Package 'LaMa'

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Type Package

Title Fast Numerical Maximum Likelihood Estimation for Latent Markov Models

Version 2.0.3

Description A variety of latent Markov models, including hidden Markov models, hidden semi-Markov models,
state-space models and continuous-time variants can be formulated and estimated within the same framework via directly maximising the likelihood function using the so-called forward algorithm.
Applied researchers often need custom models that standard software does not easily support.
Writing tailored 'R' code offers flexibility but suffers from slow estimation speeds.
We address these issues by providing easy-to-use functions (written in 'C++' for speed) for common tasks like the forward algorithm.
These functions can be combined into custom models in a Lego-type approach, offering up to 10-20 times faster estimation via standard numerical optimisers.
To aid in building fully custom likelihood functions, several vignettes are included that show how to simulate data from and estimate all the above model classes.

URL https://janoleko.github.io/LaMa/

License GPL-3

Encoding UTF-8

Imports Rcpp, mgcv, Matrix, stats, utils, MASS, mvtnorm, splines, methods, CircStats, circular, sn

LinkingTo Rcpp, RcppArmadillo

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Contents

`buildSmoothDens` *Build the design and penalty matrices for smooth density estimation*

Description

This high-level function can be used to prepare objects needed to estimate mixture models of smooth densities using P-Splines.

Usage

```
buildSmoothDens(data, type = "real", par, k = 20, degree = 3, diff_order = 2)
```

Arguments

`data`	named data frame of different data streams
`type`	type of each data stream, either `"real"` for data on the reals, `"positive"` for data on the positive reals or `"circular"` for angular data. Needs to be a vector corresponding to the number of data streams in `data`.
`par`	nested named list of initial means and sds/concentrations for each data stream
`k`	number of basis functions for each data stream
`degree`	degree of the B-spline basis functions for each data stream, defaults to cubic B-splines
`diff_order`	order of differencing used for the P-Spline penalty matrix for each data stream. Defaults to second-order differences.

Details

Under the hood, `make_matrices_dens` is used for the actual construction of the design and penalty matrices.

You can provide one or multiple data streams of different types (real, positive, circular) and specify initial means and standard deviations/ concentrations for each data stream. This information is then converted into suitable spline coefficients. `buildSmoothDens` then constructs the design and

penalty matrices for standardised B-splines basis functions (integrating to one) for each data stream. For types `"real"` and `"circular"` the knots are placed equidistant in the range of the data, for type `"positive"` the knots are placed using polynomial spacing.

Value

a nested list containing the design matrices `Z`, the penalty matrices `S`, the initial coefficients `coef` the prediction design matrices `Z_predict`, the prediction grids `xseq`, and details for the basis expansion for each data stream.

Examples

```
## 3 data streams, each with one distribution
# normal data with mean 0 and sd 1
x1 = rnorm(100, mean = 0, sd = 1)
# gamma data with mean 5 and sd 3
x2 = rgamma2(100, mean = 5, sd = 3)
# circular data
x3 = rvm(100, mu = 0, kappa = 2)

data = data.frame(x1 = x1, x2 = x2, x3 = x3)

par = list(x1 = list(mean = 0, sd = 1),
           x2 = list(mean = 5, sd = 3),
           x3 = list(mean = 0, concentration = 2))

SmoothDens = buildSmoothDens(data,
                             type = c("real", "positive", "circular"),
                             par)

# extracting objects for x1
Z1 = SmoothDens$Z$x1
S1 = SmoothDens$S$x1
coefs1 = SmoothDens$coef$x1

## one data stream, but mixture of two distributions
# normal data with mean 0 and sd 1
x = rnorm(100, mean = 0, sd = 1)
data = data.frame(x = x)

# now parameters for mixture of two normals
par = list(x = list(mean = c(0, 5), sd = c(1,1)))

SmoothDens = buildSmoothDens(data, par = par)

# extracting objects
Z = SmoothDens$Z$x
S = SmoothDens$S$x
coefs = SmoothDens$coef$x
```

calc_trackInd — *Calculate the index of the first observation of each track based on an ID variable*

Description

Function to conveniently calculate the trackInd variable that is needed internally when fitting a model to longitudinal data with multiple tracks.

Usage

```
calc_trackInd(ID)
```

Arguments

ID	ID variable of track IDs that is of the same length as the data to be analysed

Value

A vector of indices of the first observation of each track which can be passed to the forward and forward_g to sum likelihood contributions of each track

Examples

```
uniqueID = c("Animal1", "Animal2", "Animal3")
ID = rep(uniqueID, c(100, 200, 300))
trackInd = calc_trackInd(ID)
```

dgmrf2 — *Reparametrised multivariate Gaussian distribution*

Description

Density function of the multivariate Gaussian distribution reparametrised in terms of its precision matrix (inverse variance). This implementation is particularly useful for defining the **joint log-likelihood** with penalised splines or i.i.d. random effects that have a multivariate Gaussian distribution with fixed precision/ penalty matrix λS. As S is fixed and only scaled by λ, it is more efficient to precompute the determinant of S (for the normalisation constant) and only scale the quadratic form by λ when multiple spline parameters/ random effects with different λ's but the same penalty matrix S are evaluated.

Usage

```
dgmrf2(x, mu = 0, S, lambda, logdetS = NULL, log = FALSE)
```

Arguments

x	density evaluation point, either a vector or a matrix
mu	mean parameter. Either scalar or vector
S	unscaled precision matrix
lambda	precision scaling parameter Can be a vector if x is a matrix. Then each row of x is evaluated with the corresponding lambda. This is benefitial from an efficiency perspective because the determinant of S is only computed once.
logdetS	Optional precomputed log determinant of the precision matrix S. If the precision matrix does not depend on parameters, it can be precomputed and passed to the function.
log	logical; if TRUE, densities are returned on the log scale.

Details

This implementation allows for automatic differentiation with RTMB.

Value

vector of density values

Examples

```
x = matrix(runif(30), nrow = 3)

# iid random effects
S = diag(10)
sigma = c(1, 2, 3) # random effect standard deviations
lambda = 1 / sigma^2
d = dgmrf2(x, 0, S, lambda)

# P-splines
L = diff(diag(10), diff = 2) # second-order difference matrix
S = t(L) %*% L
lambda = c(1,2,3)
d = dgmrf2(x, 0, S, lambda, log = TRUE)
```

---

dirichlet *Dirichlet distribution*

Description

Density of the Dirichlet distribution.

Usage

```
ddirichlet(x, alpha, log = TRUE)
```

Arguments

x	vector or matrix of quantiles
alpha	vector or matrix of shape parameters
log	logical; if TRUE, densities p are returned as $\log(p)$.

Details

This implementation of ddirichlet allows for automatic differentiation with RTMB.

Value

ddirichlet gives the density.

Examples

```
ddirichlet(c(0.2, 0.3, 0.5), c(1, 2, 3))
```

---

forward — R*hrefhttps://www.taylorfrancis.com/books/mono/10.1201/b20790/hidden-markov-models-time-series-walter-zucchini-iain-macdonald-roland-langrockForward algorithm with homogeneous transition probability matrix*

Description

Calculates the log-likelihood of a sequence of observations under a homogeneous hidden Markov model using the **forward algorithm**.

Usage

```
forward(delta, Gamma, allprobs, trackID = NULL, ad = NULL, report = TRUE)
```

Arguments

delta	initial or stationary distribution of length N, or matrix of dimension c(k,N) for k independent tracks, if trackID is provided
Gamma	transition probability matrix of dimension c(N,N), or array of k transition probability matrices of dimension c(N,N,k), if trackID is provided
allprobs	matrix of state-dependent probabilities/ density values of dimension c(n, N)
trackID	optional vector of length n containing IDs If provided, the total log-likelihood will be the sum of each track's likelihood contribution. In this case, Gamma can be a matrix, leading to the same transition probabilities for each track, or an array of dimension c(N,N,k), with one (homogeneous) transition probability matrix for each track. Furthermore, instead of a single vector delta corresponding to the initial distribution, a delta matrix of initial distributions, of dimension c(k,N), can be provided, such that each track starts with it's own initial distribution.

ad	optional logical, indicating whether automatic differentiation with RTMB should be used. By default, the function determines this itself.
report	logical, indicating whether delta, Gamma and allprobs should be reported from the fitted model. Defaults to TRUE, but only works if ad = TRUE.

Value

log-likelihood for given data and parameters

See Also

Other forward algorithms: forward_g(), forward_hsmm(), forward_ihsmm(), forward_p(), forward_phsmm()

Examples

```
## negative log likelihood function
nll = function(par, step) {
 # parameter transformations for unconstrained optimisation
 Gamma = tpm(par[1:2]) # multinomial logit link
 delta = stationary(Gamma) # stationary HMM
 mu = exp(par[3:4])
 sigma = exp(par[5:6])
 # calculate all state-dependent probabilities
 allprobs = matrix(1, length(step), 2)
 ind = which(!is.na(step))
 for(j in 1:2) allprobs[ind,j] = dgamma2(step[ind], mu[j], sigma[j])
 # simple forward algorithm to calculate log-likelihood
 -forward(delta, Gamma, allprobs)
}

## fitting an HMM to the trex data
par = c(-2,-2,            # initial tpm params (logit-scale)
        log(c(0.3, 2.5)), # initial means for step length (log-transformed)
        log(c(0.2, 1.5))) # initial sds for step length (log-transformed)
mod = nlm(nll, par, step = trex$step[1:1000])
```

---

forward_g *General* R*hrefhttps://www.taylorfrancis.com/books/mono/10.1201/b20790/hidden-markov-models-time-series-walter-zucchini-iain-macdonald-roland-langrockforward algorithm with time-varying transition probability matrix*

Description

Calculates the log-likelihood of a sequence of observations under a hidden Markov model with time-varying transition probabilities using the **forward algorithm**.

Usage

```
forward_g(delta, Gamma, allprobs, trackID = NULL, ad = NULL, report = TRUE)
```

Arguments

`delta`	initial or stationary distribution of length N, or matrix of dimension c(k,N) for k independent tracks, if `trackID` is provided
`Gamma`	array of transition probability matrices of dimension c(N,N,n-1), as in a time series of length n, there are only n-1 transitions. If an array of dimension c(N,N,n) for a single track is provided, the first slice will be ignored. If the elements of $\Gamma^{(t)}$ depend on covariate values at t or covariates t+1 is your choice in the calculation of the array, prior to using this function. When conducting the calculation by using tpm_g(), the choice comes down to including the covariate matrix Z[-1,] oder Z[-n,]. If trackInd is provided, Gamma needs to be an array of dimension c(N,N,n), matching the number of rows of allprobs. For each track, the transition matrix at the beginning will be ignored. If the parameters for Gamma are pooled across tracks or not, depends on your calculation of Gamma. If pooled, you can use tpm_g(Z, beta) to calculate the entire array of transition matrices when Z is of dimension c(n,p). This function can also be used to fit continuous-time HMMs, where each array entry is the Markov semigroup $\Gamma(\Delta t) = \exp(Q\Delta t)$ and Q is the generator of the continuous-time Markov chain.
`allprobs`	matrix of state-dependent probabilities/ density values of dimension c(n, N)
`trackID`	optional vector of length n containing IDs If provided, the total log-likelihood will be the sum of each track's likelihood contribution. In this case, `Gamma` needs to be an array of dimension c(N,N,n), matching the number of rows of allprobs. For each track, the transition matrix at the beginning of the track will be ignored (as there is no transition between tracks). Furthermore, instead of a single vector `delta` corresponding to the initial distribution, a `delta` matrix of initial distributions, of dimension c(k,N), can be provided, such that each track starts with it's own initial distribution.
`ad`	optional logical, indicating whether automatic differentiation with `RTMB` should be used. By default, the function determines this itself.
`report`	logical, indicating whether `delta`, `Gamma` and `allprobs` should be reported from the fitted model. Defaults to `TRUE`, but only works if `ad = TRUE`.

