

Package ‘hmmTMB’

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Type Package

Title Fit Hidden Markov Models using Template Model Builder

Version 1.1.0

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Description Fitting hidden Markov models using automatic differentiation and Laplace approximation, allowing for fast inference and flexible covariate effects (including random effects and smoothing splines) on model parameters. The package is described by Michelot (2022) <doi:10.48550/arXiv.2211.14139>.

URL <https://github.com/TheoMichelot/hmmTMB>

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Depends R6, mgcv, TMB, ggplot2

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LinkingTo TMB, RcppEigen

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as_character_formula	<i>Read formula with as.character without splitting</i>
----------------------	---

Description

Read formula with as.character without splitting

Usage

as_character_formula(x, ...)

Arguments

- | | |
|-----|-----------|
| x | R formula |
| ... | Unused |

Details

Citation: this function was taken from the R package formula.tools: Christopher Brown (2018). formula.tools: Programmatic Utilities for Manipulating Formulas, Expressions, Calls, Assignments and Other R Objects. R package version 1.7.1. <https://CRAN.R-project.org/package=formula.tools>

as_sparse	<i>Transforms matrix to dgTMatrix</i>
-----------	---------------------------------------

Description

Transforms matrix to dgTMatrix

Usage

```
as_sparse(x)
```

Arguments

x Matrix or vector. If this is a vector, it is formatted into a single-column matrix.

Value

Sparse matrix of class dgTMatrix

bdiag_check	<i>Create block diagonal matrix (safe version)</i>
-------------	--

Description

This version of bdiag checks whether the matrices passed as arguments are NULL. This avoids errors that would arise if using bdiag directly.

Usage

```
bdiag_check(...)
```

Arguments

... Matrix or list of matrices (only the first argument is used)

Value

Block diagonal matrix

check_contiguous	<i>Check values in vector are contiguous</i>
------------------	--

Description

Check values in vector are contiguous

Usage

```
check_contiguous(x)
```

Arguments

x	Vector of values (can be numeric, character, factor)
---	--

Value

Logical: are values contiguous?

cov_grid	<i>Grid of covariates</i>
----------	---------------------------

Description

Grid of covariates

Usage

```
cov_grid(var, data = NULL, obj = NULL, covs = NULL, formulas, n_grid = 1000)
```

Arguments

var	Name of variable
data	Data frame containing the covariates. If not provided, data are extracted from obj
obj	HMM model object containing data and formulas
covs	Optional named list for values of covariates (other than 'var') that should be used in the plot (or dataframe with single row). If this is not specified, the mean value is used for numeric variables, and the first level for factor variables.
formulas	List of formulas used in the model
n_grid	Grid size (number of points). Default: 1000.

Value

Data frame of covariates, with 'var' defined over a grid, and other covariates fixed to their mean (numeric) or first level (factor).

Dist*R6 class for probability distribution*

Description

Contains the probability density/mass function, and the link and inverse link functions for a probability distribution.

Methods**Public methods:**

- `Dist$new()`
- `Dist$name()`
- `Dist$pdf()`
- `Dist$cdf()`
- `Dist$rng()`
- `Dist$link()`
- `Dist$invlink()`
- `Dist$npar()`
- `Dist$parnames()`
- `Dist$parapprox()`
- `Dist$fixed()`
- `Dist$code()`
- `Dist$name_long()`
- `Dist$set_npar()`
- `Dist$set_parnames()`
- `Dist$set_code()`
- `Dist$pdf_apply()`
- `Dist$rng_apply()`
- `Dist$par_alt()`
- `Dist$n2w()`
- `Dist$w2n()`
- `Dist$clone()`

Method `new()`: Create a Dist object

Usage:

```
Dist$new(  
  name,  
  pdf,  
  rng,  
  cdf = NULL,  
  link,  
  invlink,
```

```

    npar,
    parnames,
    parapprox = NULL,
    fixed = NULL,
    name_long = name,
    par_alt = NULL
  )

```

Arguments:

`name` Name of distribution

`pdf` Probability density/mass function of the distribution (e.g. `dnorm` for normal distribution).

`rng` Random generator function of the distribution (e.g. `rnorm` for normal distribution).

`cdf` Cumulative distribution function of the distribution (e.g., `pnorm` for normal distribution).

This is used to compute pseudo-residuals.

`link` Named list of link functions for distribution parameters

`invlink` Named list of inverse link functions for distribution parameters

`npar` Number of parameters of the distribution

`parnames` Character vector with name of each parameter

`parapprox` Function that takes a sample and produces approximate values for the unknown parameters

`fixed` Vector with element for each parameter which is TRUE if parameter is fixed

`name_long` Long version of the name of the distribution, possibly more user-readable than `name`.

`par_alt` Function that takes a vector of the distribution parameters as input and returns them in a different format. Only relevant for some distributions (e.g., MVN, where the SDs and correlations can be reformatted into a covariance matrix)

Returns: A new `Dist` object

Method `name()`: Return name of `Dist` object

Usage:

```
Dist$name()
```

Method `pdf()`: Return pdf of `Dist` object

Usage:

```
Dist$pdf()
```

Method `cdf()`: Return cdf of `Dist` object

Usage:

```
Dist$cdf()
```

Method `rng()`: Return random generator function of `Dist` object

Usage:

```
Dist$rng()
```

Method `link()`: Return link function of `Dist` object

Usage:

Dist\$link()

Method invlink(): Return inverse link function of Dist object

Usage:

Dist\$invlink()

Method npar(): Return number of parameters of Dist object

Usage:

Dist\$npar()

Method parnames(): Return names of parameters

Usage:

Dist\$parnames()

Method parapprox(): Return function that approximates parameters

Usage:

Dist\$parapprox()

Method fixed(): Return which parameters are fixed

Usage:

Dist\$fixed()

Method code(): Return code of Dist object

Usage:

Dist\$code()

Method name_long(): Human-readable name of Dist object

Usage:

Dist\$name_long()

Method set_npar(): Set number of parameters this distribution has

Usage:

Dist\$set_npar(new_npar)

Arguments:

new_npar Number of parameters

Method set_parnames(): Set parameter names

Usage:

Dist\$set_parnames(new_parnames)

Arguments:

new_parnames Parameter names

Method set_code(): Set distribution code

Usage:

Dist\$set_code(new_code)

Arguments:

`new_code` Distribution code

Method `pdf_apply()`: Evaluate probability density/mass function

This method is used in the `Dist$obs_probs()` method. It is a wrapper around `Dist$pdf()`, which prepares the parameters and passes them to the function.

Usage:

```
Dist$pdf_apply(x, par, log = FALSE)
```

Arguments:

`x` Value at which the function should be evaluated

`par` Vector of parameters. The entries should be named if they are not in the same order as expected by the R function. (E.g. shape/scale rather than shape/rate for gamma distribution.)

`log` Logical. If TRUE, the log-density is returned. Default: FALSE.

Returns: Probability density/mass function evaluated at `x` for parameters `par`

Method `rng_apply()`: Random number generator

This method is a wrapper around `Dist$rng()`, which prepares the parameters and passes them to the function.

Usage:

```
Dist$rng_apply(n, par)
```

Arguments:

`n` Number of realisations to generate

`par` Vector of parameters. The entries should be named if they are not in the same order as expected by the R function. (E.g. shape/scale rather than shape/rate for gamma distribution.)

Returns: Vector of `n` realisations of this distribution

Method `par_alt()`: Alternative parameter formatting*Usage:*

```
Dist$par_alt(par)
```

Arguments:

`par` Vector of distribution parameters

Returns: Formatted parameters

Method `n2w()`: Natural to working parameter transformation

This method transforms parameters from the natural scale (i.e., their domain of definition) to the "working" or "linear predictor" scale (i.e., the real line). It is a wrapper for `Dist$link()`.

Usage:

```
Dist$n2w(par)
```

Arguments:

`par` List of parameters

Returns: Vector of parameters on the working scale

Method w2n(): Working to natural parameter transformation

This method transforms parameters from the "working" or "linear predictor" scale (i.e., the real line) to the natural scale (i.e., their domain of definition). It is a wrapper for `Dist$invlink()`.

Usage:

```
Dist$w2n(wpar, as_matrix = FALSE)
```

Arguments:

`wpar` Vector of working parameters

`as_matrix` Logical. If TRUE, the natural parameters are returned as a matrix with one row for each state and one column for each parameter. If FALSE, the natural parameters are returned as a list (default).

Returns: List or matrix of parameters on natural scale

Method clone(): The objects of this class are cloneable with this method.

Usage:

```
Dist$clone(deep = FALSE)
```

Arguments:

`deep` Whether to make a deep clone.

dvm

Density function of von Mises distribution

Description

Density function of von Mises distribution

Usage

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

Arguments

<code>x</code>	Angle
<code>mu</code>	Mean parameter
<code>kappa</code>	Concentration parameter
<code>log</code>	Should log-density be returned?

