

Package ‘MatrixHMM’

July 21, 2025

Title Parsimonious Families of Hidden Markov Models for Matrix-Variate Longitudinal Data

Version 1.0.0

Description Implements three families of parsimonious hidden Markov models (HMMs) for matrix-variate longitudinal data using the Expectation-Conditional Maximization (ECM) algorithm. The package supports matrix-variate normal, t, and contaminated normal distributions as emission distributions. For each hidden state, parsimony is achieved through the eigen-decomposition of the covariance matrices associated with the emission distribution. This approach results in a comprehensive set of 98 parsimonious HMMs for each type of emission distribution. Atypical matrix detection is also supported, utilizing the fitted (heavy-tailed) models.

License GPL (>= 3)

Encoding UTF-8

RoxygenNote 7.3.2

Imports data.table, doSNOW, foreach, LaplacesDemon, mclust, progress, snow, tensor, tidyr, withr

Depends R (>= 2.10)

LazyData true

NeedsCompilation no

Author Salvatore D. Tomarchio [aut, cre]

Maintainer Salvatore D. Tomarchio <daniele.tomarchio@unict.it>

Repository CRAN

Date/Publication 2024-08-28 08:00:06 UTC

Contents

atp.MVCN	2
atp.MVT	3
Eigen.HMM_fit	4
Eigen.HMM_init	5
extract.bestM	6
r.HMM	7
simData	8
simData2	9

Index**10**

atp.MVCN	<i>Atypical Detection Points Using Matrix-Variate Contaminated Normal Hidden Markov Models</i>
----------	------------------------------------------------------------------------------------------------

Description

Detects atypical matrices via matrix-variate contaminated normal Hidden Markov Models.

Usage

```
atp.MVCN(Y, pgood, class)
```

Arguments

Y	An array with dimensions $p \times r \times \text{num} \times t$, where p is the number of variables in the rows of each data matrix, r is the number of variables in the columns of each data matrix, num is the number of data observations, and t is the number of time points.
pgood	An array with dimensions $\text{num} \times t \times k$ containing the estimated probability of being typical for each point, given the time and state.
class	An $\text{num} \times t$ matrix containing the state memberships.

Value

An $\text{num} \times t$ matrix containing, for each observation and time, a 0 if it that matrix is typical and 1 otherwise.

Examples

```
data("simData2")
Y <- simData2$Y
init <- Eigen.HMM_init(Y = Y, k = 2, density = "MVCN", mod.row = "EEE", mod.col = "EE", nstartR = 1)
fit <- Eigen.HMM_fit(Y = Y, init.par = init, nThreads = 1)
atp <- atp.MVCN(Y = Y,
                pgood = fit[["results"]][[1]][[1]][[1]][["pgood"]],
                class = fit[["results"]][[1]][[1]][[1]][["class"]])
which(atp==1)
which(simData2[["atp.tr"]]==1)
```

atp.MVT	<i>Atypical Detection Points Using Matrix-Variate t Hidden Markov Models</i>
---------	-------------------------------------------------------------------------------------------

Description

Detects atypical matrices via matrix-variate t Hidden Markov Models given a specified value of epsilon.

Usage

```
atp.MVT(Y, M, U, V, class, epsilon)
```

Arguments

Y	An array with dimensions $p \times r \times \text{num} \times t$, where p is the number of variables in the rows of each data matrix, r is the number of variables in the columns of each data matrix, num is the number of data observations, and t is the number of time points.
M	An array with dimensions $p \times p \times k$, where k is the number of states, containing the mean matrices.
U	An array with dimensions $p \times p \times k$, where k is the number of states, containing the row covariance (scale) matrices.
V	An array with dimensions $r \times r \times k$, where k is the number of states, containing the column covariance (scale) matrices.
class	An $\text{num} \times t$ matrix containing the state memberships.
epsilon	A numeric value specifying the selected percentile of the chi-squared distribution with pr degrees of freedom.

Value

An $\text{num} \times t$ matrix containing, for each observation and time, a 0 if it that matrix is typical and 1 otherwise.

Examples

```
data("simData2")
Y <- simData2$Y
init <- Eigen.HMM_init(Y = Y, k = 2, density = "MVT", mod.row = "EEE", mod.col = "EE", nstartR = 1)
fit <- Eigen.HMM_fit(Y = Y, init.par = init, nThreads = 1)
atp <- atp.MVT(Y = Y, M = fit[["results"]][[1]][[1]][[1]][["M"]],
               U = fit[["results"]][[1]][[1]][[1]][["U"]],
               V = fit[["results"]][[1]][[1]][[1]][["V"]],
               class = fit[["results"]][[1]][[1]][[1]][["class"]],
               epsilon = 0.99)
which(atp==1)
which(simData2[["atp.tr"]]==1)
```

Eigen.HMM_fit

*Fitting Parsimonious Hidden Markov Models for Matrix-Variate Longitudinal Data***Description**

Fits parsimonious Hidden Markov Models for matrix-variate longitudinal data using ECM algorithms. The models are based on the matrix-variate normal, matrix-variate t , and matrix-variate contaminated normal distributions. Parallel computing is implemented and highly recommended for faster model fitting.