Value

log-likelihood for given data and parameters

See Also

Other forward algorithms: `forward()`, `forward_hsmm()`, `forward_ihsmm()`, `forward_p()`, `forward_phsmm()`

Examples

```
## Simple usage
```

```
Gamma = array(c(0.9, 0.2, 0.1, 0.8), dim = c(2,2,10))
delta = c(0.5, 0.5)
allprobs = matrix(0.5, 10, 2)
forward_g(delta, Gamma, allprobs)


## Full model fitting example
## negative log likelihood function
nll = function(par, step, Z) {
 # parameter transformations for unconstrained optimisation
 beta = matrix(par[1:6], nrow = 2)
 Gamma = tpm_g(Z, beta) # multinomial logit link for each time point
 delta = stationary(Gamma[,,1]) # stationary HMM
 mu = exp(par[7:8])
 sigma = exp(par[9:10])
 # calculate all state-dependent probabilities
 allprobs = matrix(1, length(step), 2)
 ind = which(!is.na(step))
 for(j in 1:2) allprobs[ind,j] = dgamma2(step[ind], mu[j], sigma[j])
 # simple forward algorithm to calculate log-likelihood
 -forward_g(delta, Gamma, allprobs)
}

## fitting an HMM to the trex data
par = c(-1.5,-1.5,        # initial tpm intercepts (logit-scale)
        rep(0, 4),        # initial tpm slopes
        log(c(0.3, 2.5)), # initial means for step length (log-transformed)
        log(c(0.2, 1.5))) # initial sds for step length (log-transformed)
mod = nlm(nll, par, step = trex$step[1:500], Z = trigBasisExp(trex$tod[1:500]))
```

---

forward_hsmm R*hrefhttps://www.taylorfrancis.com/books/mono/10.1201/b20790/hidden-markov-models-time-series-walter-zucchini-iain-macdonald-roland-langrockForward algorithm for homogeneous hidden semi-Markov models*

Description

Calculates the (approximate) log-likelihood of a sequence of observations under a homogeneous hidden semi-Markov model using a modified **forward algorithm**.

Usage

```
forward_hsmm(
  dm,
  omega,
  allprobs,
  trackID = NULL,
  delta = NULL,
```

```
  eps = 1e-10,
  report = TRUE
)
```

Arguments

dm	list of length N containing vectors of dwell-time probability mass functions (PMFs) for each state. The vector lengths correspond to the approximating state aggregate sizes, hence there should be little probablity mass not covered by these.
omega	matrix of dimension c(N,N) of conditional transition probabilites, also called embedded transition probability matrix. Contains the transition probabilities given that the current state is left. Hence, the diagonal elements need to be zero and the rows need to sum to one. Can be constructed using tpm_emb.
allprobs	matrix of state-dependent probabilities/ density values of dimension c(n, N) which will automatically be converted to the appropriate dimension.
trackID	optional vector of length n containing IDs If provided, the total log-likelihood will be the sum of each track's likelihood contribution. In this case, dm can be a nested list, where the top layer contains k dm lists as described above. omega can then also be an array of dimension c(N,N,k) with one conditional transition probability matrix for each track. Furthermore, instead of a single vector delta corresponding to the initial distribution, a delta matrix of initial distributions, of dimension c(k,N), can be provided, such that each track starts with it's own initial distribution.
delta	optional vector of initial state probabilities of length N By default, the stationary distribution is computed (which is typically recommended).
eps	small value to avoid numerical issues in the approximating transition matrix construction. Usually, this should not be changed.
report	logical, indicating whether initial distribution, approximating transition probability matrix and allprobs matrix should be reported from the fitted model. Defaults to TRUE.

Details

Hidden semi-Markov models (HSMMs) are a flexible extension of HMMs, where the state duration distribution is explicitly modelled by a distribution on the positive integers. For direct numerical maximum likelihood estimation, HSMMs can be represented as HMMs on an enlarged state space (of size M) and with structured transition probabilities.

This function is designed to be used with automatic differentiation based on the R package RTMB. It will be very slow without it!

Value

log-likelihood for given data and parameters

See Also

Other forward algorithms: `forward()`, `forward_g()`, `forward_ihsmm()`, `forward_p()`, `forward_phsmm()`

Examples

```
# currently no examples
```

`forward_ihsmm` R*hrefhttps://www.taylorfrancis.com/books/mono/10.1201/b20790/hidden-markov-models-time-series-walter-zucchini-iain-macdonald-roland-langrockForward algorithm for hidden semi-Markov models with inhomogeneous state durations and/ or conditional transition probabilities*

Description

Calculates the (approximate) log-likelihood of a sequence of observations under an inhomogeneous hidden semi-Markov model using a modified **forward algorithm**.

Usage

```
forward_ihsmm(
  dm,
  omega,
  allprobs,
  trackID = NULL,
  delta = NULL,
  startInd = NULL,
  eps = 1e-10,
  report = TRUE
)
```

Arguments

`dm`	list of length N containing matrices (or vectors) of dwell-time probability mass functions (PMFs) for each state. If the dwell-time PMFs are constant, the vectors are the PMF of the dwell-time distribution fixed in time. The vector lengths correspond to the approximating state aggregate sizes, hence there should be little probablity mass not covered by these. If the dwell-time PMFs are inhomogeneous, the matrices need to have n rows, where n is the number of observations. The number of columns again corresponds to the size of the approximating state aggregates. In the latter case, the first `max(sapply(dm, ncol)) - 1` observations will not be used because the first approximating transition probability matrix needs to be computed based on the first `max(sapply(dm, ncol))` covariate values (represented by `dm`).

`omega` matrix of dimension c(N,N) or array of dimension c(N,N,n) of conditional transition probabilites, also called embedded transition probability matrix.

It contains the transition probabilities given the current state is left. Hence, the diagonal elements need to be zero and the rows need to sum to one. Such a matrix can be constructed using `tpm_emb` and an array using `tpm_emb_g`.

`allprobs` matrix of state-dependent probabilities/ density values of dimension c(n, N)

`trackID` trackID optional vector of length n containing IDs

If provided, the total log-likelihood will be the sum of each track's likelihood contribution. Instead of a single vector `delta` corresponding to the initial distribution, a `delta` matrix of initial distributions, of dimension c(k,N), can be provided, such that each track starts with it's own initial distribution.

`delta` optional vector of initial state probabilities of length N

By default, instead of this, the stationary distribution is computed corresponding to the first approximating transition probability matrix of each track is computed. Contrary to the homogeneous case, this is not theoretically motivated but just for convenience.

`startInd` optional integer index at which the forward algorithm starts.

When approximating inhomogeneous HSMMs by inhomogeneous HMMs, the first transition probability matrix that can be constructed is at time `max(sapply(dm, ncol))` (as it depends on the previous covariate values). Hence, when not provided, `startInd` is chosen to be `max(sapply(dm, ncol))`. Fixing `startInd` at a value **larger** than max(aggregate sizes) is useful when models with different aggregate sizes are fitted to the same data and are supposed to be compared. In that case it is important that all models use the same number of observations.

`eps` small value to avoid numerical issues in the approximating transition matrix construction. Usually, this should not be changed.

`report` logical, indicating whether initial distribution, approximating transition probability matrix and `allprobs` matrix should be reported from the fitted model. Defaults to `TRUE`.

Details

Hidden semi-Markov models (HSMMs) are a flexible extension of HMMs, where the state duration distribution is explicitly modelled by a distribution on the positive integers. This function can be used to fit HSMMs where the state-duration distribution and/ or the conditional transition probabilities vary with covariates. For direct numerical maximum likelihood estimation, HSMMs can be represented as HMMs on an enlarged state space (of size M) and with structured transition probabilities.

This function is designed to be used with automatic differentiation based on the `R` package `RTMB`. It will be very slow without it!

Value

log-likelihood for given data and parameters

See Also

Other forward algorithms: `forward()`, `forward_g()`, `forward_hsmm()`, `forward_p()`, `forward_phsmm()`

Examples

```
# currently no examples
```

`forward_p` R*hrefhttps://www.taylorfrancis.com/books/mono/10.1201/b20790/hidden-markov-models-time-series-walter-zucchini-iain-macdonald-roland-langrockForward algorithm with for periodically varying transition probability matrices*

Description

Calculates the log-likelihood of a sequence of observations under a hidden Markov model with periodically varying transition probabilities using the **forward algorithm**.

Usage

```
forward_p(
  delta,
  Gamma,
  allprobs,
  tod,
  trackID = NULL,
  ad = NULL,
  report = TRUE
)
```

Arguments

`delta`	initial or stationary distribution of length N, or matrix of dimension c(k,N) for k independent tracks, if `trackID` is provided
`Gamma`	array of transition probability matrices of dimension c(N,N,L). Here we use the definition $\Pr(S_t = j \mid S_{t-1} = i) = \gamma_{ij}^{(t)}$ such that the transition probabilities between time point $t-1$ and t are an element of $\Gamma^{(t)}$.
`allprobs`	matrix of state-dependent probabilities/ density values of dimension c(n, N)
`tod`	(Integer valued) variable for cycle indexing in 1, ..., L, mapping the data index to a generalised time of day (length n) For half-hourly data L = 48. It could, however, also be day of year for daily data and L = 365.

trackID	optional vector of length n containing IDs If provided, the total log-likelihood will be the sum of each track's likelihood contribution. Instead of a single vector delta corresponding to the initial distribution, a delta matrix of initial distributions of dimension c(k,N), can be provided, such that each track starts with it's own initial distribution.
ad	optional logical, indicating whether automatic differentiation with RTMB should be used. By default, the function determines this itself.
report	logical, indicating whether delta, Gamma and allprobs should be reported from the fitted model. Defaults to TRUE, but only works if ad = TRUE.

Details

When the transition probability matrix only varies periodically (e.g. as a function of time of day), there are only L unique matrices if L is the period length (e.g. $L = 24$ for hourly data and time-of-day variation). Thus, it is much more efficient to only calculate these L matrices and index them by a time variable (e.g. time of day or day of year) instead of calculating such a matrix for each index in the data set (which would be redundant). This function allows for that by only expecting a transition probability matrix for each time point in a period and an integer valued $(1, \dots, L)$ time variable that maps the data index to the according time.

Value

log-likelihood for given data and parameters

See Also

Other forward algorithms: forward(), forward_g(), forward_hsmm(), forward_ihsmm(), forward_phsmm()

Examples

```
## negative log likelihood function
nll = function(par, step, tod) {
 # parameter transformations for unconstrained optimisation
 beta = matrix(par[1:6], nrow = 2)
 Gamma = tpm_p(1:24, beta = beta) # multinomial logit link for each time point
 delta = stationary_p(Gamma, tod[1]) # stationary HMM
 mu = exp(par[7:8])
 sigma = exp(par[9:10])
 # calculate all state-dependent probabilities
 allprobs = matrix(1, length(step), 2)
 ind = which(!is.na(step))
 for(j in 1:2) allprobs[ind,j] = dgamma2(step[ind], mu[j], sigma[j])
 # simple forward algorithm to calculate log-likelihood
 -forward_p(delta, Gamma, allprobs, tod)
}

## fitting an HMM to the nessi data
par = c(-2,-2,            # initial tpm intercepts (logit-scale)
        rep(0, 4),        # initial tpm slopes
        log(c(0.3, 2.5)), # initial means for step length (log-transformed)
```

```
        log(c(0.2, 1.5))) # initial sds for step length (log-transformed)
mod = nlm(nll, par, step = trex$step[1:500], tod = trex$tod[1:500])
```

---

forward_phsmm — R*hrefhttps://www.taylorfrancis.com/books/mono/10.1201/b20790/hidden-markov-models-time-series-walter-zucchini-iain-macdonald-roland-langrockForward algorithm for hidden semi-Markov models with periodically inhomogeneous state durations and/ or conditional transition probabilities*

Description

Hidden semi-Markov models (HSMMs) are a flexible extension of HMMs, where the state duration distribution is explicitly modelled by a distribution on the positive integers. This function can be used to fit HSMMs where the state-duration distribution and/ or the conditional transition probabilities vary with covariates. For direct numerical maximum likelihood estimation, HSMMs can be represented as HMMs on an enlarged state space (of size M) and with structured transition probabilities.

This function can be used to fit HSMMs where the state-duration distribution and/ or the conditional transition probabilities vary periodically. In the special case of periodic variation (as compared to arbitrary covariate influence), this version is to be preferred over forward_ihsmm because it computes the **correct periodically stationary distribution** and no observations are lost for the approximation.

This function is designed to be used with automatic differentiation based on the R package RTMB. It will be very slow without it!

Usage

```
forward_phsmm(
  dm,
  omega,
  allprobs,
  tod,
  trackID = NULL,
  delta = NULL,
  eps = 1e-10,
  report = TRUE
)
```

Arguments

dm	list of length N containing matrices (or vectors) of dwell-time probability mass functions (PMFs) for each state. If the dwell-time PMFs are constant, the vectors are the PMF of the dwell-time distribution fixed in time. The vector lengths correspond to the approximating state aggregate sizes, hence there should be little probablity mass not covered by these.

If the dwell-time PMFs are inhomogeneous, the matrices need to have L rows, where L is the cycle length. The number of columns again correpond to the size of the approximating state aggregates.

`omega` matrix of dimension c(N,N) or array of dimension c(N,N,L) of conditional transition probabilites, also called embedded transition probability matrix

It contains the transition probabilities given the current state is left. Hence, the diagonal elements need to be zero and the rows need to sum to one. Such a matrix can be constructed using `tpm_emb` and an array using `tpm_emb_g`.