Value

Von Mises density

dwrpcauchy	<i>Density function of wrapped Cauchy distribution</i>
------------	--

Description

Density function of wrapped Cauchy distribution

Usage

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

Arguments

x	Angle
mu	Mean parameter
rho	Concentration parameter
log	Should log-density be returned?

Value

Wrapped Cauchy density

find_re	<i>Find s(, $bs = "re"$) terms in formula</i>
---------	---

Description

This function is used to identify the variables "x" which are included as $s(x, bs = "re")$ in the formula, in particular to check that they are factors.

Usage

```
find_re(form)
```

Arguments

form	Model formula
------	---------------

Value

Vector of names of variables for which a random effect term is included in the model.

gdeterminant	<i>Generalized matrix determinant</i>
--------------	---------------------------------------

Description

Generalized determinant = product of non-zero eigenvalues (see e.g., Wood 2017). Used for (log)determinant of penalty matrices, required in log-likelihood function.

Usage

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

Arguments

x	Numeric matrix
eps	Threshold below which eigenvalues are ignored (default: 1e-10)
log	Logical: should the log-determinant be returned?

Value

Generalized determinant of input matrix

HMM	<i>R6 class for hidden Markov model</i>
-----	---

Description

Encapsulates the observation and hidden state models for a hidden Markov model.

Methods**Public methods:**

- [HMM\\$new\(\)](#)
- [HMM\\$obs\(\)](#)
- [HMM\\$hid\(\)](#)
- [HMM\\$out\(\)](#)
- [HMM\\$tmb_obj\(\)](#)
- [HMM\\$tmb_obj_joint\(\)](#)
- [HMM\\$tmb_rep\(\)](#)
- [HMM\\$states\(\)](#)
- [HMM\\$coeff_fe\(\)](#)
- [HMM\\$coeff_re\(\)](#)
- [HMM\\$coeff_list\(\)](#)

- `HMM$fixpar()`
- `HMM$coeff_array()`
- `HMM$lambda()`
- `HMM$update_par()`
- `HMM$sd_re()`
- `HMM$par()`
- `HMM$set_priors()`
- `HMM$priors()`
- `HMM$iters()`
- `HMM$out_stan()`
- `HMM$llk()`
- `HMM$edf()`
- `HMM$suggest_initial()`
- `HMM$setup()`
- `HMM$fit_stan()`
- `HMM$fit()`
- `HMM$mle()`
- `HMM$forward_backward()`
- `HMM$pseudores()`
- `HMM$viterbi()`
- `HMM$sample_states()`
- `HMM$state_probs()`
- `HMM$post_coeff()`
- `HMM$post_linpred()`
- `HMM$post_fn()`
- `HMM$predict()`
- `HMM$confint()`
- `HMM$simulate()`
- `HMM$check()`
- `HMM$plot_ts()`
- `HMM$plot_dist()`
- `HMM$plot()`
- `HMM$AIC_marginal()`
- `HMM$AIC_conditional()`
- `HMM$print_obspar()`
- `HMM$print_tpm()`
- `HMM$formulation()`
- `HMM$print()`
- `HMM$clone()`

Method `new()`: Create new HMM object

Usage:

```
HMM$new(obs = NULL, hid = NULL, file = NULL, init = NULL, fixpar = NULL)
```

Arguments:

obs Observation object, created with `Observation$new()`. This contains the formulation for the observation model.

hid MarkovChain object, created with `MarkovChain$new()`. This contains the formulation for the state process model.

file Path to specification file for HMM. If this argument is used, then **obs** and **hid** are unnecessary.

init HMM object, used to initialise the parameters for this model. If **init** is passed, then all parameters that are included in **init** and in the present model are copied. This may be useful when fitting increasingly complex models: start from a simple model, then pass it as **init** to create a more complex model, and so on.

fixpar Named list, with optional elements: 'hid', 'obs', 'delta0', 'lambda_obs', and 'lambda_hid'. Each element is a named vector of parameters in `coeff_fe` that should either be fixed (if the corresponding element is set to NA) or estimated to a common value (using integers or factor levels). See examples in the vignettes, and check the TMB documentation to understand the inner workings (argument `map` of `TMB::MakeADFun()`).

Returns: A new HMM object

Examples:

```
# Load data set (included with R)
data(nottem)
data <- data.frame(temp = as.vector(t(nottem)))

# Create hidden state and observation models
hid <- MarkovChain$new(data = data, n_states = 2)
par0 <- list(temp = list(mean = c(40, 60), sd = c(5, 5)))
obs <- Observation$new(data = data, n_states = 2,
                      dists = list(temp = "norm"),
                      par = par0)

# Create HMM
hmm <- HMM$new(hid = hid, obs = obs)
```

Method `obs()`: Observation object for this model

Usage:

```
HMM$obs()
```

Method `hid()`: MarkovChain object for this model

Usage:

```
HMM$hid()
```

Method `out()`: Output of optimiser after model fitting

Usage:

```
HMM$out()
```

Method `tmb_obj()`: Model object created by TMB. This is the output of the TMB function `MakeADFun`, and it is a list including elements

fn Objective function
 gr Gradient function of fn
 par Vector of initial parameters on working scale

Usage:

HMM\$tmb_obj()

Method tmb_obj_joint(): Model object created by TMB for the joint likelihood of the fixed and random effects. This is the output of the TMB function MakeADFun, and it is a list including elements

fn Objective function
 gr Gradient function of fn
 par Vector of initial parameters on working scale

Usage:

HMM\$tmb_obj_joint()

Method tmb_rep(): Output of the TMB function sdreport, which includes estimates and standard errors for all model parameters.

Usage:

HMM\$tmb_rep()

Method states(): Vector of estimated states, after viterbi has been run

Usage:

HMM\$states()

Method coeff_fe(): Coefficients for fixed effect parameters

Usage:

HMM\$coeff_fe()

Method coeff_re(): Coefficients for random effect parameters

Usage:

HMM\$coeff_re()

Method coeff_list(): List of all model coefficients

These are the parameters estimated by the model, including fixed and random effect parameters for the observation parameters and the transition probabilities, (transformed) initial probabilities, and smoothness parameters.

Usage:

HMM\$coeff_list()

Method fixpar(): Fixed parameters

Usage:

HMM\$fixpar(all = FALSE)

Arguments:

all Logical. If FALSE, only user-specified fixed parameters are returned, but not parameters that are fixed by definition (e.g., size of binomial distribution).

Method `coeff_array()`: Array of working parameters

Usage:

`HMM$coeff_array()`

Method `lambda()`: Smoothness parameters

Usage:

`HMM$lambda()`

Method `update_par()`: Update parameters stored inside model object

Usage:

`HMM$update_par(par_list = NULL, iter = NULL)`

Arguments:

`par_list` List with elements for `coeff_fe_obs`, `coeff_fe_hid`, `coeff_re_obs`, `coeff_re_hid`, `log_delta0`, `log_lambda_hid`, and `log_lambda_obs`

`iter` Optional argument to update model parameters based on MCMC iterations (if using `rstan`). Either the index of the iteration to use, or "mean" if the posterior mean should be used.

Method `sd_re()`: Standard deviation of smooth terms (or random effects)

This function transforms the smoothness parameter of each smooth term into a standard deviation, given by $SD = 1/\sqrt{\lambda}$. It is particularly helpful to get the standard deviations of independent normal random effects.

Usage:

`HMM$sd_re()`

Returns: List of standard deviations for observation model and hidden state model.

Method `par()`: Model parameters

Usage:

`HMM$par(t = 1)`

Arguments:

`t` returns parameters at time `t`, default is `t = 1`

Returns: A list with elements:

`obspar` Parameters of observation model

`tpm` Transition probability matrix of hidden state model

Method `set_priors()`: Set priors for coefficients

Usage:

`HMM$set_priors(new_priors = NULL)`

Arguments:

`new_priors` is a named list of matrices with optional elements `coeff_fe_obs`, `coeff_fe_hid`, `log_lambda_obs`, and `log_lambda_hid`. Each matrix has two columns (first col = mean, second col = sd) specifying parameters for normal priors.

Method `priors()`: Extract stored priors

Usage:

HMM\$priors()

Method `iters()`: Iterations from stan MCMC fit

Usage:

HMM\$iters(type = "response")

Arguments:

type Either "response" for parameters on the response (natural) scale, or "raw" for parameters on the linear predictor scale.

Returns: see output of `as.matrix` in stan

Method `out_stan()`: fitted stan object from MCMC fit

Usage:

HMM\$out_stan()

Returns: the stanfit object

Method `llk()`: Log-likelihood at current parameters

Usage:

HMM\$llk()

Returns: Log-likelihood

Method `edf()`: Effective degrees of freedom

Usage:

HMM\$edf()

Returns: Number of effective degrees of freedom (accounting for flexibility in non-parametric terms implied by smoothing)

Method `suggest_initial()`: Suggest initial parameter values

Uses K-means clustering to split the data into naive "states", and estimates observation parameters within each of these states. This is meant to help with selecting initial parameter values before model fitting, but users should still think about the values carefully, and try multiple set of initial parameter values to ensure convergence to the global maximum of the likelihood function.