Usage

```
Eigen.HMM_fit(
  Y,
  init.par = NULL,
  tol = 0.001,
  maxit = 500,
  nThreads = 1,
  verbose = FALSE
)
```

Arguments

<code>Y</code>	An array with dimensions $p \times r \times \text{num} \times t$, where p is the number of variables in the rows of each data matrix, r is the number of variables in the columns of each data matrix, num is the number of data observations, and t is the number of time points.
<code>init.par</code>	A list of initial values for starting the algorithms, as generated by the <code>Eigen.HMM_init()</code> function.
<code>tol</code>	A numeric value specifying the tolerance level for the ECM algorithms' convergence.
<code>maxit</code>	A numeric value specifying the maximum number of iterations for the ECM algorithms.
<code>nThreads</code>	A positive integer indicating the number of cores to use for parallel processing.
<code>verbose</code>	A logical value indicating whether to display the running output.

Value

A list containing the following elements:

<code>results</code>	A list of the results from the fitted models.
<code>c.time</code>	A numeric value providing information on the computational time required to fit all models for each state.
<code>models</code>	A data frame listing the models that were fitted.

Examples

```
data(simData)
Y <- simData$Y
init <- Eigen.HMM_init(Y = Y, k = 2, density = "MVT", mod.row = "EEE", mod.col = "EE", nstartR = 10)
fit <- Eigen.HMM_fit(Y = Y, init.par = init, nThreads = 1)
```

Eigen.HMM_init	<i>Initialization for ECM Algorithms in Matrix-Variate Hidden Markov Models</i>
----------------	---------------------------------------------------------------------------------

Description

Initializes the ECM algorithms used for fitting parsimonious matrix-variate Hidden Markov Models (HMMs). Parallel computing is implemented and highly recommended for faster computations.

Usage

```
Eigen.HMM_init(
  Y,
  k,
  density,
  mod.row = "all",
  mod.col = "all",
  nstartR = 50,
  nThreads = 1,
  verbose = FALSE,
  seed = 3
)
```

Arguments

Y	An array with dimensions $p \times r \times \text{num} \times t$, where p is the number of variables in the rows of each data matrix, r is the number of variables in the columns of each data matrix, num is the number of data observations, and t is the number of time points.
k	An integer or vector indicating the number of states in the model(s).
density	A character string specifying the distribution to use in the HMM. Possible values are: "MVN" for the matrix-variate normal distribution, "MVT" for the matrix-variate t-distribution, and "MVCN" for the matrix-variate contaminated normal distribution.
mod.row	A character string indicating the parsimonious structure of the row covariance (or scale) matrices. Possible values are: "EII", "VII", "EEI", "VEI", "EVI", "VVI", "EEE", "VEE", "EVE", "EEV", "VVE", "VEV", "EVV", "VVV", or "all". When "all" is specified, all 14 parsimonious structures are considered.

mod.col	A character string indicating the parsimonious structure of the column covariance (or scale) matrices. Possible values are: "II", "EI", "VI", "EE", "VE", "EV", "VV", or "all". When "all" is specified, all 7 parsimonious structures are considered.
nstartR	An integer specifying the number of random starts to consider.
nThreads	A positive integer indicating the number of cores to use for parallel processing.
verbose	A logical value indicating whether to display the running output.
seed	A positive integer specifying the seed for random generation.

Value

A list containing the following elements:

results	A list of the results from the initialization.
k	The number of states fitted in each model.
req.model	A data frame listing the models that were initialized.
init.used	A data frame listing the initializations used for the required models.
index	A numeric vector to be used by the Eigen.HMM_fit() function.
dens	The density used for the HMMs.

Examples

```
data(simData)
Y <- simData$Y
init <- Eigen.HMM_init(Y = Y, k = 2, density = "MVT", mod.row = "EEE", mod.col = "EE", nstartR = 10)
```

extract.bestM	<i>Selection of the best fitting model(s)</i>
---------------	-----------------------------------------------

Description

This functions extracts the best fitting model(s) according to the Bayesian information criterion (BIC).

Usage

```
extract.bestM(results, top = 1)
```

Arguments

results	The output of the Eigen.HMM_fit() function.
top	Integer. Specifies the number of top-ranked models to display based on the Bayesian Information Criterion (BIC).