`allprobs` matrix of state-dependent probabilities/ density values of dimension c(n, N)

`tod` (Integer valued) variable for cycle indexing in 1, ..., L, mapping the data index to a generalised time of day (length n). For half-hourly data L = 48. It could, however, also be day of year for daily data and L = 365.

`trackID` optional vector of length n containing IDs

If provided, the total log-likelihood will be the sum of each track's likelihood contribution. Instead of a single vector `delta` corresponding to the initial distribution, a `delta` matrix of initial distributions, of dimension c(k,N), can be provided, such that each track starts with it's own initial distribution.

`delta` Optional vector of initial state probabilities of length N. By default, instead of this, the stationary distribution is computed corresponding to the first approximating t.p.m. of each track is computed. Contrary to the homogeneous case, this is not theoretically motivated but just for convenience.

`eps` small value to avoid numerical issues in the approximating transition matrix construction. Usually, this should not be changed.

`report` logical, indicating whether initial distribution, approximating transition probability matrix and `allprobs` matrix should be reported from the fitted model. Defaults to `TRUE`.

Details

Calculates the (approximate) log-likelihood of a sequence of observations under a periodically inhomogeneous hidden semi-Markov model using a modified **forward algorithm**.

Value

log-likelihood for given data and parameters

See Also

Other forward algorithms: `forward()`, `forward_g()`, `forward_hsmm()`, `forward_ihsmm()`, `forward_p()`

Examples

```
# currently no examples
```

forward_s — R*hrefhttps://www.taylorfrancis.com/books/mono/10.1201/b20790/hidden-markov-models-time-series-walter-zucchini-iain-macdonald-roland-langrockForward algorithm for hidden semi-Markov models with homogeneous transition probability matrix*

Description

Hidden semi-Markov models (HSMMs) are a flexible extension of HMMs that can be approximated by HMMs on an enlarged state space (of size M) and with structured transition probabilities.

Usage

```
forward_s(delta, Gamma, allprobs, sizes)
```

Arguments

delta	initial or stationary distribution of length N, or matrix of dimension c(k,N) for k independent tracks, if trackID is provided
Gamma	transition probability matrix of dimension c(M,M)
allprobs	matrix of state-dependent probabilities/ density values of dimension c(n, N) which will automatically be converted to the appropriate dimension.
sizes	state aggregate sizes that are used for the approximation of the semi-Markov chain.

Value

log-likelihood for given data and parameters

Examples

```
## generating data from homogeneous 2-state HSMM
mu = c(0, 6)
lambda = c(6, 12)
omega = matrix(c(0,1,1,0), nrow = 2, byrow = TRUE)
# simulation
# for a 2-state HSMM the embedded chain always alternates between 1 and 2
s = rep(1:2, 100)
C = x = numeric(0)
for(t in 1:100){
  dt = rpois(1, lambda[s[t]])+1 # shifted Poisson
  C = c(C, rep(s[t], dt))
  x = c(x, rnorm(dt, mu[s[t]], 1.5)) # fixed sd 2 for both states
}

## negative log likelihood function
mllk = function(theta.star, x, sizes){
  # parameter transformations for unconstraint optimization
```

```
  omega = matrix(c(0,1,1,0), nrow = 2, byrow = TRUE) # omega fixed (2-states)
  lambda = exp(theta.star[1:2]) # dwell time means
  dm = list(dpois(1:sizes[1]-1, lambda[1]), dpois(1:sizes[2]-1, lambda[2]))
  Gamma = tpm_hsmm2(omega, dm)
  delta = stationary(Gamma) # stationary
  mu = theta.star[3:4]
  sigma = exp(theta.star[5:6])
  # calculate all state-dependent probabilities
  allprobs = matrix(1, length(x), 2)
  for(j in 1:2){ allprobs[,j] = dnorm(x, mu[j], sigma[j]) }
  # return negative for minimization
  -forward_s(delta, Gamma, allprobs, sizes)
}

## fitting an HSMM to the data
theta.star = c(log(5), log(10), 1, 4, log(2), log(2))
mod = nlm(mllk, theta.star, x = x, sizes = c(20, 30), stepmax = 5)
```

`forward_sp` R*hrefhttps://www.taylorfrancis.com/books/mono/10.1201/b20790/hidden-markov-models-time-series-walter-zucchini-iain-macdonald-roland-langrockForward algorithm for hidden semi-Markov models with periodically varying transition probability matrices*

Description

Hidden semi-Markov models (HSMMs) are a flexible extension of HMMs that can be approximated by HMMs on an enlarged state space (of size M) and with structured transition probabilities. Recently, this inference procedure has been generalised to allow either the dwell-time distributions or the conditional transition probabilities to depend on external covariates such as the time of day. This special case is implemented here. This function allows for that, by expecting a transition probability matrix for each time point in a period, and an integer valued $(1, \ldots, L)$ time variable that maps the data index to the according time.

Usage

```
forward_sp(delta, Gamma, allprobs, sizes, tod)
```

Arguments

`delta`	initial or stationary distribution of length N, or matrix of dimension c(k,N) for k independent tracks, if `trackID` is provided
`Gamma`	array of transition probability matrices of dimension c(M,M,L). Here we use the definition $\Pr(S_t = j \mid S_{t-1} = i) = \gamma_{ij}^{(t)}$ such that the transition probabilities between time point $t-1$ and t are an element of $\Gamma^{(t)}$.
`allprobs`	matrix of state-dependent probabilities/ density values of dimension c(n, N) which will automatically be converted to the appropriate dimension.

sizes	state aggregate sizes that are used for the approximation of the semi-Markov chain.
tod	(Integer valued) variable for cycle indexing in 1, ..., L, mapping the data index to a generalised time of day (length n). For half-hourly data L = 48. It could, however, also be day of year for daily data and L = 365.

Value

log-likelihood for given data and parameters

Examples

```
## generating data from homogeneous 2-state HSMM
mu = c(0, 6)
beta = matrix(c(log(4),log(6),-0.2,0.2,-0.1,0.4), nrow=2)
# time varying mean dwell time
Lambda = exp(cbind(1, trigBasisExp(1:24, 24, 1))%*%t(beta))
omega = matrix(c(0,1,1,0), nrow = 2, byrow = TRUE)
# simulation
# for a 2-state HSMM the embedded chain always alternates between 1 and 2
s = rep(1:2, 100)
C = x = numeric(0)
tod = rep(1:24, 50) # time of day variable
time = 1
for(t in 1:100){
  dt = rpois(1, Lambda[tod[time], s[t]])+1 # dwell time depending on time of day
  time = time + dt
  C = c(C, rep(s[t], dt))
  x = c(x, rnorm(dt, mu[s[t]], 1.5)) # fixed sd 2 for both states
}
tod = tod[1:length(x)]

## negative log likelihood function
mllk = function(theta.star, x, sizes, tod){
  # parameter transformations for unconstraint optimization
  omega = matrix(c(0,1,1,0), nrow = 2, byrow = TRUE) # omega fixed (2-states)
  mu = theta.star[1:2]
  sigma = exp(theta.star[3:4])
  beta = matrix(theta.star[5:10], nrow=2)
  # time varying mean dwell time
  Lambda = exp(cbind(1, trigBasisExp(1:24, 24, 1))%*%t(beta))
  dm = list()
  for(j in 1:2){
    dm[[j]] = sapply(1:sizes[j]-1, dpois, lambda = Lambda[,j])
  }
  Gamma = tpm_phsmm2(omega, dm)
  delta = stationary_p(Gamma, tod[1])
  # calculate all state-dependent probabilities
  allprobs = matrix(1, length(x), 2)
  for(j in 1:2){ allprobs[,j] = dnorm(x, mu[j], sigma[j]) }
  # return negative for minimization
  -forward_sp(delta, Gamma, allprobs, sizes, tod)
```

```
}

## fitting an HSMM to the data
theta.star = c(1, 4, log(2), log(2), # state-dependent parameters
                 log(4), log(6), rep(0,4)) # state process parameters dm
# mod = nlm(mllk, theta.star, x = x, sizes = c(10, 15), tod = tod, stepmax = 5)
```

---

gamma2 *Reparametrised gamma distribution*

Description

Density, distribution function, quantile function and random generation for the gamma distribution reparametrised in terms of mean and standard deviation.

Usage

```
dgamma2(x, mean = 1, sd = 1, log = FALSE)

pgamma2(q, mean = 1, sd = 1, lower.tail = TRUE, log.p = FALSE)

qgamma2(p, mean = 1, sd = 1, lower.tail = TRUE, log.p = FALSE)

rgamma2(n, mean = 1, sd = 1)
```

Arguments

x, q	vector of quantiles
mean	mean parameter, must be positive scalar.
sd	standard deviation parameter, must be positive scalar.
log, log.p	logical; if TRUE, probabilities/ densities p are returned as $\log(p)$.
lower.tail	logical; if TRUE, probabilities are $P[X <= x]$, otherwise, $P[X > x]$.
p	vector of probabilities
n	number of observations. If length(n) > 1, the length is taken to be the number required.

Details

This implementation allows for automatic differentiation with RTMB.

Value

dgamma2 gives the density, pgamma2 gives the distribution function, qgamma2 gives the quantile function, and rgamma2 generates random deviates.

Examples

```
x = rgamma2(1)
d = dgamma2(x)
p = pgamma2(x)
q = qgamma2(p)
```

`gdeterminant` *Computes generalised determinant*

Description

Computes generalised determinant

Usage

```
gdeterminant(x, eps = 1e-10, log = TRUE)
```

Arguments

`x`	square matrix
`eps`	eigenvalues smaller than this will be treated as zero
`log`	logical. If `TRUE`, the log-determinant is returned. If `FALSE`, the determinant is returned.

Value

generalised log-determinant of `x`

`generator` *Build the generator matrix of a continuous-time Markov chain*

Description

This function builds the **infinitesimal generator matrix** for a **continuous-time Markov chain** from an unconstrained parameter vector.

Usage

```
generator(param, byrow = FALSE, report = TRUE)
```

Arguments

param	unconstrained parameter vector of length N*(N-1) where N is the number of states of the Markov chain
byrow	logical indicating if the transition probability matrix should be filled by row
report	logical, indicating whether the generator matrix Q should be reported from the fitted model. Defaults to TRUE, but only works if when automatic differentiation with RTMB is used.

Value

infinitesimal generator matrix of dimension c(N,N)

See Also

Other transition probability matrix functions: tpm(), tpm_cont(), tpm_emb(), tpm_emb_g(), tpm_g(), tpm_p()

Examples

```
# 2 states: 2 free off-diagonal elements
generator(rep(-1, 2))
# 3 states: 6 free off-diagonal elements
generator(rep(-2, 6))
```

---

make_matrices *Build the design matrix and the penalty matrix for models involving penalised splines based on a formula and a data set*

Description

Build the design matrix and the penalty matrix for models involving penalised splines based on a formula and a data set

Usage

```
make_matrices(formula, data, knots = NULL)
```

Arguments

formula	right side of a formula as used in mgcv
data	data frame containing the variables in the formula
knots	optional list containing user specified knot values to be used for basis construction For most bases the user simply supplies the knots to be used, which must match up with the k value supplied (note that the number of knots is not always just k). See mgcv documentation for more details.

Value

a list containing the design matrix `Z`, the penalty matrix `S`, the `formula`, the `data` and the `knots`

Examples

```
modmat = make_matrices(~ s(x), data.frame(x = 1:10))
```

`make_matrices_dens` *Build a standardised P-Spline design matrix and the associated P-Spline penalty matrix*

Description

This function builds the B-spline design matrix for a given data vector. Importantly, the B-spline basis functions are normalised such that the integral of each basis function is 1, hence this basis can be used for spline-based density estimation, when the basis functions are weighted by non-negative weights summing to one.

Usage

```
make_matrices_dens(
  x,
  k,
  type = "real",
  degree = 3,
  npoints = 10000,
  diff_order = 2,
  pow = 0.5
)
```

Arguments

`x`	data vector
`k`	number of basis functions
`type`	type of the data, either `"real"` for data on the reals, `"positive"` for data on the positive reals or `"circular"` for circular data like angles.
`degree`	degree of the B-spline basis functions, defaults to cubic B-splines
`npoints`	number of points used in the numerical integration for normalizing the B-spline basis functions
`diff_order`	order of differencing used for the P-Spline penalty matrix for each data stream. Defaults to second-order differences.
`pow`	power for polynomial knot spacing Such non-equidistant knot spacing is only used for `type = "positive"`.

Value

list containing the design matrix `Z`, the penalty matrix `S`, the prediction design matrix `Z_predict`, the prediction grid `xseq`, and details for the basis expansion.