Usage:

HMM\$suggest_initial()

Returns: List of initial parameters

Method `setup()`: TMB setup

This creates an attribute `tmb_obj`, which can be used to evaluate the negative log-likelihood function.

Usage:

HMM\$setup(silent = TRUE)

Arguments:

silent Logical. If TRUE, all tracing outputs are hidden (default).

Method `fit_stan()`: Fit model using `tmbstan`

Consult documentation of the `tmbstan` package for more information. After this method has been called, the Stan output can be accessed using the method `out_stan()`. This Stan output can for example be visualised using functions from the `rstan` package. The parameters stored in this HMM object are automatically updated to the mean posterior estimate, although this can be changed using `update_par()`.

Usage:

```
HMM$fit_stan(..., silent = FALSE)
```

Arguments:

... Arguments passed to `tmbstan`

`silent` Logical. If `FALSE`, all tracing outputs are shown (default).

Method `fit()`: Model fitting

The negative log-likelihood of the model is minimised using the function `nlminb()`. TMB uses the Laplace approximation to integrate the random effects out of the likelihood.

After the model has been fitted, the output of `nlminb()` can be accessed using the method `out()`. The estimated parameters can be accessed using the methods `par()` (for the HMM parameters, possibly dependent on covariates), `predict()` (for uncertainty quantification and prediction of the HMM parameters for new covariate values), `coeff_fe()` (for estimated fixed effect coefficients on the linear predictor scale), and `coeff_re()` (for estimated random effect coefficients on the linear predictor scale).

Usage:

```
HMM$fit(silent = FALSE, ...)
```

Arguments:

`silent` Logical. If `FALSE`, all tracing outputs are shown (default).

... Other arguments to `nlminb` which is used to optimise the likelihood. This currently only supports the additional argument `control`, which is a list of control parameters such as `eval.max` and `iter.max` (see `?nlminb`)

Examples:

```
# Load data set (included with R)
data(nottem)
data <- data.frame(temp = as.vector(t(nottem)))

# Create hidden state and observation models
hid <- MarkovChain$new(data = data, n_states = 2)
par0 <- list(temp = list(mean = c(40, 60), sd = c(5, 5)))
obs <- Observation$new(data = data, n_states = 2,
                      dists = list(temp = "norm"),
                      par = par0)

# Create HMM
hmm <- HMM$new(hid = hid, obs = obs)

# Fit HMM
hmm$fit(silent = TRUE)
```

Method `mle()`: Get maximum likelihood estimates once model fitted

Usage:

`HMM$mle()`

Returns: list of maximum likelihood estimates as described as input for the function `update_par()`

Method `forward_backward()`: Forward-backward algorithm

The forward probability for time step t and state j is the joint pdf/pmf of observations up to time t and of being in state j at time t , $p(Z[1], Z[2], \dots, Z[t], S[t] = j)$. The backward probability for time t and state j is the conditional pdf/pmf of observations between time $t + 1$ and n , given state j at time t , $p(Z[t+1], Z[t+2], \dots, Z[n] \mid S[t] = j)$. This function returns their logarithm, for use in other methods `state_probs`, and `sample_states`.

Usage:

`HMM$forward_backward()`

Returns: Log-forward and log-backward probabilities

Method `pseudores()`: Pseudo-residuals

Compute pseudo-residuals for the fitted model. If the fitted model is the "true" model, the pseudo-residuals follow a standard normal distribution. Deviations from normality suggest lack of fit.

Usage:

`HMM$pseudores()`

Returns: List (of length the number of variables), where each element is a vector of pseudo-residuals (of length the number of data points)

Method `viterbi()`: Viterbi algorithm

Usage:

`HMM$viterbi()`

Returns: Most likely state sequence

Method `sample_states()`: Sample posterior state sequences using forward-filtering backward-sampling

The forward-filtering backward-sampling algorithm returns a sequence of states, similarly to the Viterbi algorithm, but it generates it from the posterior distribution of state sequences, i.e., accounting for uncertainty in the state classification. Multiple generated sequences will therefore generally not be the same.

Usage:

`HMM$sample_states(nsamp = 1, full = FALSE)`

Arguments:

`nsamp` Number of samples to produce

`full` If TRUE and model fit by `fit_stan` then parameter estimates are sampled from the posterior samples before simulating each sequence

Returns: Matrix where each column is a different sample of state sequences, and each row is a time of observation

Method `state_probs()`: Compute posterior probability of being in each state

Usage:

`HMM$state_probs()`

Returns: matrix with a row for each observation and a column for each state

Method `post_coeff()`: Posterior sampling for model coefficients

Usage:

`HMM$post_coeff(n_post)`

Arguments:

`n_post` Number of posterior samples

Returns: Matrix with one column for each coefficient and one row for each posterior draw

Method `post_linpred()`: Posterior sampling for linear predictor

Usage:

`HMM$post_linpred(n_post)`

Arguments:

`n_post` Number of posterior samples

Returns: List with elements `obs` and `hid`, where each is a matrix with one column for each predictor and one row for each posterior draw

Method `post_fn()`: Create posterior simulations of a function of a model component

Usage:

`HMM$post_fn(fn, n_post, comp = NULL, ..., level = 0, return_post = FALSE)`

Arguments:

`fn` Function which takes a vector of linear predictors as input and produces either a scalar or vector output

`n_post` Number of posterior simulations

`comp` Either "obs" for observation model linear predictor, or "hid" for hidden model linear predictor

`...` Arguments passed to `fn`

`level` Confidence interval level if required (e.g., 0.95 for 95 confidence intervals). Default is 0, i.e., confidence intervals are not returned.

`return_post` Logical indicating whether to return the posterior samples. If FALSE (default), only mean estimates and confidence intervals are returned

Returns: A list with elements:

post If `return_post = TRUE`, this is a vector (for scalar outputs of `fn`) or matrix (for vector outputs) with a column for each simulation

mean Mean over posterior samples

lcl Lower confidence interval bound (if `level != 0`)

ucl Upper confidence interval bound (if `level != 0`)

Method `predict()`: Predict estimates from a fitted model

By default, this returns point estimates of the HMM parameters for a new data frame of covariates. See the argument '`n_post`' to also get confidence intervals.

Usage:

```
HMM$predict(
  what,
  t = 1,
  newdata = NULL,
  n_post = 0,
  level = 0.95,
  return_post = FALSE,
  as_list = TRUE
)
```

Arguments:

what Which estimates to predict? Options include transition probability matrices "tpm", stationary distributions "delta", or observation distribution parameters "obspar"

t Time points to predict at

newdata New dataframe to use for prediction

n_post If greater than zero then n_post posterior samples are produced, and used to create confidence intervals.

level Level of the confidence intervals, e.g. CI = 0.95 will produce 95% confidence intervals (default)

return_post Logical. If TRUE, a list of posterior samples is returned.

as_list Logical. If confidence intervals are required for the transition probabilities or observation parameters, this argument determines whether the MLE, lower confidence limit and upper confidence limit are returned as separate elements in a list (if TRUE; default), or whether they are combined into a single array (if FALSE). Ignored if **what** = "delta" or if **n_post** = 0.

... Other arguments to the respective functions for `hid$tpm`, `hid$delta`, `obs$par`

Returns: Maximum likelihood estimates (mle) of predictions, and confidence limits (lcl and ucl) if requested. The format of the output depends on whether confidence intervals are required (specified through **n_post**), and on the argument **as_list**.

Examples:

```
# Load data set (included with R)
data(nottem)
data <- data.frame(temp = as.vector(t(nottem)))

# Create hidden state and observation models
hid <- MarkovChain$new(data = data, n_states = 2)
par0 <- list(temp = list(mean = c(40, 60), sd = c(5, 5)))
obs <- Observation$new(data = data, n_states = 2,
  dists = list(temp = "norm"),
  par = par0)

# Create HMM
hmm <- HMM$new(hid = hid, obs = obs)

# Fit HMM
hmm$fit(silent = TRUE)
```

```
# Get transition probability matrix with confidence intervals
hmm$predict(what = "tpm", n_post = 1000)
```

Method `confint()`: Confidence intervals for working parameters

This function computes standard errors for all fixed effect model parameters based on the diagonal of the inverse of the Hessian matrix, and then derives Wald-type confidence intervals.

Usage:

```
HMM$confint(level = 0.95)
```

Arguments:

`level` Level of confidence intervals. Defaults to 0.95, i.e., 95% confidence intervals.