Value

A list containing the required best fitting model(s).

Examples

```
data(simData)
Y <- simData$Y
init <- Eigen.HMM_init(Y = Y, k = 2, density = "MVT", mod.row = "EEE", mod.col = "EE", nstartR = 10)
fit <- Eigen.HMM_fit(Y = Y, init.par = init, nThreads = 1)
win <- extract.bestM(results = fit, top = 1)
```

r.HMM

Random Number Generation for Matrix-Variate Hidden Markov Models

Description

Generates random numbers for matrix-variate Hidden Markov Models (HMMs) based on matrix-variate normal, t, and contaminated normal distributions.

Usage

```
r.HMM(density, num, t, PI, M, U, V, IP, nu, alpha, eta)
```

Arguments

density	A character string specifying the distribution to use for the HMM. Possible values are: "MVN" for the matrix-variate normal distribution, "MVT" for the matrix-variate t-distribution, and "MVCN" for the matrix-variate contaminated normal distribution.
num	An integer specifying the number of random matrices to generate.
t	An integer specifying the number of time points.
PI	A matrix representing the transition probability matrix.
M	An array with dimensions $p \times r \times k$, where k is the number of states, containing the mean matrices.
U	An array with dimensions $p \times p \times k$, where k is the number of states, containing the row covariance (scale) matrices.
V	An array with dimensions $r \times r \times k$, where k is the number of states, containing the column covariance (scale) matrices.
IP	A numeric vector of length k containing the initial probability weights.
nu	A numeric vector of length k containing the degrees of freedom for each state in the MVT distribution.
alpha	A numeric vector of length k containing the proportion of typical points in each state for the MVCN distribution.
eta	A numeric vector of length k containing the inflation parameters for each state in the MVCN distribution.

Value

A list containing the following elements:

Y An array with dimensions $p \times r \times \text{num} \times t$ containing the generated data.
obs.states An $\text{num} \times t$ matrix containing the state memberships.

Examples

```
p <- 2
r <- 3
num <- 50
t <- 3
k <- 2
IP <- c(0.5, 0.5)
PI <- matrix(c(0.9, 0.1, 0.3, 0.7), nrow = k, ncol = k, byrow = TRUE)
M <- array(NA, dim = c(p, r, k))
M[,1]<- matrix(c(0,1,1,
                -1,-1.5,-1),nrow = p, ncol = r, byrow = TRUE)
M[,2]<- M[,1]+3
U <- array(NA, dim = c(p, p, k))
V <- array(NA, dim = c(r, r, k))
U[, , 1] <- U[, , 2] <- matrix(c(1.73, -0.59, -0.59, 2.52), nrow = p, ncol = p, byrow = TRUE)
V[, , 1] <- V[, , 2] <- matrix(c(0.69, 0.23, -0.03,
                                0.23, 0.48, 0.16,
                                -0.03, 0.16, 0.88), nrow = r, ncol = r, byrow = TRUE)

nu <- c(4.5, 6.5)
simData <- r.HMM(density = "MVT", num = num, t = t, PI = PI,
                M = M, U = U, V = V, IP = IP, nu = nu)
```

simData

A Simulated Dataset from a Matrix-Variate t Hidden Markov Model

Description

A simulated dataset generated from a matrix-variate t Hidden Markov Model with 2 states and an EE - EE covariance structure.

Usage

```
data(simData)
```

Format

A list containing two elements:

- 1) An array with $p = 2$ variables in the rows, $r = 3$ variables in the columns, $\text{num} = 50$ matrices, and $t = 3$ time points.
- 2) An $\text{num} \times t$ matrix containing the state memberships.

simData2*A Simulated Dataset with Atypical Matrices*

Description

A simulated dataset containing atypical matrices. The data are initially generated from a matrix-variate normal Hidden Markov Model with 2 states and an EE - EE covariance structure. Atypical matrices are then introduced by randomly replacing some of the original matrices with values from a uniform distribution.

Usage

```
data(simData2)
```

Format

A list containing three elements:

- 1) An array with $p = 2$ variables in the rows, $r = 3$ variables in the columns, $num = 50$ matrices, and $t = 3$ time points.
- 2) An $num \times t$ matrix containing the state memberships.
- 3) An $num \times t$ matrix identifying the atypical matrices, where atypical matrices are coded with a 1.

Index

* datasets

simData, [8](#)

simData2, [9](#)

atp.MVCN, [2](#)

atp.MVT, [3](#)

Eigen.HMM_fit, [4](#)

Eigen.HMM_init, [5](#)

extract.bestM, [6](#)

r.HMM, [7](#)

simData, [8](#)

simData2, [9](#)