Examples

```
modmat = make_matrices_dens(x = (-50):50, k = 20)
modmat = make_matrices_dens(x = 1:100, k = 20, type = "positive")
modmat = make_matrices_dens(x = seq(-pi,pi), k = 20, type = "circular")
```

`nessi` *Loch Ness Monster Acceleration Data*

Description

A small group of researchers managed to put an accelerometer on the Loch Ness Monster and collected data for a few days. Now we have a data set of the overall dynamic body acceleration (ODBA) of the creature.

Usage

```
nessi
```

Format

A data frame with 5.000 rows and 3 variables:

ODBA overall dynamci body acceleration

logODBA logarithm of overall dynamic body acceleration

state hidden state variable

Source

Generated for example purposes.

`penalty` *Computes penalty based on quadratic form*

Description

This function computes quadratic penalties of the form

$$0.5 \sum_i \lambda_i b_i^T S_i b_i,$$

with smoothing parameters λ_i, coefficient vectors b_i, and fixed penalty matrices S_i.

It is intended to be used inside the **penalised negative log-likelihood function** when fitting models with penalised splines or simple random effects via **quasi restricted maximum likelihood** (qREML) with the `qreml` function. For `qreml` to work, the likelihood function needs to be compatible with the `RTMB` R package to enable automatic differentiation.

Usage

```
penalty(re_coef, S, lambda)
```

Arguments

`re_coef`	coefficient vector/ matrix or list of coefficient vectors/ matrices Each list entry corresponds to a different smooth/ random effect with its own associated penalty matrix in `S`. When several smooths/ random effects of the same kind are present, it is convenient to pass them as a matrix, where each row corresponds to one smooth/ random effect. This way all rows can use the same penalty matrix.
`S`	fixed penalty matrix or list of penalty matrices matching the structure of `re_coef` and also the dimension of the individuals smooths/ random effects
`lambda`	penalty strength parameter vector that has a length corresponding to the **total number** of random effects/ spline coefficients in `re_coef` E.g. if `re_coef` contains one vector and one matrix with 4 rows, then `lambda` needs to be of length 5.

Details

Caution: The formatting of `re_coef` needs to match the structure of the parameter list in your penalised negative log-likelihood function, i.e. you cannot have two random effect vectors of different names (different list elements in the parameter list), combine them into a matrix inside your likelihood and pass the matrix to `penalty`. If these are seperate random effects, each with its own name, they need to be passed as a list to `penalty`. Moreover, the ordering of `re_coef` needs to match the character vector `random` specified in `qreml`.

Value

returns the penalty value and reports to `qreml`.

See Also

qreml for the **qREML** algorithm

Examples

```
# Example with a single random effect
re = rep(0, 5)
S = diag(5)
lambda = 1
penalty(re, S, lambda)

# Example with two random effects,
# where one element contains two random effects of similar structure
re = list(matrix(0, 2, 5), rep(0, 4))
S = list(diag(5), diag(4))
lambda = c(1,1,2) # length = total number of random effects
penalty(re, S, lambda)

# Full model-fitting example
data = trex[1:1000,] # subset

# initial parameter list
par = list(logmu = log(c(0.3, 1)), # step mean
           logsigma = log(c(0.2, 0.7)), # step sd
           beta0 = c(-2,-2), # state process intercept
           betaspline = matrix(rep(0, 18), nrow = 2)) # state process spline coefs

# data object with initial penalty strength lambda
dat = list(step = data$step, # step length
           tod = data$tod, # time of day covariate
           N = 2, # number of states
           lambda = rep(10,2)) # initial penalty strength

# building model matrices
modmat = make_matrices(~ s(tod, bs = "cp"),
                       data = data.frame(tod = 1:24),
                       knots = list(tod = c(0,24))) # wrapping points
dat$Z = modmat$Z # spline design matrix
dat$S = modmat$S # penalty matrix

# penalised negative log-likelihood function
pnll = function(par) {
  getAll(par, dat) # makes everything contained available without $
  Gamma = tpm_g(Z, cbind(beta0, betaspline)) # transition probabilities
  delta = stationary_p(Gamma, t = 1) # initial distribution
  mu = exp(logmu) # step mean
  sigma = exp(logsigma) # step sd
  # calculating all state-dependent densities
  allprobs = matrix(1, nrow = length(step), ncol = N)
  ind = which(!is.na(step)) # only for non-NA obs.
  for(j in 1:N) allprobs[ind,j] = dgamma2(step[ind],mu[j],sigma[j])
  -forward_g(delta, Gamma[,,tod], allprobs) +
```

```
      penalty(betaspline, S, lambda) # this does all the penalization work
}

# model fitting
mod = qreml(pnll, par, dat, random = "betaspline")
```

`pred_matrix` *Build the prediction design matrix based on new data and model_matrices object created by* `make_matrices`

Description

Build the prediction design matrix based on new data and model_matrices object created by `make_matrices`

Usage

```
pred_matrix(model_matrices, newdata)
```

Arguments

`model_matrices`	model_matrices object as returned from `make_matrices`
`newdata`	data frame containing the variables in the formula and new data for which to evaluate the basis

Value

prediction design matrix for `newdata` with the same basis as used for `model_matrices`

Examples

```
modmat = make_matrices(~ s(x), data.frame(x = 1:10))
Z_predict = pred_matrix(modmat, data.frame(x = 1:10 - 0.5))
```

`pseudo_res` *Calculate pseudo-residuals*

Description

For HMMs, pseudo-residuals are used to assess the goodness-of-fit of the model. These are based on the cumulative distribution function (CDF)

$$F_{X_t}(x_t) = F(x_t \mid x_1, \ldots, x_{t-1}, x_{t+1}, \ldots, x_T)$$

and can be used to quantify whether an observation is extreme relative to its model-implied distribution.

This function calculates such residuals via probability integral transform, based on the local state probabilities obtained by `stateprobs` or `stateprobs_g` and the respective parametric family.

Usage

```
pseudo_res(
  obs,
  dist,
  par,
  stateprobs = NULL,
  mod = NULL,
  normal = TRUE,
  discrete = NULL,
  randomise = TRUE,
  seed = NULL
)
```

Arguments

obs	vector of continuous-valued observations (of length n)
dist	character string specifying which parametric CDF to use (e.g., "norm" for normal or "pois" for Poisson)
par	named parameter list for the parametric CDF Names need to correspond to the parameter names in the specified distribution (e.g. list(mean = c(1,2), sd = c(1,1)) for a normal distribution and 2 states). This argument is as flexible as the parametric distribution allows. For example you can have a matrix of parameters with one row for each observation and one column for each state.
stateprobs	matrix of local state probabilities for each observation (of dimension c(n,N), where N is the number of states) as computed by stateprobs, stateprobs_g or stateprobs_p
mod	optional model object containing initial distribution delta, transition probability matrix Gamma, matrix of state-dependent probabilities allprobs, and potentially a trackID variable If you are using automatic differentiation either with RTMB::MakeADFun or qreml and include forward, forward_g or forward_p in your likelihood function, the objects needed for state decoding are automatically reported after model fitting. Hence, you can pass the model object obtained from running RTMB::report() or from qreml directly to this function and avoid calculating local state proabilities manually. In this case, a call should look like pseudo_res(obs, "norm", par, mod = mod).
normal	logical, if TRUE, returns Gaussian pseudo residuals These will be approximately standard normally distributed if the model is correct.
discrete	logical, if TRUE, computes discrete pseudo residuals (which slightly differ in their definition) By default, will be determined using dist argument, but only works for standard discrete distributions. When used with a special discrete distribution, set to TRUE manually. See pseudo_res_discrete for details.

randomise	for discrete pseudo residuals only. Logical, if TRUE, return randomised pseudo residuals. Recommended for discrete observations.
seed	for discrete pseudo residuals only. Integer, seed for random number generation

Details

When used for discrete pseudo-residuals, this function is just a wrapper for pseudo_res_discrete.

Value

vector of pseudo residuals

Examples

```
## continuous-valued observations
obs = rnorm(100)
stateprobs = matrix(0.5, nrow = 100, ncol = 2)
par = list(mean = c(1,2), sd = c(1,1))
pres = pseudo_res(obs, "norm", par, stateprobs)

## discrete-valued observations
obs = rpois(100, lambda = 1)
stateprobs = matrix(0.5, nrow = 100, ncol = 2)
par = list(lambda = c(1,2))
pres = pseudo_res(obs, "pois", par, stateprobs)
```

---

pseudo_res_discrete *Calculate pseudo-residuals for discrete-valued observations*

Description

For HMMs, pseudo-residuals are used to assess the goodness-of-fit of the model. These are based on the cumulative distribution function (CDF)

$$F_{X_t}(x_t) = F(x_t \mid x_1, \ldots, x_{t-1}, x_{t+1}, \ldots, x_T)$$

and can be used to quantify whether an observation is extreme relative to its model-implied distribution.

This function calculates such residuals for **discrete-valued** observations, based on the local state probabilities obtained by stateprobs or stateprobs_g and the respective parametric family.

Usage

```
pseudo_res_discrete(
  obs,
  dist,
  par,
  stateprobs,
```

```
  normal = TRUE,
  randomise = TRUE,
  seed = NULL
)
```

Arguments

obs	vector of discrete-valued observations (of length n)
dist	character string specifying which parametric CDF to use (e.g., "norm" for normal or "pois" for Poisson)
par	named parameter list for the parametric CDF Names need to correspond to the parameter names in the specified distribution (e.g. list(mean = c(1,2), sd = c(1,1)) for a normal distribution and 2 states). This argument is as flexible as the parametric distribution allows. For example you can have a matrix of parameters with one row for each observation and one column for each state.
stateprobs	matrix of local state probabilities for each observation (of dimension c(n,N), where N is the number of states)
normal	logical, if TRUE, returns Gaussian pseudo residuals These will be approximately standard normally distributed if the model is correct.
randomise	logical, if TRUE, return randomised pseudo residuals. Recommended for discrete observations.
seed	integer, seed for random number generation

Details

For discrete observations, calculating pseudo residuals is slightly more involved, as the CDF is a step function. Therefore, one can calculate the lower and upper CDF values for each observation. By default, this function does exactly that and then randomly samples the interval in between to give approximately Gaussian psuedo-residuals. If randomise is set to FALSE, the lower, upper and mean pseudo-residuasl are returned.

Value

vector of pseudo residuals

Examples

```
obs = rpois(100, lambda = 1)
stateprobs = matrix(0.5, nrow = 100, ncol = 2)
par = list(lambda = c(1,2))
pres = pseudo_res_discrete(obs, "pois", par, stateprobs)
```

qreml *Quasi restricted maximum likelihood (qREML) algorithm for models with penalised splines or simple i.i.d. random effects*

Description

This algorithm can be used very flexibly to fit statistical models that involve **penalised splines** or simple **i.i.d. random effects**, i.e. that have penalties of the form

$$0.5 \sum_i \lambda_i b_i^T S_i b_i,$$

with smoothing parameters λ_i, coefficient vectors b_i, and fixed penalty matrices S_i.

The **qREML** algorithm is typically much faster than REML or marginal ML using the full Laplace approximation method, but may be slightly less accurate regarding the estimation of the penalty strength parameters.

Under the hood, `qreml` uses the R package `RTMB` for automatic differentiation in the inner optimisation. The user has to specify the **penalised negative log-likelihood function** `pnll` structured as dictated by `RTMB` and use the `penalty` function to compute the quadratic-form penalty inside the likelihood.

Usage

```
qreml(
  pnll,
  par,
  dat,
  random,
  map = NULL,
  psname = "lambda",
  alpha = 0.15,
  smoothing = 1,
  maxiter = 100,
  tol = 1e-04,
  control = list(reltol = 1e-10, maxit = 1000),
  silent = 1,
  joint_unc = TRUE,
  saveall = FALSE,
  epsilon = c(0.01, 0.1)
)
```

Arguments

`pnll`	penalised negative log-likelihood function that is structured as dictated by `RTMB` and uses the `penalty` function from `LaMa` to compute the penalty Needs to be a function of the named list of initial parameters `par` only.

par	named list of initial parameters The random effects/ spline coefficients can be vectors or matrices, the latter summarising several random effects of the same structure, each one being a row in the matrix.
dat	initial data list that contains the data used in the likelihood function, hyperparameters, and the **initial penalty strength** vector If the initial penalty strength vector is **not** called `lambda`, the name it has in `dat` needs to be specified using the `psname` argument below. Its length needs to match the to the total number of random effects.
random	vector of names of the random effects/ penalised parameters in `par` **Caution:** The ordering of `random` needs to match the order of the random effects passed to `penalty` inside the likelihood function.
map	optional map for fixed effects in the likelihood function
psname	optional name given to the penalty strength parameter in `dat`. Defaults to `"lambda"`.
alpha	optional hyperparamater for exponential smoothing of the penalty strengths. For larger values smoother convergence is to be expected but the algorithm may need more iterations.
smoothing	optional scaling factor for the final penalty strength parameters Increasing this beyond one will lead to a smoother final model. Can be an integer or a vector of length equal to the length of the penalty strength parameter.
maxiter	maximum number of iterations in the outer optimisation over the penalty strength parameters.
tol	Convergence tolerance for the penalty strength parameters.
control	list of control parameters for `optim` to use in the inner optimisation. Here, `optim` uses the `BFGS` method which cannot be changed. We advise against changing the default values of `reltol` and `maxit` as this can decrease the accuracy of the Laplace approximation.
silent	integer silencing level: 0 corresponds to full printing of inner and outer iterations, 1 to printing of outer iterations only, and 2 to no printing.
joint_unc	logical, if `TRUE`, joint `RTMB` object is returned allowing for joint uncertainty quantification
saveall	logical, if `TRUE`, then all model objects from each iteration are saved in the final model object.
epsilon	vector of two values specifying the cycling detection parameters. If the relative change of the new penalty strength to the previous one is larger than `epsilon[1]` but the change to the one before is smaller than `epsilon[2]`, the algorithm will average the two last values to prevent cycling.