Returns: List of matrices with three columns: mle (maximum likelihood estimate), lcl (lower confidence limit), ucl (upper confidence limit), and se (standard error). One such matrix is produced for the working parameters of the observation model, the working parameters of the hidden state model, the smoothness parameters of the observation model, and the smoothness parameters of the hidden state model.

Method `simulate()`: Simulate from hidden Markov model

Usage:

```
HMM$simulate(n, data = NULL, silent = FALSE)
```

Arguments:

`n` Number of time steps to simulate

`data` Optional data frame including covariates

`silent` if TRUE then no messages are printed

Returns: Data frame including columns of data (if provided), and simulated data variables

Method `check()`: Compute goodness-of-fit statistics using simulation

Many time series are simulated from the fitted model, and the statistic(s) of interest are calculated for each. A histogram of those values can for example be used to compare to the observed value of the statistic. An observation far in the tails of the distribution of simulated statistics suggests lack of fit.

Usage:

```
HMM$check(check_fn, nsims = 100, full = FALSE, silent = FALSE)
```

Arguments:

`check_fn` Goodness-of-fit function which accepts "data" as input and returns a statistic (either a vector or a single number) to be compared between observed data and simulations.

`nsims` Number of simulations to perform

`full` If model fitted with 'fit_stan', then `full = TRUE` will sample from posterior for each simulation

`silent` Logical. If FALSE, simulation progress is shown. (Default: TRUE)

Returns: List with elements:

obs_stat: Vector of values of goodness-of-fit statistics for the observed data

stats: Matrix of values of goodness-of-fit statistics for the simulated data sets (one row for each statistic, and one column for each simulation)

plot: ggplot object

Method plot_ts(): Time series plot coloured by states

Creates a plot of the data coloured by the most likely state sequence, as estimated by the Viterbi algorithm. If one variable name is passed as input, it is plotted against time. If two variables are passed, they are plotted against each other.

Usage:

```
HMM$plot_ts(var, var2 = NULL, line = TRUE)
```

Arguments:

var Name of the variable to plot.

var2 Optional name of a second variable, for 2-d plot.

line Logical. If TRUE (default), lines are drawn between successive data points. Can be set to FALSE if another geom is needed (e.g., geom_point).

Returns: A ggplot object

Method plot_dist(): Plot observation distributions weighted by frequency in Viterbi

This is a wrapper around Observation\$plot_dist, where the distribution for each state is weighted by the proportion of time spent in that state (according to the Viterbi state sequence).

Usage:

```
HMM$plot_dist(var = NULL)
```

Arguments:

var Name of data variable. If NULL, a list of plots are returned (one for each observation variable)

Returns: Plot of distributions with data histogram

Method plot(): Plot a model component

Usage:

```
HMM$plot(
  what,
  var = NULL,
  covs = NULL,
  i = NULL,
  j = NULL,
  n_grid = 50,
  n_post = 1000
)
```

Arguments:

what Name of model component to plot: should be one of "tpm" (transition probabilities), "delta" (stationary state probabilities), or "obspar" (state-dependent observation parameters)

var Name of covariate to plot on x-axis

covs Optional named list for values of covariates (other than 'var') that should be used in the plot (or dataframe with single row). If this is not specified, the mean value is used for numeric variables, and the first level for factor variables.

- i If plotting tpm then rows of tpm; if plotting delta then indices of states to plot; if plotting obspar then full names of parameters to plot (e.g., obsvar.mean)
- j If plotting tpm then columnss of tpm to plot; if plotting delta then this is ignored.; if plotting obspar then indices of states to plot
- n_grid Number of points in grid over x-axis (default: 50)
- n_post Number of posterior simulations to use when computing confidence intervals; default: 1000. See predict function for more detail.

Returns: A ggplot object

Method `AIC_marginal()`: Marginal Akaike Information Criterion

The marginal AIC is for example defined by Wood (2017), as $AIC = -2L + 2k$ where L is the maximum marginal log-likelihood (of fixed effects), and k is the number of degrees of freedom of the fixed effect component of the model

Usage:

`HMM$AIC_marginal()`

Returns: Marginal AIC

Method `AIC_conditional()`: Conditional Akaike Information Criterion

The conditional AIC is for example defined by Wood (2017), as $AIC = -2L + 2k$ where L is the maximum joint log-likelihood (of fixed and random effects), and k is the number of effective degrees of freedom of the model (accounting for flexibility in non-parametric terms implied by smoothing)

Usage:

`HMM$AIC_conditional()`

Returns: Conditional AIC

Method `print_obspar()`: Print observation parameters at $t = 1$

Usage:

`HMM$print_obspar()`

Method `print_tpm()`: Print observation parameters at $t = 1$

Usage:

`HMM$print_tpm()`

Method `formulation()`: Print model formulation

Usage:

`HMM$formulation()`

Method `print()`: Print HMM object

Usage:

`HMM$print()`

Method `clone()`: The objects of this class are cloneable with this method.

Usage:

`HMM$clone(deep = FALSE)`

Arguments:

deep Whether to make a deep clone.

Examples

```

## -----
## Method `HMM$new`
## -----

# Load data set (included with R)
data(nottem)
data <- data.frame(temp = as.vector(t(nottem)))

# Create hidden state and observation models
hid <- MarkovChain$new(data = data, n_states = 2)
par0 <- list(temp = list(mean = c(40, 60), sd = c(5, 5)))
obs <- Observation$new(data = data, n_states = 2,
                      dists = list(temp = "norm"),
                      par = par0)

# Create HMM
hmm <- HMM$new(hid = hid, obs = obs)

## -----
## Method `HMM$fit`
## -----

# Load data set (included with R)
data(nottem)
data <- data.frame(temp = as.vector(t(nottem)))

# Create hidden state and observation models
hid <- MarkovChain$new(data = data, n_states = 2)
par0 <- list(temp = list(mean = c(40, 60), sd = c(5, 5)))
obs <- Observation$new(data = data, n_states = 2,
                      dists = list(temp = "norm"),
                      par = par0)

# Create HMM
hmm <- HMM$new(hid = hid, obs = obs)

# Fit HMM
hmm$fit(silent = TRUE)

## -----
## Method `HMM$predict`
## -----

# Load data set (included with R)
data(nottem)
data <- data.frame(temp = as.vector(t(nottem)))

# Create hidden state and observation models
hid <- MarkovChain$new(data = data, n_states = 2)
par0 <- list(temp = list(mean = c(40, 60), sd = c(5, 5)))
obs <- Observation$new(data = data, n_states = 2,

```



```

                                dists = list(temp = "norm"),
                                par = par0)

# Create HMM
hmm <- HMM$new(hid = hid, obs = obs)

# Fit HMM
hmm$fit(silent = TRUE)

# Get transition probability matrix with confidence intervals
hmm$predict(what = "tpm", n_post = 1000)
```

hmmTMB_cols	<i>hmmTMB colour palette</i>
-------------	------------------------------

Description

hmmTMB colour palette

Usage

hmmTMB_cols

Format

An object of class character of length 6.

invmlgit	<i>Multivariate inverse logit function</i>
----------	--

Description

Multivariate inverse logit function

Usage

invmlgit(x)

Arguments

x Numeric vector

is_whole_number	<i>Check if number of whole number</i>
-----------------	--

Description

Check if number of whole number

Usage

```
is_whole_number(x, tol = 1e-10)
```

Arguments

x	number to check or vector of numbers
tol	how far away from whole number is ok?

Value

TRUE if it is a whole number within tolerance

logLik.HMM	<i>logLik function for SDE objects</i>
------------	--

Description

This function makes it possible to call generic R methods such as AIC and BIC on HMM objects. It is based on the number of degrees of freedom of the *conditional* AIC (rather than marginal AIC), i.e., including degrees of freedom from the smooth/random effect components of the model.

Usage

```
## S3 method for class 'HMM'
logLik(object, ...)
```

Arguments

object	HMM model object
...	For compatibility with S3 method

Value

Maximum log-likelihood value for the model, with attributes df (degrees of freedom) and nobs (number of observations)

logsumexp	<i>Log of sum of exponentials</i>
-----------	-----------------------------------

Description

Log of sum of exponentials

Usage

```
logsumexp(x)
```

Arguments

x	Numeric vector
---	----------------

make_cov	<i>Make covariance matrix from standard deviations and correlations</i>
----------	---

Description

Make covariance matrix from standard deviations and correlations

Usage

```
make_cov(sds, corr)
```

Arguments

sds	Vector of standard deviations
corr	Vector of correlations (must be of length $m*(m-1)/2$ if sds is of length m)

Value

An m by m covariance matrix

make_formulas

Process formulas and store in nested list

Description

Process formulas and store in nested list

Usage

```
make_formulas(input_forms, var_names, par_names, n_states)
```

Arguments

input_forms	Nested list of formulas, with two levels: observed variable, and parameter of the observation distribution. The formulas can contain state-specific terms, e.g. " $\sim \text{state1}(x1) + x2$ ".
var_names	character vector name of each observation variable
par_names	list with element for each observation variable that contains character vector of name of each parameter in its distribution
n_states	Number of states

Details

Formulas for the observation parameters can be different for the different states, using special functions of the form "state1", "state2", etc. This method processes the list of formulas passed by the user to extract the state-specific formulas. Missing formulas are assumed to be intercept-only ~ 1 .