Value

returns a model list influenced by the users report statements in `pnll`

See Also

`penalty` to compute the penalty inside the likelihood function

Examples

```
data = trex[1:1000,] # subset

# initial parameter list
par = list(logmu = log(c(0.3, 1)), # step mean
           logsigma = log(c(0.2, 0.7)), # step sd
           beta0 = c(-2,-2), # state process intercept
           betaspline = matrix(rep(0, 18), nrow = 2)) # state process spline coefs

# data object with initial penalty strength lambda
dat = list(step = data$step, # step length
           tod = data$tod, # time of day covariate
           N = 2, # number of states
           lambda = rep(10,2)) # initial penalty strength

# building model matrices
modmat = make_matrices(~ s(tod, bs = "cp"),
                       data = data.frame(tod = 1:24),
                       knots = list(tod = c(0,24))) # wrapping points
dat$Z = modmat$Z # spline design matrix
dat$S = modmat$S # penalty matrix

# penalised negative log-likelihood function
pnll = function(par) {
  getAll(par, dat) # makes everything contained available without $
  Gamma = tpm_g(Z, cbind(beta0, betaspline), ad = TRUE) # transition probabilities
  delta = stationary_p(Gamma, t = 1, ad = TRUE) # initial distribution
  mu = exp(logmu) # step mean
  sigma = exp(logsigma) # step sd
  # calculating all state-dependent densities
  allprobs = matrix(1, nrow = length(step), ncol = N)
  ind = which(!is.na(step)) # only for non-NA obs.
  for(j in 1:N) allprobs[ind,j] = dgamma2(step[ind],mu[j],sigma[j])
  -forward_g(delta, Gamma[,,tod], allprobs) +
      penalty(betaspline, S, lambda) # this does all the penalization work
}

# model fitting
mod = qreml(pnll, par, dat, random = "betaspline")
```

`sdreportMC` *Monte Carlo version of* `sdreport`

Description

After optimisation of an AD model, `sdreportMC` can be used to calculate samples of confidence intervals of all model parameters and `REPORT()`ed quantities including nonlinear functions of random effects and parameters.

Usage

```
sdreportMC(
  obj,
  what,
  Hessian = NULL,
  CI = FALSE,
  n = 1000,
  probs = c(0.025, 0.975)
)
```

Arguments

obj	object returned by MakeADFun() after optimisation
what	vector of strings with names of parameters and REPORT()ed quantities to be reported
Hessian	optional Hessian matrix. If not provided, it will be computed from the object
CI	logical. If TRUE, only confidence intervals instead of samples will be returned
n	number of samples to draw from the multivariate normal distribution of the MLE
probs	vector of probabilities for the confidence intervals (ignored if no CIs are computed)

Details

Caution: Currently does not work for models with fixed parameters (i.e. that use the map argument of MakeADFun.)

Value

named list corresponding to the elements of what. Each element has the structure of the corresponding quantity with an additional dimension added for the samples. For example, if a quantity is a vector, the list contains a matrix. If a quantity is a matrix, the list contains an array.

Examples

```
# fitting an HMM to the trex data and running sdreportMC
## negative log-likelihood function
nll = function(par) {
  getAll(par, dat) # makes everything contained available without $
  Gamma = tpm(eta) # computes transition probability matrix from unconstrained eta
  delta = stationary(Gamma) # computes stationary distribution
  # exponentiating because all parameters strictly positive
  mu = exp(logmu)
  sigma = exp(logsigma)
  kappa = exp(logkappa)
  # reporting statements for sdreportMC
  REPORT(mu)
  REPORT(sigma)
  REPORT(kappa)
  # calculating all state-dependent densities
```

```
  allprobs = matrix(1, nrow = length(step), ncol = N)
  ind = which(!is.na(step) & !is.na(angle)) # only for non-NA obs.
  for(j in 1:N){
    allprobs[ind,j] = dgamma2(step[ind],mu[j],sigma[j])*dvm(angle[ind],0,kappa[j])
  }
  -forward(delta, Gamma, allprobs) # simple forward algorithm
}

## initial parameter list
par = list(
 logmu = log(c(0.3, 1)),       # initial means for step length (log-transformed)
  logsigma = log(c(0.2, 0.7)), # initial sds for step length (log-transformed)
  logkappa = log(c(0.2, 0.7)), # initial concentration for turning angle (log-transformed)
  eta = rep(-2, 2)             # initial t.p.m. parameters (on logit scale)
)
## data and hyperparameters
dat = list(
  step = trex$step[1:500],   # hourly step lengths
  angle = trex$angle[1:500], # hourly turning angles
  N = 2
)

## creating AD function
obj = MakeADFun(nll, par, silent = TRUE) # creating the objective function

## optimising
opt = nlminb(obj$par, obj$fn, obj$gr) # optimization

## running sdreportMC
# `mu` has report statement, `delta` is automatically reported by `forward()`
sdrMC = sdreportMC(obj,
                   what = c("mu", "delta"),
                   n = 50)
dim(sdrMC$delta)
# now a matrix with 50 samples (rows)
```

---

skewnorm *Skew normal distribution*

Description

Density, distribution function, quantile function and random generation for the skew normal distribution.

Usage

```
dskewnorm(x, xi = 0, omega = 1, alpha = 0, log = FALSE)

pskewnorm(q, xi = 0, omega = 1, alpha = 0, ...)
```

```
qskewnorm(p, xi = 0, omega = 1, alpha = 0, ...)

rskewnorm(n, xi = 0, omega = 1, alpha = 0)
```

Arguments

x, q	vector of quantiles
xi	location parameter
omega	scale parameter, must be positive.
alpha	skewness parameter, +/- Inf is allowed.
log	logical; if TRUE, probabilities/ densities p are returned as $\log(p)$.
...	additional parameters to be passed to the sn package functions for pskewnorm and qskewnorm.
p	vector of probabilities
n	number of observations. If length(n) > 1, the length is taken to be the number required.

Details

This implementation of dskewnorm allows for automatic differentiation with RTMB while the other functions are imported from the sn package.

Value

dskewnorm gives the density, pskewnorm gives the distribution function, qskewnorm gives the quantile function, and rskewnorm generates random deviates.

Examples

```
x = rskewnorm(1)
d = dskewnorm(x)
p = pskewnorm(x)
q = qskewnorm(p)
```

---

stateprobs *Calculate conditional local state probabilities for homogeneous HMMs*

Description

Computes

$$\Pr(S_t = j \mid X_1, ..., X_T)$$

for homogeneous HMMs

Usage

```
stateprobs(delta, Gamma, allprobs, trackID = NULL, mod = NULL)
```

Arguments

delta	initial or stationary distribution of length N, or matrix of dimension c(k,N) for k independent tracks, if trackID is provided
Gamma	transition probability matrix of dimension c(N,N), or array of k transition probability matrices of dimension c(N,N,k), if trackID is provided
allprobs	matrix of state-dependent probabilities/ density values of dimension c(n, N)
trackID	optional vector of length n containing IDs If provided, the total log-likelihood will be the sum of each track's likelihood contribution. In this case, Gamma can be a matrix, leading to the same transition probabilities for each track, or an array of dimension c(N,N,k), with one (homogeneous) transition probability matrix for each track. Furthermore, instead of a single vector delta corresponding to the initial distribution, a delta matrix of initial distributions, of dimension c(k,N), can be provided, such that each track starts with it's own initial distribution.
mod	optional model object containing initial distribution delta, transition probability matrix Gamma, matrix of state-dependent probabilities allprobs, and potentially a trackID variable If you are using automatic differentiation either with RTMB::MakeADFun or qreml and include forward in your likelihood function, the objects needed for state decoding are automatically reported after model fitting. Hence, you can pass the model object obtained from running RTMB::report() or from qreml directly to this function.

Value

matrix of conditional state probabilities of dimension c(n,N)

See Also

Other decoding functions: stateprobs_g(), stateprobs_p(), viterbi(), viterbi_g(), viterbi_p()

Examples

```
Gamma = tpm(c(-1,-2))
delta = stationary(Gamma)
allprobs = matrix(runif(200), nrow = 100, ncol = 2)

probs = stateprobs(delta, Gamma, allprobs)
```

`stateprobs_g` *Calculate conditional local state probabilities for inhomogeneous HMMs*

Description

Computes

$$\Pr(S_t = j \mid X_1, ..., X_T)$$

for inhomogeneous HMMs

Usage

```
stateprobs_g(delta, Gamma, allprobs, trackID = NULL, mod = NULL)
```

Arguments

`delta`	initial or stationary distribution of length N, or matrix of dimension c(k,N) for k independent tracks, if `trackID` is provided
`Gamma`	array of transition probability matrices of dimension c(N,N,n-1), as in a time series of length n, there are only n-1 transitions If an array of dimension c(N,N,n) for a single track is provided, the first slice will be ignored. If `trackID` is provided, `Gamma` needs to be an array of dimension c(N,N,n), where n is the number of rows in `allprobs`. Then for each track the first transition matrix will be ignored.
`allprobs`	matrix of state-dependent probabilities/ density values of dimension c(n, N)
`trackID`	optional vector of k track IDs, if multiple tracks need to be decoded separately
`mod`	optional model object containing initial distribution `delta`, transition probability matrix `Gamma`, matrix of state-dependent probabilities `allprobs`, and potentially a `trackID` variable If you are using automatic differentiation either with `RTMB::MakeADFun` or `qreml` and include `forward_g` in your likelihood function, the objects needed for state decoding are automatically reported after model fitting. Hence, you can pass the model object obtained from running `RTMB::report()` or from `qreml` directly to this function.

Value

matrix of conditional state probabilities of dimension c(n,N)

See Also

Other decoding functions: `stateprobs()`, `stateprobs_p()`, `viterbi()`, `viterbi_g()`, `viterbi_p()`

Examples

```
Gamma = tpm_g(runif(99), matrix(c(-1,-1,1,-2), nrow = 2, byrow = TRUE))
delta = c(0.5, 0.5)
allprobs = matrix(runif(200), nrow = 100, ncol = 2)

probs = stateprobs_g(delta, Gamma, allprobs)
```

`stateprobs_p` *Calculate conditional local state probabilities for periodically inhomogeneous HMMs*

Description

Computes

$$\Pr(S_t = j \mid X_1, ..., X_T)$$

for periodically inhomogeneous HMMs

Usage

```
stateprobs_p(delta, Gamma, allprobs, tod, trackID = NULL, mod = NULL)
```

Arguments

`delta`	initial or stationary distribution of length N, or matrix of dimension c(k,N) for k independent tracks, if `trackID` is provided This could e.g. be the periodically stationary distribution (for each track) as computed by `stationary_p`.
`Gamma`	array of transition probability matrices for each time point in the cycle of dimension c(N,N,L), where L is the length of the cycle.
`allprobs`	matrix of state-dependent probabilities/ density values of dimension c(n, N)
`tod`	(Integer valued) variable for cycle indexing in 1, ..., L, mapping the data index to a generalised time of day (length n). For half-hourly data L = 48. It could, however, also be day of year for daily data and L = 365.
`trackID`	optional vector of k track IDs, if multiple tracks need to be decoded separately
`mod`	optional model object containing initial distribution `delta`, transition probability matrix `Gamma`, matrix of state-dependent probabilities `allprobs`, and potentially a `trackID` variable If you are using automatic differentiation either with `RTMB::MakeADFun` or `qreml` and include `forward_p` in your likelihood function, the objects needed for state decoding are automatically reported after model fitting. Hence, you can pass the model object obtained from running `RTMB::report()` or from `qreml` directly to this function.

Value

matrix of conditional state probabilities of dimension c(n,N)

See Also

Other decoding functions: stateprobs(), stateprobs_g(), viterbi(), viterbi_g(), viterbi_p()

Examples

```
L = 24
beta = matrix(c(-1, 2, -1, -2, 1, -1), nrow = 2, byrow = TRUE)
Gamma = tpm_p(1:L, L, beta, degree = 1)
delta = stationary_p(Gamma, 1)
allprobs = matrix(runif(200), nrow = 100, ncol = 2)
tod = rep(1:24, 5)[1:100]

probs = stateprobs_p(delta, Gamma, allprobs, tod)
```

---

stationary *Compute the stationary distribution of a homogeneous Markov chain*

Description

A homogeneous, finite state Markov chain that is irreducible and aperiodic converges to a unique stationary distribution, here called δ. As it is stationary, this distribution satisfies

$$\delta\Gamma = \delta,$$

subject to $\sum_{j=1}^{N} \delta_j = 1$, where Γ is the transition probability matrix. This function solves the linear system of equations above.

Usage

```
stationary(Gamma)
```

Arguments

Gamma	transition probability matrix of dimension c(N,N)

Value

stationary distribution of the Markov chain with the given transition probability matrix

See Also

tpm to create a transition probabilty matrix using the multinomial logistic link (softmax)

Other stationary distribution functions: stationary_cont(), stationary_p()

Examples

```
Gamma = tpm(c(rep(-2,3), rep(-3,3)))
delta = stationary(Gamma)
```

stationary_cont — *Compute the stationary distribution of a continuous-time Markov chain*

Description

A well-behaved continuous-time Markov chain converges to a unique stationary distribution, here called π. This distribution satisfies

$$\pi Q = 0,$$

subject to $\sum_{j=1}^{N} \pi_j = 1$, where Q is the infinitesimal generator of the Markov chain. This function solves the linear system of equations above for a given generator matrix.

Usage

```
stationary_cont(Q)
```

Arguments

Q	infinitesimal generator matrix of dimension c(N,N)

Value

stationary distribution of the continuous-time Markov chain with given generator matrix

See Also

generator to create a generator matrix

Other stationary distribution functions: stationary(), stationary_p()

Examples

```
Q = generator(c(-2,-2))
Pi = stationary_cont(Q)
```

stationary_p — *Compute the periodically stationary distribution of a periodically inhomogeneous Markov chain*

Description

If the transition probability matrix of an inhomogeneous Markov chain varies only periodically (with period length L), it converges to a so-called periodically stationary distribution. This happens, because the thinned Markov chain, which has a full cycle as each time step, has homogeneous transition probability matrix

$$\Gamma_t = \Gamma^{(t)}\Gamma^{(t+1)} \dots \Gamma^{(t+L-1)}$$

for all $t = 1, \dots, L$. The stationary distribution for time t satifies $\delta^{(t)}\Gamma_t = \delta^{(t)}$.

This function calculates said periodically stationary distribution.

Usage

```
stationary_p(Gamma, t = NULL, ad = NULL)
```

Arguments

Gamma	array of transition probability matrices of dimension c(N,N,L)
t	integer index of the time point in the cycle, for which to calculate the stationary distribution If t is not provided, the function calculates all stationary distributions for each time point in the cycle.
ad	optional logical, indicating whether automatic differentiation with RTMB should be used. By default, the function determines this itself.

Value

either the periodically stationary distribution at time t or all periodically stationary distributions.

See Also

tpm_p and tpm_g to create multiple transition matrices based on a cyclic variable or design matrix

Other stationary distribution functions: stationary(), stationary_cont()

Examples

```
# setting parameters for trigonometric link
beta = matrix(c(-1, 2, -1, -2, 1, -1), nrow = 2, byrow = TRUE)
Gamma = tpm_p(beta = beta, degree = 1)
# periodically stationary distribution for specific time point
delta = stationary_p(Gamma, 4)

# all periodically stationary distributions
Delta = stationary_p(Gamma)
```

---

stationary_p_sparse *Sparse version of* stationary_p

Description

This is function computes the periodically stationary distribution of a Markov chain given a list of L **sparse** transition probability matrices. Compatible with automatic differentiation by RTMB

Usage

```
stationary_p_sparse(Gamma, t = NULL)
```

Arguments

Gamma	sist of length L containing sparse transition probability matrices for one cycle.
t	integer index of the time point in the cycle, for which to calculate the stationary distribution If t is not provided, the function calculates all stationary distributions for each time point in the cycle.

Value

either the periodically stationary distribution at time t or all periodically stationary distributions.

Examples

```
## periodic HSMM example (here the approximating tpm is sparse)
N = 2 # number of states
L = 24 # cycle length
# time-varying mean dwell times
Z = trigBasisExp(1:L) # trigonometric basis functions design matrix
beta = matrix(c(2, 2, 0.1, -0.1, -0.2, 0.2), nrow = 2)
Lambda = exp(cbind(1, Z) %*% t(beta))
sizes = c(20, 20) # approximating chain with 40 states
# state dwell-time distributions
dm = lapply(1:N, function(i) sapply(1:sizes[i]-1, dpois, lambda = Lambda[,i]))
omega = matrix(c(0,1,1,0), nrow = N, byrow = TRUE) # embedded t.p.m.

# calculating extended-state-space t.p.m.s
Gamma = tpm_phsmm(omega, dm)
# Periodically stationary distribution for specific time point
delta = stationary_p_sparse(Gamma, 4)

# All periodically stationary distributions
Delta = stationary_p_sparse(Gamma)
```

---

stationary_sparse *Sparse version of* stationary

Description

This is function computes the stationary distribution of a Markov chain with a given **sparse** transition probability matrix. Compatible with automatic differentiation by RTMB

Usage

```
stationary_sparse(Gamma)
```

Arguments

Gamma	sparse transition probability matrix of dimension c(N,N)

Value

stationary distribution of the Markov chain with the given transition probability matrix

Examples

```
## HSMM example (here the approximating tpm is sparse)
# building the t.p.m. of the embedded Markov chain
omega = matrix(c(0,1,1,0), nrow = 2, byrow = TRUE)
# defining state aggregate sizes
sizes = c(20, 30)
# defining state dwell-time distributions
lambda = c(5, 11)
dm = list(dpois(1:sizes[1]-1, lambda[1]), dpois(1:sizes[2]-1, lambda[2]))
# calculating extended-state-space t.p.m.
Gamma = tpm_hsmm(omega, dm)
delta = stationary_sparse(Gamma)
```

---

tpm *Build the transition probability matrix from unconstrained parameter vector*

Description

Markov chains are parametrised in terms of a transition probability matrix Γ, for which each row contains a conditional probability distribution of the next state given the current state. Hence, each row has entries between 0 and 1 that need to sum to one.

For numerical optimisation, we parametrise in terms of unconstrained parameters, thus this function computes said matrix from an unconstrained parameter vector via the inverse multinomial logistic link (also known as softmax) applied to each row.

Usage

```
tpm(param, byrow = FALSE)
```

Arguments

param	unconstrained parameter vector of length N*(N-1) where N is the number of states of the Markov chain
byrow	logical indicating if the transition probability matrix should be filled by row Defaults to FALSE, but should be set to TRUE if one wants to work with a matrix of beta parameters returned by popular HMM packages like moveHMM, momentuHMM, or hmmTMB.

Value

Transition probability matrix of dimension c(N,N)

See Also

Other transition probability matrix functions: `generator()`, `tpm_cont()`, `tpm_emb()`, `tpm_emb_g()`, `tpm_g()`, `tpm_p()`

Examples

```
# 2 states: 2 free off-diagonal elements
par1 = rep(-1, 2)
Gamma1 = tpm(par1)

# 3 states: 6 free off-diagonal elements
par2 = rep(-2, 6)
Gamma2 = tpm(par2)
```

---

tpm_cont *Calculate continuous time transition probabilities*

Description

A continuous-time Markov chain is described by an infinitesimal generator matrix Q. When observing data at time points $t_1, \dots, t_n$ the transition probabilites between t_i and t_{i+1} are caluclated as

$$\Gamma(\Delta t_i) = \exp(Q \Delta t_i),$$

where $\exp()$ is the matrix exponential. The mapping $\Gamma(\Delta t)$ is also called the **Markov semigroup**. This function calculates all transition matrices based on a given generator and time differences.

Usage

```
tpm_cont(Q, timediff, ad = NULL, report = TRUE)
```

Arguments

`Q`	infinitesimal generator matrix of the continuous-time Markov chain of dimension c(N,N)
`timediff`	time differences between observations of length n-1 when based on n observations
`ad`	optional logical, indicating whether automatic differentiation with `RTMB` should be used. By default, the function determines this itself.
`report`	logical, indicating whether `Q` should be reported from the fitted model. Defaults to `TRUE`, but only works if `ad = TRUE`.

Value

array of continuous-time transition matrices of dimension c(N,N,n-1)

See Also

Other transition probability matrix functions: generator(), tpm(), tpm_emb(), tpm_emb_g(), tpm_g(), tpm_p()

Examples

```
# building a Q matrix for a 3-state cont.-time Markov chain
Q = generator(rep(-2, 6))

# draw random time differences
timediff = rexp(100, 10)

# compute all transition matrices
Gamma = tpm_cont(Q, timediff)
```

---

tpm_emb *Build the embedded transition probability matrix of an HSMM from unconstrained parameter vector*

Description

Hidden semi-Markov models are defined in terms of state durations and an **embedded** transition probability matrix that contains the conditional transition probabilities given that the **current state is left**. This matrix necessarily has diagonal entries all equal to zero as self-transitions are impossible.

This function builds such an embedded/ conditional transition probability matrix from an unconstrained parameter vector. For each row of the matrix, the inverse multinomial logistic link is applied.

For a matrix of dimension c(N,N), the number of free off-diagonal elements is N*(N-2), hence also the length of param. This means, for 2 states, the function needs to be called without any arguments, for 3-states with a vector of length 3, for 4 states with a vector of length 8, etc.

Compatible with automatic differentiation by RTMB

Usage

```
tpm_emb(param = NULL)
```

Arguments

param	unconstrained parameter vector of length N*(N-2) where N is the number of states of the Markov chain If the function is called without param, it will return the conditional transition probability matrix for a 2-state HSMM, which is fixed with 0 diagonal entries and off-diagonal entries equal to 1.

Value

embedded/ conditional transition probability matrix of dimension c(N,N)

See Also

Other transition probability matrix functions: `generator()`, `tpm()`, `tpm_cont()`, `tpm_emb_g()`, `tpm_g()`, `tpm_p()`

Examples

```
# 2 states: no free off-diagonal elements
omega = tpm_emb()

# 3 states: 3 free off-diagonal elements
param = rep(0, 3)
omega = tpm_emb(param)

# 4 states: 8 free off-diagonal elements
param = rep(0, 8)
omega = tpm_emb(param)
```

---

tpm_emb_g *Build all embedded transition probability matrices of an inhomogeneous HSMM*

Description

Hidden semi-Markov models are defined in terms of state durations and an **embedded** transition probability matrix that contains the conditional transition probabilities given that the **current state is left**. This matrix necessarily has diagonal entries all equal to zero as self-transitions are impossible. We can allow this matrix to vary with covariates, which is the purpose of this function.

It builds all embedded/ conditional transition probability matrices based on a design and parameter matrix. For each row of the matrix, the inverse multinomial logistic link is applied.

For a matrix of dimension c(N,N), the number of free off-diagonal elements is N*(N-2) which determines the number of rows of the parameter matrix.

Compatible with automatic differentiation by `RTMB`

Usage

```
tpm_emb_g(Z, beta, report = TRUE)
```

Arguments

`Z`	covariate design matrix with or without intercept column, i.e. of dimension c(n, p) or c(n, p+1) If `Z` has only p columns, an intercept column of ones will be added automatically.

beta	matrix of coefficients for the off-diagonal elements of the embedded transition probability matrix Needs to be of dimension c(N*(N-2), p+1), where the first column contains the intercepts. p can be 0, in which case the model is homogeneous.
report	logical, indicating whether the coefficient matrix beta should be reported from the fitted model. Defaults to TRUE.

Value

array of embedded/ conditional transition probability matrices of dimension c(N,N,n)

See Also

Other transition probability matrix functions: generator(), tpm(), tpm_cont(), tpm_emb(), tpm_g(), tpm_p()

Examples

```
## parameter matrix for 3-state HSMM
beta = matrix(c(rep(0, 3), -0.2, 0.2, 0.1), nrow = 3)
# no intercept
Z = rnorm(100)
omega = tpm_emb_g(Z, beta)
# intercept
Z = cbind(1, Z)
omega = tpm_emb_g(Z, beta)
```

---

tpm_g *Build all transition probability matrices of an inhomogeneous HMM*

Description

In an HMM, we often model the influence of covariates on the state process by linking them to the transition probabiltiy matrix. Most commonly, this is done by specifying a linear predictor

$$\eta_{ij}^{(t)} = \beta_0^{(ij)} + \beta_1^{(ij)} z_{t1} + \cdots + \beta_p^{(ij)} z_{tp}$$

for each off-diagonal element ($i \neq j$) of the transition probability matrix and then applying the inverse multinomial logistic link (also known as softmax) to each row. This function efficiently calculates all transition probabilty matrices for a given design matrix Z and parameter matrix beta.