Value

Nested list of formulas, with three levels: observed variable, parameter of the observation distribution, and state.

Examples

```
input_forms <- list(step = list(shape = ~ state1(x1) + x2,
                                scale = ~ x1),
                    count = list(lambda = ~ state1(x1) + state2(s(x2, bs = "cs"))))

make_formulas(input_forms = input_forms,
              var_names = names(input_forms),
              par_names = lapply(input_forms, names),
              n_states = 2)
```

make_matrices	<i>Create model matrices</i>
---------------	------------------------------

Description

Create model matrices

Usage

```
make_matrices(formulas, data, new_data = NULL, gam_args = NULL)
```

Arguments

formulas	List of formulas (possibly nested, e.g. for use within Observation)
data	Data frame including covariates
new_data	Optional new data set, including covariates for which the design matrices should be created. This needs to be passed in addition to the argument 'data', for cases where smooth terms or factor covariates are included, and the original data set is needed to determine the full range of covariate values.
gam_args	Named list of additional arguments for <code>mgcv::gam()</code> , such as knots.

Value

A list of

- X_fe Design matrix for fixed effects
- X_re Design matrix for random effects
- S Smoothness matrix
- log_det_S Vector of log-determinants of smoothness matrices
- ncol_fe Number of columns of X_fe for each parameter
- ncol_re Number of columns of X_re and S for each random effect

MarkovChain	<i>R6 class for HMM hidden process model</i>
-------------	--

Description

Contains the parameters and model formulas for the hidden process model.

Methods**Public methods:**

- `MarkovChain$new()`
- `MarkovChain$formula()`
- `MarkovChain$formulas()`
- `MarkovChain$tpm()`
- `MarkovChain$ref()`
- `MarkovChain$ref_mat()`
- `MarkovChain$ref_delta0()`
- `MarkovChain$coeff_fe()`
- `MarkovChain$delta()`
- `MarkovChain$delta0()`
- `MarkovChain$stationary()`
- `MarkovChain$fixpar()`
- `MarkovChain$coeff_re()`
- `MarkovChain$X_fe()`
- `MarkovChain$X_re()`
- `MarkovChain$lambda()`
- `MarkovChain$sd_re()`
- `MarkovChain$nstates()`
- `MarkovChain$terms()`
- `MarkovChain$unique_ID()`
- `MarkovChain$initial_state()`
- `MarkovChain$empty()`
- `MarkovChain$gam_args()`
- `MarkovChain$update_tpm()`
- `MarkovChain$update_coeff_fe()`
- `MarkovChain$update_coeff_re()`
- `MarkovChain$update_X_fe()`
- `MarkovChain$update_X_re()`
- `MarkovChain$update_delta0()`
- `MarkovChain$update_lambda()`
- `MarkovChain$update_fixpar()`
- `MarkovChain$make_mat()`
- `MarkovChain$make_mat_grid()`
- `MarkovChain$tpm2par()`
- `MarkovChain$par2tpm()`
- `MarkovChain$linpred()`
- `MarkovChain$simulate()`
- `MarkovChain$formulation()`
- `MarkovChain$print()`
- `MarkovChain$clone()`

Method `new()`: Create new MarkovChain object

Usage:

```
MarkovChain$new(
  data = NULL,
  formula = NULL,
  n_states,
  tpm = NULL,
  initial_state = "estimated",
  fixpar = NULL,
  ref = 1:n_states,
  gam_args = NULL
)
```

Arguments:

`data` Data frame, needed to create model matrices, and to identify the number of time series (which each have a separate initial distribution)

`formula` Either (1) R formula, used for all transition probabilities, or (2) matrix of character strings giving the formula for each transition probability, with "." along the diagonal (or for reference elements; see `ref` argument). (Default: no covariate dependence.)

`n_states` Number of states. If not specified, then `formula` needs to be provided as a matrix, and `n_states` is deduced from its dimensions.

`tpm` Optional transition probability matrix, to initialise the model parameters (intercepts in model with covariates). If not provided, the default is a matrix with 0.9 on the diagonal.

`initial_state` Specify model for initial state distribution. There are five different options:

- "estimated": a separate initial distribution is estimated for each ID (default)
- "stationary": the initial distribution is fixed to the stationary distribution of the transition probability matrix for the first time point of each ID
- "shared": a common initial distribution is estimated for all IDs
- integer value between 1 and `n_states`: used as the known initial state for all IDs
- vector of integers between 1 and `n_states` (of length the number of IDs): each element is used as the known initial state for the corresponding ID

`fixpar` List with optional elements "hid" (fixed parameters for transition probabilities), "lambda_hid" (fixed smoothness parameters), and "delta0" (fixed parameters for initial distribution). Each element is a named vector of coefficients that should either be fixed (if the corresponding element is set to NA) or estimated to a common value (using integers or factor levels).

`ref` Vector of indices for reference transition probabilities, of length `n_states`. The *i*-th element is the index for the reference in the *i*-th row of the transition probability matrix. For example, `ref = c(1, 1)` means that the first element of the first row $\Pr(1>1)$ and the first element of the second row $\Pr(2>1)$ are used as reference elements and are not estimated. If this is not provided, the diagonal transition probabilities are used as references.

`gam_args` Named list of arguments passed to `mgcv::gam()` in `MarkovChain$make_mat()`, e.g., "knots". Use at your own risk.

Returns: A new MarkovChain object

Examples:

```
# Load data set from MSwM package
data(energy, package = "MSwM")
```

```
# Create 2-state covariate-free model and initialise transition
# probability matrix
hid <- MarkovChain$new(data = energy, n_states = 2,
                      tpm = matrix(c(0.8, 0.3, 0.2, 0.7), 2, 2))

# Create 2-state model with non-linear effect of Oil on all transition
# probabilities
hid <- MarkovChain$new(data = energy, n_states = 2,
                      formula = ~ s(Oil, k = 5, bs = "cs"))

# Create 2-state model with quadratic effect of Oil on Pr(1 > 2)
structure <- matrix(c(".", "~poly(Oil, 2)",
                      "~1", "."),
                    ncol = 2, byrow = TRUE)
hid <- MarkovChain$new(data = energy, n_states = 2,
                      formula = structure)
```

Method formula(): Formula of MarkovChain model

Usage:

```
MarkovChain$formula()
```

Method formulas(): List of formulas for MarkovChain model

Usage:

```
MarkovChain$formulas()
```

Method tpm(): Get transition probability matrices

Usage:

```
MarkovChain$tpm(t = 1, linpred = NULL)
```

Arguments:

t Time index or vector of time indices; default = 1. If t = "all" then all transition probability matrices are returned.

linpred Optional custom linear predictor

Returns: Array with one slice for each transition probability matrix

Method ref(): Indices of reference elements in transition probability matrix

Usage:

```
MarkovChain$ref()
```

Method ref_mat(): Matrix of reference elements in transition probability matrix

Usage:

```
MarkovChain$ref_mat()
```

Method ref_delta0(): Indices of reference elements in initial distribution

Usage:

```
MarkovChain$ref_delta0()
```


Method `coeff_fe()`: Current parameter estimates (fixed effects)

Usage:

`MarkovChain$coeff_fe()`

Method `delta()`: Stationary distribution

Usage:

`MarkovChain$delta(t = NULL, linpred = NULL)`

Arguments:

`t` Time point(s) for which stationary distribution should be returned. If `t = "all"`, all deltas are returned; else this should be a vector of time indices. If `NULL` (default), the stationary distribution for the first time step is returned.

`linpred` Optional custom linear predictor

Returns: Matrix of stationary distributions. Each row corresponds to a row of the design matrices, and each column corresponds to a state.

Method `delta0()`: Initial distribution

Usage:

`MarkovChain$delta0(log = FALSE, as_matrix = TRUE)`

Arguments:

`log` Logical indicating whether to return the log of the initial probabilities (default: `FALSE`). If `TRUE`, then the last element is excluded, as it is not estimated.

`as_matrix` Logical indicating whether the output should be formatted as a matrix (default). If `as_matrix` is `FALSE` and `log` is `TRUE`, the result is formatted as a column vector.

Returns: Matrix with one row for each time series ID, and one column for each state. For each ID, the *i*-th element of the corresponding row is the probability $\Pr(S[1] = i)$

Method `stationary()`: Use stationary distribution as initial distribution?