Usage

```
tpm_g(Z, beta, byrow = FALSE, ad = NULL, report = TRUE)
```

Arguments

Z	covariate design matrix with or without intercept column, i.e. of dimension c(n, p) or c(n, p+1) If Z has only p columns, an intercept column of ones will be added automatically.
beta	matrix of coefficients for the off-diagonal elements of the transition probability matrix Needs to be of dimension c(N*(N-1), p+1), where the first column contains the intercepts.
byrow	logical indicating if each transition probability matrix should be filled by row Defaults to FALSE, but should be set to TRUE if one wants to work with a matrix of beta parameters returned by popular HMM packages like moveHMM, momentuHMM, or hmmTMB.
ad	optional logical, indicating whether automatic differentiation with RTMB should be used. By default, the function determines this itself.
report	logical, indicating whether the coefficient matrix beta should be reported from the fitted model. Defaults to TRUE, but only works if ad = TRUE.

Value

array of transition probability matrices of dimension c(N,N,n)

See Also

Other transition probability matrix functions: generator(), tpm(), tpm_cont(), tpm_emb(), tpm_emb_g(), tpm_p()

Examples

```
Z = matrix(runif(200), ncol = 2)
beta = matrix(c(-1, 1, 2, -2, 1, -2), nrow = 2, byrow = TRUE)
Gamma = tpm_g(Z, beta)
```

---

tpm_hsmm *Builds the transition probability matrix of an HSMM-approximating HMM*

Description

Hidden semi-Markov models (HSMMs) are a flexible extension of HMMs, where the state duration distribution is explicitly modelled. For direct numerical maximum likelihood estimation, HSMMs can be represented as HMMs on an enlarged state space (of size M) and with structured transition probabilities.

This function computes the transition matrix to approximate a given HSMM by an HMM with a larger state space.

Usage

```
tpm_hsmm(omega, dm, Fm = NULL, sparse = TRUE, eps = 1e-10)
```

Arguments

omega	embedded transition probability matrix of dimension c(N,N) as computed by tpm_emb.
dm	state dwell-time distributions arranged in a list of length(N). Each list element needs to be a vector of length N_i, where N_i is the state aggregate size.
Fm	optional list of length N containing the cumulative distribution functions of the dwell-time distributions.
sparse	logical, indicating whether the output should be a **sparse** matrix. Defaults to TRUE.
eps	rounding value: If an entry of the transition probabily matrix is smaller, than it is rounded to zero. Usually, this should not be changed.

Value

extended-state-space transition probability matrix of the approximating HMM

Examples

```
# building the t.p.m. of the embedded Markov chain
omega = matrix(c(0,1,1,0), nrow = 2, byrow = TRUE)
# defining state aggregate sizes
sizes = c(20, 30)
# defining state dwell-time distributions
lambda = c(5, 11)
dm = list(dpois(1:sizes[1]-1, lambda[1]), dpois(1:sizes[2]-1, lambda[2]))
# calculating extended-state-space t.p.m.
Gamma = tpm_hsmm(omega, dm)
```

---

tpm_hsmm2 *Build the transition probability matrix of an HSMM-approximating HMM*

Description

Hidden semi-Markov models (HSMMs) are a flexible extension of HMMs. For direct numerical maximum likelihood estimation, HSMMs can be represented as HMMs on an enlarged state space (of size M) and with structured transition probabilities. This function computes the transition matrix of an HSMM.

Usage

```
tpm_hsmm2(omega, dm, eps = 1e-10)
```

Arguments

omega	embedded transition probability matrix of dimension c(N,N)
dm	state dwell-time distributions arranged in a list of length(N). Each list element needs to be a vector of length N_i, where N_i is the state aggregate size.
eps	rounding value: If an entry of the transition probabily matrix is smaller, than it is rounded to zero.

Value

extended-state-space transition probability matrix of the approximating HMM

Examples

```
# building the t.p.m. of the embedded Markov chain
omega = matrix(c(0,1,1,0), nrow = 2, byrow = TRUE)
# defining state aggregate sizes
sizes = c(20, 30)
# defining state dwell-time distributions
lambda = c(5, 11)
dm = list(dpois(1:sizes[1]-1, lambda[1]), dpois(1:sizes[2]-1, lambda[2]))
# calculating extended-state-space t.p.m.
Gamma = tpm_hsmm(omega, dm)
```

---

tpm_ihsmm *Builds all transition probability matrices of an inhomogeneous-HSMM-approximating HMM*

Description

Hidden semi-Markov models (HSMMs) are a flexible extension of HMMs. For direct numerical maximum likelihood estimation, HSMMs can be represented as HMMs on an enlarged state space (of size M) and with structured transition probabilities.

This function computes the transition matrices of a periodically inhomogeneos HSMMs.

Usage

```
tpm_ihsmm(omega, dm, eps = 1e-10)
```

Arguments

omega	embedded transition probability matrix Either a matrix of dimension c(N,N) for homogeneous conditional transition probabilities (as computed by tpm_emb), or an array of dimension c(N,N,n) for inhomogeneous conditional transition probabilities (as computed by tpm_emb_g).
dm	state dwell-time distributions arranged in a list of length N Each list element needs to be a matrix of dimension c(n, N_i), where each row t is the (approximate) probability mass function of state i at time t.

eps — rounding value: If an entry of the transition probabily matrix is smaller, than it is rounded to zero. Usually, this should not be changed.

Value

list of dimension length `n - max(sapply(dm, ncol))`, containing sparse extended-state-space transition probability matrices for each time point (except the first `max(sapply(dm, ncol)) - 1`).

Examples

```
N = 2
# time-varying mean dwell times
n = 100
z = runif(n)
beta = matrix(c(2, 2, 0.1, -0.1), nrow = 2)
Lambda = exp(cbind(1, z) %*% t(beta))
sizes = c(15, 15) # approximating chain with 30 states
# state dwell-time distributions
dm = lapply(1:N, function(i) sapply(1:sizes[i]-1, dpois, lambda = Lambda[,i]))

## homogeneous conditional transition probabilites
# diagonal elements are zero, rowsums are one
omega = matrix(c(0,1,1,0), nrow = N, byrow = TRUE)

# calculating extended-state-space t.p.m.s
Gamma = tpm_ihsmm(omega, dm)

## inhomogeneous conditional transition probabilites
# omega can be an array
omega = array(omega, dim = c(N,N,n))

# calculating extended-state-space t.p.m.s
Gamma = tpm_ihsmm(omega, dm)
```

---

tpm_p — *Build all transition probability matrices of a periodically inhomogeneous HMM*

Description

Given a periodically varying variable such as time of day or day of year and the associated cycle length, this function calculates the transition probability matrices by applying the inverse multinomial logistic link (also known as softmax) to linear predictors of the form

$$\eta_{ij}^{(t)} = \beta_0^{(ij)} + \sum_{k=1}^{K} \left(\beta_{1k}^{(ij)} \sin(\frac{2\pi kt}{L}) + \beta_{2k}^{(ij)} \cos(\frac{2\pi kt}{L}) \right)$$

for the off-diagonal elements ($i \neq j$) of the transition probability matrix. This is relevant for modeling e.g. diurnal variation and the flexibility can be increased by adding smaller frequencies (i.e. increasing K).

Usage

```
tpm_p(
  tod = 1:24,
  L = 24,
  beta,
  degree = 1,
  Z = NULL,
  byrow = FALSE,
  ad = NULL,
  report = TRUE
)
```

Arguments

tod	equidistant sequence of a cyclic variable For time of day and e.g. half-hourly data, this could be 1, ..., L and L = 48, or 0.5, 1, 1.5, ..., 24 and L = 24.
L	length of one full cycle, on the scale of tod
beta	matrix of coefficients for the off-diagonal elements of the transition probability matrix Needs to be of dimension c(N *(N-1), 2*degree+1), where the first column contains the intercepts.
degree	degree of the trigonometric link function For each additional degree, one sine and one cosine frequency are added.
Z	pre-calculated design matrix (excluding intercept column) Defaults to NULL if trigonometric link should be calculated. From an efficiency perspective, Z should be pre-calculated within the likelihood function, as the basis expansion should not be redundantly calculated. This can be done by using trigBasisExp.
byrow	logical indicating if each transition probability matrix should be filled by row Defaults to FALSE, but should be set to TRUE if one wants to work with a matrix of beta parameters returned by popular HMM packages like moveHMM, momentuHMM, or hmmTMB.
ad	optional logical, indicating whether automatic differentiation with RTMB should be used. By default, the function determines this itself.
report	logical, indicating whether the coefficient matrix beta should be reported from the fitted model. Defaults to TRUE, but only works if ad = TRUE.

Details

Note that using this function inside the negative log-likelihood function is convenient, but it performs the basis expansion into sine and cosine terms each time it is called. As these do not change during the optimisation, using tpm_g with a pre-calculated (by trigBasisExp) design matrix would be more efficient.

Value

array of transition probability matrices of dimension c(N,N,length(tod))

See Also

Other transition probability matrix functions: `generator()`, `tpm()`, `tpm_cont()`, `tpm_emb()`, `tpm_emb_g()`, `tpm_g()`

Examples

```
# hourly data
tod = seq(1, 24, by = 1)
L = 24
beta = matrix(c(-1, 2, -1, -2, 1, -1), nrow = 2, byrow = TRUE)
Gamma = tpm_p(tod, L, beta, degree = 1)

# half-hourly data
## integer tod sequence
tod = seq(1, 48, by = 1)
L = 48
beta = matrix(c(-1, 2, -1, -2, 1, -1), nrow = 2, byrow = TRUE)
Gamma1 = tpm_p(tod, L, beta, degree = 1)

## equivalent specification
tod = seq(0.5, 24, by = 0.5)
L = 24
beta = matrix(c(-1, 2, -1, -2, 1, -1), nrow = 2, byrow = TRUE)
Gamma2 = tpm_p(tod, L, beta, degree = 1)

all(Gamma1 == Gamma2) # same result
```

---

tpm_phsmm *Builds all transition probability matrices of an periodic-HSMM-approximating HMM*

Description

Hidden semi-Markov models (HSMMs) are a flexible extension of HMMs. For direct numerical maximum likelihood estimation, HSMMs can be represented as HMMs on an enlarged state space (of size M) and with structured transition probabilities.

This function computes the transition matrices of a periodically inhomogeneos HSMMs.

Usage

```
tpm_phsmm(omega, dm, eps = 1e-10)
```

Arguments

omega	embedded transition probability matrix Either a matrix of dimension c(N,N) for homogeneous conditional transition probabilities (as computed by tpm_emb), or an array of dimension c(N,N,L) for inhomogeneous conditional transition probabilities (as computed by tpm_emb_g).
dm	state dwell-time distributions arranged in a list of length N Each list element needs to be a matrix of dimension c(L, N_i), where each row t is the (approximate) probability mass function of state i at time t.
eps	rounding value: If an entry of the transition probabily matrix is smaller, than it is rounded to zero. Usually, this should not be changed.

Value

list of dimension length L, containing sparse extended-state-space transition probability matrices of the approximating HMM for each time point of the cycle.

Examples

```
N = 2 # number of states
L = 24 # cycle length
# time-varying mean dwell times
Z = trigBasisExp(1:L) # trigonometric basis functions design matrix
beta = matrix(c(2, 2, 0.1, -0.1, -0.2, 0.2), nrow = 2)
Lambda = exp(cbind(1, Z) %*% t(beta))
sizes = c(20, 20) # approximating chain with 40 states
# state dwell-time distributions
dm = lapply(1:N, function(i) sapply(1:sizes[i]-1, dpois, lambda = Lambda[,i]))

## homogeneous conditional transition probabilites
# diagonal elements are zero, rowsums are one
omega = matrix(c(0,1,1,0), nrow = N, byrow = TRUE)

# calculating extended-state-space t.p.m.s
Gamma = tpm_phsmm(omega, dm)

## inhomogeneous conditional transition probabilites
# omega can be an array
omega = array(omega, dim = c(N,N,L))

# calculating extended-state-space t.p.m.s
Gamma = tpm_phsmm(omega, dm)
```

---

tpm_phsmm2 *Build all transition probability matrices of an periodic-HSMM-approximating HMM*

Description

Hidden semi-Markov models (HSMMs) are a flexible extension of HMMs. For direct numerical maximum likelihood estimation, HSMMs can be represented as HMMs on an enlarged state space (of size M) and with structured transition probabilities. This function computes the transition matrices of a periodically inhomogeneos HSMMs.