Usage:

`MarkovChain$stationary()`

Method `fixpar()`: Fixed parameters

Usage:

`MarkovChain$fixpar(all = FALSE)`

Arguments:

`all` Logical. If `FALSE`, only user-specified fixed parameters are returned, but not parameters that are fixed for some other reason (e.g., from `'.'` in formula)

Method `coeff_re()`: Current parameter estimates (random effects)

Usage:

`MarkovChain$coeff_re()`

Method `X_fe()`: Fixed effect design matrix

Usage:

`MarkovChain$X_fe()`

Method `X_re()`: Random effect design matrix

Usage:

`MarkovChain$X_re()`

Method `lambda()`: Smoothness parameters

Usage:

`MarkovChain$lambda()`

Method `sd_re()`: Standard deviation of smooth terms

This function transforms the smoothness parameter of each smooth term into a standard deviation, given by $SD = 1/\sqrt{\lambda}$. It is particularly helpful to get the standard deviations of independent normal random effects.

Usage:

`MarkovChain$sd_re()`

Method `nstates()`: Number of states

Usage:

`MarkovChain$nstates()`

Method `terms()`: Terms of model formulas

Usage:

`MarkovChain$terms()`

Method `unique_ID()`: Number of time series

Usage:

`MarkovChain$unique_ID()`

Method `initial_state()`: Initial state (see constructor argument)

Usage:

`MarkovChain$initial_state()`

Method `empty()`: Empty model? (for simulation only)

Usage:

`MarkovChain$empty()`

Method `gam_args()`: Extra arguments for `mgcv::gam` (passed to `make_matrices`)

Usage:

`MarkovChain$gam_args()`

Method `update_tpm()`: Update transition probability matrix

Usage:

`MarkovChain$update_tpm(tpm)`

Arguments:

`tpm` New transition probability matrix

Method `update_coeff_fe()`: Update coefficients for fixed effect parameters

Usage:

`MarkovChain$update_coeff_fe(coeff_fe)`

Arguments:

`coeff_fe` Vector of coefficients for fixed effect parameters

Method `update_coeff_re()`: Update coefficients for random effect parameters

Usage:

`MarkovChain$update_coeff_re(coeff_re)`

Arguments:

`coeff_re` Vector of coefficients for random effect parameters

Method `update_X_fe()`: Update design matrix for fixed effects

Usage:

`MarkovChain$update_X_fe(X_fe)`

Arguments:

`X_fe` new design matrix for fixed effects

Method `update_X_re()`: Update design matrix for random effects

Usage:

`MarkovChain$update_X_re(X_re)`

Arguments:

`X_re` new design matrix for random effects

Method `update_delta0()`: Update initial distribution

Usage:

`MarkovChain$update_delta0(delta0)`

Arguments:

`delta0` Either a matrix where the i-th row is the initial distribution for the i-th time series in the data, or a vector which is then used for all time series. Entries of each row of `delta0` should sum to one.

Method `update_lambda()`: Update smoothness parameters

Usage:

`MarkovChain$update_lambda(lambda)`

Arguments:

`lambda` New smoothness parameter vector

Method `update_fixpar()`: Update information about fixed parameters

Usage:

`MarkovChain$update_fixpar(fixpar)`

Arguments:

`fixpar` New list of fixed parameters, in the same format expected by `MarkovChain$new()`

Method `make_mat()`: Make model matrices

Usage:

```
MarkovChain$make_mat(data, new_data = NULL)
```

Arguments:

`data` Data frame containing all needed covariates

`new_data` Optional new data set, including covariates for which the design matrices should be created. This needs to be passed in addition to the argument 'data', for cases where smooth terms or factor covariates are included, and the original data set is needed to determine the full range of covariate values.

Returns: A list with elements:

X_fe Design matrix for fixed effects

X_re Design matrix for random effects

S Smoothness matrix for random effects

ncol_fe Number of columns of X_fe for each parameter

ncol_re Number of columns of X_re and S for each random effect

Method `make_mat_grid()`: Design matrices for grid of covariates

Used in plotting functions such as `HMM$plot_tpm` and `HMM$plot_stat_dist`

Usage:

```
MarkovChain$make_mat_grid(var, data, covs = NULL, n_grid = 1000)
```

Arguments:

`var` Name of variable

`data` Data frame containing the covariates

`covs` Optional named list for values of covariates (other than 'var') that should be used in the plot (or dataframe with single row). If this is not specified, the mean value is used for numeric variables, and the first level for factor variables.

`n_grid` Grid size (number of points). Default: 1000.

Returns: A list with the same elements as the output of `make_mat`, plus a data frame of covariates values.

Method `tpm2par()`: Transform transition probabilities to working scale

Apply the multinomial logit link function to get the corresponding parameters on the working scale (i.e., linear predictor scale).

Usage:

```
MarkovChain$tpm2par(tpm)
```

Arguments:

`tpm` Transition probability matrix

Returns: Vector of parameters on linear predictor scale

Method `par2tpm()`: Transform working parameters to transition probabilities

Apply the inverse multinomial logit link function to transform the parameters on the working scale (i.e., linear predictor scale) into the transition probabilities.

Usage:

```
MarkovChain$par2tpm(par)
```

Arguments:

par Vector of parameters on working scale

Returns: Transition probability matrix

Method linpred(): Linear predictor for transition probabilities

Usage:

```
MarkovChain$linpred()
```

Method simulate(): Simulate from Markov chain

Usage:

```
MarkovChain$simulate(n, data = NULL, new_data = NULL, silent = FALSE)
```

Arguments:

n Number of time steps to simulate

data Optional data frame containing all needed covariates

new_data Optional new data set, including covariates for which the design matrices should be created. This needs to be passed in addition to the argument 'data', for cases where smooth terms or factor covariates are included, and the original data set is needed to determine the full range of covariate values.

silent if TRUE then no messages are printed

Returns: Sequence of states of simulated chain

Method formulation(): Print model formulation

Usage:

```
MarkovChain$formulation()
```

Method print(): Print MarkovChain object

Usage:

```
MarkovChain$print()
```

Method clone(): The objects of this class are cloneable with this method.

Usage:

```
MarkovChain$clone(deep = FALSE)
```

Arguments:

deep Whether to make a deep clone.

Examples

```
## -----
## Method `MarkovChain$new`
## -----

# Load data set from MSwM package
data(energy, package = "MSwM")
```

```
# Create 2-state covariate-free model and initialise transition
# probability matrix
hid <- MarkovChain$new(data = energy, n_states = 2,
                       tpm = matrix(c(0.8, 0.3, 0.2, 0.7), 2, 2))

# Create 2-state model with non-linear effect of Oil on all transition
# probabilities
hid <- MarkovChain$new(data = energy, n_states = 2,
                       formula = ~ s(Oil, k = 5, bs = "cs"))

# Create 2-state model with quadratic effect of Oil on Pr(1 > 2)
structure <- matrix(c(".", "~poly(Oil, 2)",
                       "~1", "."),
                    ncol = 2, byrow = TRUE)
hid <- MarkovChain$new(data = energy, n_states = 2,
                       formula = structure)
```

mlogit	<i>Multivariate logit function</i>
--------	------------------------------------

Description

Multivariate logit function

Usage

```
mlogit(x)
```

Arguments

x Numeric vector

mvnorm_invlink	<i>Multivariate Normal inverse link function</i>
----------------	--

Description

Multivariate Normal inverse link function

Usage

```
mvnorm_invlink(x)
```

Arguments

x Vector of parameters on linear predictor scale (in the order: means, SDs, correlations)

mvnorm_link	<i>Multivariate Normal link function</i>
-------------	--

Description

Multivariate Normal link function

Usage

```
mvnorm_link(x)
```

Arguments

x Vector of parameters on natural scale (in the order: means, SDs, correlations)

na_fill	<i>Fill in NAs</i>
---------	--------------------

Description

Replace NA entries in a vector by the last non-NA value. If the first entry of the vector is NA, it is replaced by the first non-NA value. If the vector passed as input doesn't contain NAs, it is returned as is.

Usage

```
na_fill(x)
```

Arguments

x Vector in which NAs should be removed

Value

Copy of x in which NAs have been replaced by nearest available value.

Observation

R6 class for HMM observation model

Description

Contains the data, distributions, parameters, and formulas for the observation model from a hidden Markov model.

Methods

Public methods:

- `Observation$new()`
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- `Observation$formulation()`
- `Observation$print()`
- `Observation$clone()`

Method `new()`: Create new Observation object

Usage:

```
Observation$new(
  data = NULL,
  dists,
  formulas = NULL,
  n_states = NULL,
  par,
  fixpar = NULL,
  gam_args = NULL
)
```

Arguments:

`data` Data frame containing response variables (named in `dists` and `par`) and covariates (named in `formulas`)

`dists` Named list of distribution names for each data stream, with the following options: `beta`, `binom`, `cat`, `dir`, `exp`, `foldednorm`, `gamma`, `gamma2`, `lnorm`, `mvnorm`, `nbinom`, `norm`, `pois`, `t`, `truncnorm`, `tweedie`, `vm`, `weibull`, `wrpcauchy`, `zibinom`, `zgamma`, `zgamma2`, `zinbinom`, `zipois`, `zoibeta`, `ztnbinom`, `ztpois`. See vignette about list of distributions for more details, e.g., list of parameters for each distribution.

`formulas` List of formulas for observation parameters. This should be a nested list, where the outer list has one element for each observed variable, and the inner lists have one element for each parameter. Any parameter that is not included is assumed to have the formula `~1`. By default, all parameters have the formula `~1` (i.e., no covariate effects).

`n_states` Number of states (optional). If not provided, the number of states is derived from the length of entries of `par`.

`par` List of initial observation parameters. This should be a nested list, where the outer list has one element for each observed variable, and the inner lists have one element for each parameter. The choice of good initial values can be important, especially for complex models; the package vignettes discuss approaches to selecting them (e.g., see `Observation$suggest_initial()`).

`fixpar` List with optional elements `"obs"` (fixed coefficients for observation parameters), and `"lambda_obs"` (fixed smoothness parameters). Each element is a named vector of coefficients that should either be fixed (if the corresponding element is set to `NA`) or estimated to a common value (using integers or factor levels).

`gam_args` Named list of arguments passed to `mgcv::gam()` in `Observation$make_mat()`, e.g., `"knots"`. Use at your own risk.

Returns: A new Observation object

Examples:

```
# Load data set from MSwM package
data(energy, package = "MSwM")

# Initial observation parameters
par0 <- list(Price = list(mean = c(3, 6), sd = c(2, 2)))

# Model "energy" with normal distributions
obs <- Observation$new(data = energy,
                      dists = list(Price = "norm"),
                      par = par0)

# Model "energy" with gamma distributions
obs <- Observation$new(data = energy,
                      dists = list(Price = "gamma2"),
                      par = par0)

# Model with non-linear effect of EurDol on mean price
f <- list(Price = list(mean = ~ s(EurDol, k = 5, bs = "cs")))
obs <- Observation$new(data = energy,
                      dists = list(Price = "norm"),
                      par = par0,
                      formula = f)
```

Method data(): Data frame

Usage:

```
Observation$data()
```

Method dists(): List of distributions

Usage:

```
Observation$dists()
```

Method nstates(): Number of states

Usage:

```
Observation$nstates()
```

Method par(): Parameters on natural scale

Usage:

```
Observation$par(t = 1, full_names = TRUE, linpred = NULL, as_list = FALSE)
```

Arguments:

t Time index or vector of time indices; default **t = 1**. If **t = "all"**, then return observation parameters for all time points.

full_names Logical. If **TRUE**, the rows of the output are named in the format "variable.parameter" (default). If **FALSE**, the rows are names in the format "parameter". The latter is used in various internal functions, when the parameters need to be passed on to an R function.

`linpred` Optional custom linear predictor.

`as_list` Logical. If TRUE, the output is a nested list with three levels: (1) time step, (2) observed variable, (3) observation parameter. If FALSE (default), the output is an array with one row for each observation parameter, one column for each state, and one slice for each time step.

Returns: Array of parameters with one row for each observation parameter, one column for each state, and one slice for each time step. (See `as_list` argument for alternative output format.)

Examples:

```
# Load data set from MSwM package
data(energy, package = "MSwM")

# Initial observation parameters
par0 <- list(Price = list(mean = c(3, 6), sd = c(2, 2)))

# Model with linear effect of EurDol on mean price
f <- list(Price = list(mean = ~ EurDol))
obs <- Observation$new(data = energy,
                      dists = list(Price = "norm"),
                      par = par0,
                      n_states = 2,
                      formula = f)

# Set slope coefficients
obs$update_coeff_fe(coeff_fe = c(3, 2, 6, -2, log(2), log(2)))

# Observation parameter values for given data rows
obs$par(t = c(1, 10, 20))
```

Method `par_alt()`: Alternative parameter output

This function is only useful for the categorical and multivariate normal distributions, and it formats the parameters in a slightly nicer way.

Usage:

```
Observation$par_alt(var = NULL, t = 1)
```

Arguments:

`var` Name of observation variable for which parameters are required. By default, the first variable in 'dists' is used.

`t` Time index for covariate values. Only one value should be provided.

Returns: List of distribution parameters, with one element for each state

Method `inipar()`: Return initial parameter values supplied

Usage:

```
Observation$inipar()
```

Method `coeff_fe()`: Fixed effect parameters on working scale

Usage:

Observation\$coeff_fe()

Method coeff_re(): Random effect parameters

Usage:

Observation\$coeff_re()

Method X_fe(): Fixed effect design matrix

Usage:

Observation\$X_fe()

Method X_re(): Random effect design matrix

Usage:

Observation\$X_re()

Method lambda(): Smoothness parameters

Usage:

Observation\$lambda()

Method sd_re(): Standard deviation of smooth terms

This function transforms the smoothness parameter of each smooth term into a standard deviation, given by $SD = 1/\sqrt{\lambda}$. It is particularly helpful to get the standard deviations of independent normal random effects.

Usage:

Observation\$sd_re()

Method formulas(): List of model formulas for observation model

Usage:

Observation\$formulas(raw = FALSE)

Arguments:

raw Logical. If FALSE, returns the nested list created by make_formulas (default). If TRUE, returns formulas passed as input.

Method terms(): Terms of model formulas

Usage:

Observation\$terms()

Method obs_var(): Data frame of response variables

Usage:

Observation\$obs_var(expand = FALSE)

Arguments:

expand If TRUE, then multivariate variables in observations are expanded to be univariate, creating extra columns.

Returns: Data frame of observation variables

Method known_states(): Vector of known states

Usage:

```
Observation$known_states(mat = TRUE)
```

Arguments:

mat Logical.

Method fixpar(): Fixed parameters*Usage:*

```
Observation$fixpar(all = FALSE)
```

Arguments:

all Logical. If FALSE, only user-specified fixed parameters are returned, but not parameters that are fixed for some other reason (e.g., size of binomial distribution)

Method empty(): Empty model? (for simulation only)*Usage:*

```
Observation$empty()
```

Method gam_args(): Extra arguments for mgcv::gam (passed to make_matrices)*Usage:*

```
Observation$gam_args()
```

Method update_par(): Update parameters

Updates the 'par' attribute to the list passed as input, and updates the intercept elements of 'coeff_fe' using the list passed as input

Usage:

```
Observation$update_par(par)
```

Arguments:

par New list of parameters

Method update_coeff_fe(): Update coefficients for fixed effect parameters*Usage:*

```
Observation$update_coeff_fe(coeff_fe)
```

Arguments:

coeff_fe New vector of coefficients for fixed effect parameters

Method update_coeff_re(): Update random effect parameters*Usage:*

```
Observation$update_coeff_re(coeff_re)
```

Arguments:

coeff_re New vector of coefficients for random effect parameters

Method update_X_fe(): Update fixed effect design matrix*Usage:*

```
Observation$update_X_fe(X_fe)
```

Arguments:

X_fe New fixed effect design matrix

Method update_X_re(): Update random effect design matrix

Usage:

Observation\$update_X_re(X_re)

Arguments:

X_re New random effect design matrix

Method update_lambda(): Update smoothness parameters

Usage:

Observation\$update_lambda(lambda)

Arguments:

lambda New smoothness parameter vector

Method update_data(): Update data

Usage:

Observation\$update_data(data)

Arguments:

data New data frame

Method update_fixpar(): Update information about fixed parameters

Usage:

Observation\$update_fixpar(fixpar)

Arguments:

fixpar New list of fixed parameters, in the same format expected by Observation\$new()

Method make_mat(): Make model matrices

Usage:

Observation\$make_mat(new_data = NULL)

Arguments:

new_data Optional new data set, including covariates for which the design matrices should be created. If this argument is not specified, the design matrices are based on the original data frame.

Returns: A list with elements:

X_fe Design matrix for fixed effects

X_re Design matrix for random effects

S Smoothness matrix for random effects

ncol_fe Number of columns of X_fe for each parameter

ncol_re Number of columns of X_re and S for each random effect

Method make_newdata_grid(): Design matrices for grid of covariates

Usage:

```
Observation$make_newdata_grid(var, covs = NULL, n_grid = 1000)
```

Arguments:

var Name of variable

covs Optional named list for values of covariates (other than 'var') that should be used in the plot (or dataframe with single row). If this is not specified, the mean value is used for numeric variables, and the first level for factor variables.

n_grid Grid size (number of points). Default: 1000.

Returns: A list with the same elements as the output of `make_mat`, plus a data frame of covariates values.

Method `n2w()`: Natural to working parameter transformation

This function applies the link functions of the distribution parameters, to transform parameters from their natural scale to the working scale (i.e., linear predictor scale)

Usage:

```
Observation$n2w(par)
```

Arguments:

par List of parameters on natural scale

Returns: Vector of parameters on working scale

Method `w2n()`: Working to natural parameter transformation

This function applies the inverse link functions of the distribution parameters, to transform parameters from the working scale (i.e., linear predictor scale) to their natural scale.