Usage

```
tpm_phsmm2(omega, dm, eps = 1e-10)
```

Arguments

omega	embedded transition probability matrix Either a matrix of dimension c(N,N) for homogeneous conditional transition probabilities, or an array of dimension c(N,N,L) for inhomogeneous conditional transition probabilities.
dm	state dwell-time distributions arranged in a list of length(N) Each list element needs to be a matrix of dimension c(L, N_i), where each row t is the (approximate) probability mass function of state i at time t.
eps	rounding value: If an entry of the transition probabily matrix is smaller, than it is rounded to zero.

Value

array of dimension c(N,N,L), containing the extended-state-space transition probability matrices of the approximating HMM for each time point of the cycle.

Examples

```
N = 3
L = 24
# time-varying mean dwell times
Lambda = exp(matrix(rnorm(L*N, 2, 0.5), nrow = L))
sizes = c(25, 25, 25) # approximating chain with 75 states
# state dwell-time distributions
dm = list()
for(i in 1:3){
  dmi = matrix(nrow = L, ncol = sizes[i])
  for(t in 1:L){
    dmi[t,] = dpois(1:sizes[i]-1, Lambda[t,i])
  }
  dm[[i]] = dmi
}

## homogeneous conditional transition probabilites
# diagonal elements are zero, rowsums are one
omega = matrix(c(0,0.5,0.5,0.2,0,0.8,0.7,0.3,0), nrow = N, byrow = TRUE)

# calculating extended-state-space t.p.m.s
Gamma = tpm_phsmm(omega, dm)
```

```
## inhomogeneous conditional transition probabilites
# omega can be an array
omega = array(rep(omega,L), dim = c(N,N,L))
omega[1,,4] = c(0, 0.2, 0.8) # small change for inhomogeneity

# calculating extended-state-space t.p.m.s
Gamma = tpm_phsmm(omega, dm)
```

`tpm_thinned` *Compute the transition probability matrix of a thinned periodically inhomogeneous Markov chain.*

Description

If the transition probability matrix of an inhomogeneous Markov chain varies only periodically (with period length L), it converges to a so-called periodically stationary distribution. This happens, because the thinned Markov chain, which has a full cycle as each time step, has homogeneous transition probability matrix

$$\Gamma_t = \Gamma^{(t)}\Gamma^{(t+1)}\dots\Gamma^{(t+L-1)}$$

for all $t = 1, \dots, L$. This function calculates the matrix above efficiently as a preliminery step to calculating the periodically stationary distribution.

Usage

```
tpm_thinned(Gamma, t)
```

Arguments

`Gamma`	array of transition probability matrices of dimension c(N,N,L).
`t`	integer index of the time point in the cycle, for which to calculate the thinned transition probility matrix

Value

thinned transition probabilty matrix of dimension c(N,N)

Examples

```
# setting parameters for trigonometric link
beta = matrix(c(-1, -2, 2, -1, 2, -4), nrow = 2, byrow = TRUE)
# calculating periodically varying t.p.m. array (of length 24 here)
Gamma = tpm_p(beta = beta)
# calculating t.p.m. of thinned Markov chain
tpm_thinned(Gamma, 4)
```

trex *T-Rex Movement Data*

Description

Hourly step lengths and turning angles of a Tyrannosaurus rex, living 66 million years ago.

Usage

```
trex
```

Format

A data frame with 10.000 rows and 4 variables:

tod time of day variable ranging from 1 to 24

step hourly step lengths in kilometres

angle hourly turning angles in radians

state hidden state variable

Source

Generated for example purposes.

trigBasisExp *Compute the design matrix for a trigonometric basis expansion*

Description

Given a periodically varying variable such as time of day or day of year and the associated cycle length, this function performs a basis expansion to efficiently calculate a linear predictor of the form

$$\eta^{(t)} = \beta_0 + \sum_{k=1}^{K} \big(\beta_{1k} \sin(\frac{2\pi kt}{L}) + \beta_{2k} \cos(\frac{2\pi kt}{L})\big).$$

This is relevant for modeling e.g. diurnal variation and the flexibility can be increased by adding smaller frequencies (i.e. increasing K).

Usage

```
trigBasisExp(tod, L = 24, degree = 1)
```

Arguments

tod	equidistant sequence of a cyclic variable For time of day and e.g. half-hourly data, this could be 1, ..., L and L = 48, or 0.5, 1, 1.5, ..., 24 and L = 24.
L	length of one cycle on the scale of the time variable. For time of day, this would be 24.
degree	degree K of the trigonometric link above. Increasing K increases the flexibility.

Value

design matrix (without intercept column), ordered as sin1, cos1, sin2, cos2, ...

Examples

```
## hourly data
tod = rep(1:24, 10)
Z = trigBasisExp(tod, L = 24, degree = 2)

## half-hourly data
tod = rep(1:48/2, 10) # in [0,24] -> L = 24
Z1 = trigBasisExp(tod, L = 24, degree = 3)

tod = rep(1:48, 10) # in [1,48] -> L = 48
Z2 = trigBasisExp(tod, L = 48, degree = 3)

all(Z1 == Z2)
# The latter two are equivalent specifications!
```

---

viterbi *Viterbi algorithm for state decoding in homogeneous HMMs*

Description

The Viterbi algorithm allows one to decode the most probable state sequence of an HMM.

Usage

```
viterbi(delta, Gamma, allprobs, trackID = NULL, mod = NULL)
```

Arguments

delta	initial distribution of length N, or matrix of dimension c(k,N) for k independent tracks, if trackID is provided
Gamma	transition probability matrix of dimension c(N,N) or array of transition probability matrices of dimension c(N,N,k) if trackID is provided
allprobs	matrix of state-dependent probabilities/ density values of dimension c(n, N)

trackID	optional vector of k track IDs, if multiple tracks need to be decoded separately
mod	optional model object containing initial distribution delta, transition probability matrix Gamma, matrix of state-dependent probabilities allprobs, and potentially a trackID variable If you are using automatic differentiation either with RTMB::MakeADFun or qreml and include forward in your likelihood function, the objects needed for state decoding are automatically reported after model fitting. Hence, you can pass the model object obtained from running RTMB::report() or from qreml directly to this function.

Value

vector of decoded states of length n

See Also

Other decoding functions: stateprobs(), stateprobs_g(), stateprobs_p(), viterbi_g(), viterbi_p()

Examples

```
delta = c(0.5, 0.5)
Gamma = matrix(c(0.9, 0.1, 0.2, 0.8), nrow = 2, byrow = TRUE)
allprobs = matrix(runif(200), nrow = 100, ncol = 2)
states = viterbi(delta, Gamma, allprobs)
```

---

viterbi_g *Viterbi algorithm for state decoding in inhomogeneous HMMs*

Description

The Viterbi algorithm allows one to decode the most probable state sequence of an HMM.

Usage

```
viterbi_g(delta, Gamma, allprobs, trackID = NULL, mod = NULL)
```

Arguments

delta	initial distribution of length N, or matrix of dimension c(k,N) for k independent tracks, if trackID is provided
Gamma	array of transition probability matrices of dimension c(N,N,n-1), as in a time series of length n, there are only n-1 transitions If an array of dimension c(N,N,n) is provided for a single track, the first slice will be ignored. If trackID is provided, Gamma needs to be an array of dimension c(N,N,n), where n is the number of rows in allprobs. Then for each track the first transition matrix will be ignored.

allprobs	matrix of state-dependent probabilities/ density values of dimension c(n, N)
trackID	optional vector of k track IDs, if multiple tracks need to be decoded separately
mod	optional model object containing initial distribution delta, transition probability matrix Gamma, matrix of state-dependent probabilities allprobs, and potentially a trackID variable If you are using automatic differentiation either with RTMB::MakeADFun or qreml and include forward_g in your likelihood function, the objects needed for state decoding are automatically reported after model fitting. Hence, you can pass the model object obtained from running RTMB::report() or from qreml directly to this function.

Value

vector of decoded states of length n

See Also

Other decoding functions: stateprobs(), stateprobs_g(), stateprobs_p(), viterbi(), viterbi_p()

Examples

```
delta = c(0.5, 0.5)
Gamma = array(dim = c(2,2,99))
for(t in 1:99){
  gammas = rbeta(2, shape1 = 0.4, shape2 = 1)
  Gamma[,,t] = matrix(c(1-gammas[1], gammas[1],
                        gammas[2], 1-gammas[2]), nrow = 2, byrow = TRUE)
}
allprobs = matrix(runif(200), nrow = 100, ncol = 2)
states = viterbi_g(delta, Gamma, allprobs)
```

---

viterbi_p *Viterbi algorithm for state decoding in periodically inhomogeneous HMMs*

Description

The Viterbi algorithm allows one to decode the most probable state sequence of an HMM.

Usage

```
viterbi_p(delta, Gamma, allprobs, tod, trackID = NULL, mod = NULL)
```

Arguments

delta	initial distribution of length N, or matrix of dimension c(k,N) for k independent tracks, if trackID is provided This could e.g. be the periodically stationary distribution (for each track).
Gamma	array of transition probability matrices for each time point in the cycle of dimension c(N,N,L), where L is the length of the cycle
allprobs	matrix of state-dependent probabilities/ density values of dimension c(n, N)
tod	(Integer valued) variable for cycle indexing in 1, ..., L, mapping the data index to a generalised time of day (length n) For half-hourly data L = 48. It could, however, also be day of year for daily data and L = 365.
trackID	optional vector of k track IDs, if multiple tracks need to be decoded separately
mod	optional model object containing initial distribution delta, transition probability matrix Gamma, matrix of state-dependent probabilities allprobs, and potentially a trackID variable If you are using automatic differentiation either with RTMB::MakeADFun or qreml and include forward_p in your likelihood function, the objects needed for state decoding are automatically reported after model fitting. Hence, you can pass the model object obtained from running RTMB::report() or from qreml directly to this function.

Value

vector of decoded states of length n

See Also

Other decoding functions: stateprobs(), stateprobs_g(), stateprobs_p(), viterbi(), viterbi_g()

Examples

```
delta = c(0.5, 0.5)
beta = matrix(c(-2, 1, -1,
                -2, -1, 1), nrow = 2, byrow = TRUE)
Gamma = tpm_p(1:24, 24, beta)

tod = rep(1:24, 10)
n = length(tod)

allprobs = matrix(runif(2*n), nrow = n, ncol = 2)
states = viterbi_p(delta, Gamma, allprobs, tod)
```

vm *von Mises distribution*

Description

Density, distribution function and random generation for the von Mises distribution.

Usage

```
dvm(x, mu = 0, kappa = 1, log = FALSE)

pvm(q, mu = 0, kappa = 1, from = NULL, tol = 1e-20)

rvm(n, mu = 0, kappa = 1, wrap = TRUE)
```

Arguments

x, q	vector of angles measured in radians at which to evaluate the density function.
mu	mean direction of the distribution measured in radians.
kappa	non-negative numeric value for the concentration parameter of the distribution.
log	logical; if TRUE, densities are returned on the log scale.
from	value from which the integration for CDF starts. If NULL, is set to mu - pi.
tol	the precision in evaluating the distribution function
n	number of observations. If length(n) > 1, the length is taken to be the number required.
wrap	logical; if TRUE, generated angles are wrapped to the interval [-pi, pi].

Details

The implementation of dvm allows for automatic differentiation with RTMB. rvm and pvm are imported from CircStats and circular respectively.

Value

dvm gives the density, pvm gives the distribution function, and rvm generates random deviates.

Examples

```
set.seed(1)
x = rvm(10, 0, 1)
d = dvm(x, 0, 1)
p = pvm(x, 0, 1)
```

wrpcauchy *wrapped Cauchy distribution*

Description

Density and random generation for the wrapped Cauchy distribution.

Usage

```
dwrpcauchy(x, mu = 0, rho, log = FALSE)

rwrpcauchy(n, mu = 0, rho, wrap = TRUE)
```

Arguments

x	vector of angles measured in radians at which to evaluate the density function.
mu	mean direction of the distribution measured in radians.
rho	concentration parameter of the distribution, must be in the interval from 0 to 1.
log	logical; if TRUE, densities are returned on the log scale.
n	number of observations. If length(n) > 1, the length is taken to be the number required.
wrap	logical; if TRUE, generated angles are wrapped to the interval [-pi, pi].

Details

The implementation of dwrpcauchy allows for automatic differentiation with RTMB. rwrpcauchy is imported from CircStats.

Value

dwrpcauchy gives the density and rwrpcauchy generates random deviates.

Examples

```
set.seed(1)
x = rwrpcauchy(10, 0, 1)
d = dwrpcauchy(x, 0, 1)
```

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