Usage:

```
Observation$w2n(wpar)
```

Arguments:

wpar Vector of parameters on working scale

Returns: List of parameters on natural scale

Method `linpred()`: Compute linear predictor

Usage:

```
Observation$linpred()
```

Method `obs_probs()`: Observation likelihoods

Usage:

```
Observation$obs_probs(data = NULL)
```

Arguments:

data Optional dataframe to include in form of `obs_var()` output

Returns: Matrix of likelihoods of observations, with one row for each time step, and one column for each state.

Method `cdf()`: Cumulative probabilities of observations

Usage:

```
Observation$cdf()
```

Returns: List of cumulative probabilities, with one element for each observed variable. Matrix rows correspond to time steps, and columns correspond to states.

Method `suggest_initial()`: Suggest initial observation parameters

The K-means algorithm is used to define clusters of observations (supposed to approximate the HMM states). Then, for each cluster, the `parapprox` function of the relevant `Dist` object is used to obtain parameter values.

Usage:

```
Observation$suggest_initial()
```

Returns: List of initial parameters for each observation variable

Examples:

```
# Load data set from MSwM package
data(energy, package = "MSwM")

# Initial observation parameters
par0 <- list(Price = list(mean = c(3, 6), sd = c(2, 2)))

# Model "energy" with normal distributions
obs <- Observation$new(data = energy,
                       dists = list(Price = "norm"),
                       par = par0,
                       n_states = 2)

# Print observation parameters
obs$par()

# Suggest initial parameters
par0_new <- obs$suggest_initial()
par0_new

# Update model parameters to suggested
obs$update_par(par = par0_new)
obs$par()
```

Method `plot_dist()`: Plot histogram of data and pdfs

Plot histogram of observations for the variable specified by the argument name, overlaid with the pdf of the specified distribution for that data stream. Helpful to select initial parameter values for model fitting, or to visualise fitted state-dependent distributions.

Usage:

```
Observation$plot_dist(var = NULL, weights = NULL, t = 1)
```

Arguments:

`var` Name of response variable for which the histogram and pdfs should be plotted.

`weights` Optional vector of length the number of pdfs that are plotted. Useful to visualise a mixture of distributions weighted by the proportion of time spent in the different states.

`t` Index of time step to use for covariates (default: 1).

Returns: A ggplot object

Method `formulation()`: Print model formulation

Usage:

`Observation$formulation()`

Method `print()`: Print Observation object Check constructor arguments

Usage:

`Observation$print()`

Method `clone()`: The objects of this class are cloneable with this method.

Usage:

`Observation$clone(deep = FALSE)`

Arguments:

`deep` Whether to make a deep clone.

Examples

```
## -----
## Method `Observation$new`
## -----

# Load data set from MSwM package
data(energy, package = "MSwM")

# Initial observation parameters
par0 <- list(Price = list(mean = c(3, 6), sd = c(2, 2)))

# Model "energy" with normal distributions
obs <- Observation$new(data = energy,
                      dists = list(Price = "norm"),
                      par = par0)

# Model "energy" with gamma distributions
obs <- Observation$new(data = energy,
                      dists = list(Price = "gamma2"),
                      par = par0)

# Model with non-linear effect of EurDol on mean price
f <- list(Price = list(mean = ~ s(EurDol, k = 5, bs = "cs")))
obs <- Observation$new(data = energy,
                      dists = list(Price = "norm"),
                      par = par0,
                      formula = f)

## -----
## Method `Observation$par`
## -----

# Load data set from MSwM package
data(energy, package = "MSwM")
```

```

# Initial observation parameters
par0 <- list(Price = list(mean = c(3, 6), sd = c(2, 2)))

# Model with linear effect of EurDol on mean price
f <- list(Price = list(mean = ~ EurDol))
obs <- Observation$new(data = energy,
                      dists = list(Price = "norm"),
                      par = par0,
                      n_states = 2,
                      formula = f)

# Set slope coefficients
obs$update_coeff_fe(coeff_fe = c(3, 2, 6, -2, log(2), log(2)))

# Observation parameter values for given data rows
obs$par(t = c(1, 10, 20))

## -----
## Method `Observation$suggest_initial`
## -----

# Load data set from MSwM package
data(energy, package = "MSwM")

# Initial observation parameters
par0 <- list(Price = list(mean = c(3, 6), sd = c(2, 2)))

# Model "energy" with normal distributions
obs <- Observation$new(data = energy,
                      dists = list(Price = "norm"),
                      par = par0,
                      n_states = 2)

# Print observation parameters
obs$par()

# Suggest initial parameters
par0_new <- obs$suggest_initial()
par0_new

# Update model parameters to suggested
obs$update_par(par = par0_new)
obs$par()

```

prec_to_cov

Get covariance matrix from precision matrix

Description

The covariance matrix is the inverse of the precision matrix. By default, the function `solve` is used for inversion. If it fails (e.g., singular system), then `MASS::ginv` is used instead, and returns the

Moore-Penrose generalised inverse of the precision matrix.

Usage

prec_to_cov(prec_mat)

Arguments

prec_mat Precision matrix (either of 'matrix' type or sparse matrix on which as.matrix can be used)

Value

Precision matrix

quad_pos_solve	<i>Solve for positive root of quadratic $ax^2 + bx + c = 0$ when it exists</i>
----------------	---

Description

Solve for positive root of quadratic $ax^2 + bx + c = 0$ when it exists

Usage

quad_pos_solve(a, b, c)

Arguments

a coefficient of x^2
b coefficient of x
c scalar coefficient

Value

real positive root if it exists

rvm	<i>Sample from von Mises distribution</i>
-----	---

Description

Sample from von Mises distribution

Usage

```
rvm(n, mu, kappa)
```

Arguments

n	Number of samples
mu	Mean parameter
kappa	Concentration parameter

Details

Uses basic rejection sampling, based on dvm(), which might be inefficient for large kappa. Could be improved following Best & Fisher (1979), Efficient simulation of the von Mises distribution, JRSSC, 28(2), 152-157.

Value

Vector of n samples from vm(mu, kappa)

rwrpcauchy	<i>Sample from wrapped Cauchy distribution</i>
------------	--

Description

Sample from wrapped Cauchy distribution

Usage

```
rwrpcauchy(n, mu, rho)
```

Arguments

n	Number of samples
mu	Mean parameter
rho	Concentration parameter

Details

Uses basic rejection sampling, based on dwrpcauchy(), which might be inefficient for large rho.

Value

Vector of n samples from wrpcauchy(mu, rho)

strip_comments	<i>Strip comments marked with a hash from a character vector</i>
----------------	--

Description

Strip comments marked with a hash from a character vector

Usage

```
strip_comments(str)
```

Arguments

str the character vector

Value

character vector with comments removed (and lines with only comments completely removed)

update.HMM	<i>Update a model to a new model by changing one formula</i>
------------	--

Description

Update a model to a new model by changing one formula

Usage

```
## S3 method for class 'HMM'
update(object, type, i, j, change, fit = TRUE, silent = FALSE, ...)
```

Arguments

<code>object</code>	HMM model object
<code>type</code>	Character string for the part of the model that is updated (either "hid" or "obs")
<code>i</code>	If type = "hid" then i is the row of the formula containing the change. If type = "obs" then i is the observation variable name.
<code>j</code>	If type = "hid" then j is the column of the formula containing the change. If type = "obs" then j is the parameter whose formula is to be changed.
<code>change</code>	The change to make to the formula, see ?update.formula for details.
<code>fit</code>	If FALSE then change is made but model is not re-fit.
<code>silent</code>	If TRUE then no model fitting output is given
<code>...</code>	Additional arguments are ignored (for compatibility with generic S3 method)

Examples

```
# Load data set from MSwM package
data(energy, package = "MSwM")

# Create hidden state and observation models
hid <- MarkovChain$new(data = energy, n_states = 2)
par0 <- list(Price = list(mean = c(3, 6), sd = c(2, 3)))
obs <- Observation$new(data = energy, n_states = 2,
                      dists = list(Price = "norm"),
                      par = par0)

# Create HMM (no covariate effects)
hmm <- HMM$new(hid = hid, obs = obs)
hmm$hid()$formula()
hmm$obs()$formulas()

# Update transition probability formulas (one at a time)
hmm <- update(hmm, type = "hid", i = 1, j = 2,
              change = ~ . + Oil, fit = FALSE)
hmm <- update(hmm, type = "hid", i = 2, j = 1,
              change = ~ . + Gas + Coal, fit = FALSE)
hmm$hid()$formula()

# Update observation parameter formulas (one at a time)
hmm <- update(hmm, type = "obs", i = "Price", j = "mean",
              change = ~ . + EurDol, fit = FALSE)
hmm$obs()$formulas()
```

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