Package 'MatrixHMM'

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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 eigendecomposition 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.

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atp.MVCN

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atp.MVCN	Atypical Detection Points Using Matrix-Variate Contaminated Normal Hidden Markov Models

Description

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

Usage

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

Arguments

Υ	An array with dimensions $p \times r \times num \times t$, 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 $\operatorname{num} x t x k$ containing the estimated probability of being typical for each point, given the time and state.
class	An num x t matrix containing the state memberships.

Value

An num x t matrix containing, for each observation and time, a 0 if it that matrix is typical and 1 otherwise.

Examples

atp.MVT

	atp.MVT	Atypical Detection Models	on Points	Using	Matrix-Variate t	Hidden Markov
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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 $p \times r \times num \times t$, 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.
М	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 num x 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 num x t matrix containing, for each observation and time, a 0 if it that matrix is typical and 1 otherwise.

Examples

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Eigen. HMM_fit Fitting Parsimonious Hidden Markov Models for Matrix-Variate Longitudinal Data	Eigen.HMM_fit	Fitting Parsimonious Hidden Markov Models for Matrix-Variate Longitudinal Data
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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

Y	An array with dimensions $p \times r \times num \times t$, 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.
init.par	A list of initial values for starting the algorithms, as generated by the Eigen.HMM_init() function.
tol	A numeric value specifying the tolerance level for the ECM algorithms' convergence.
maxit	A numeric value specifying the maximum number of iterations for the ECM algorithms.
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.

Value

A list containing the following elements:

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

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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)</pre>
```

Eigen.HMM_init

Initialization for ECM Algorithms in Matrix-Variate Hidden Markov Models

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

Υ

An array with dimensions $p \times r \times num \times t$, 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.

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mod.col A character string indicating the parsimonious structure of the column covari-

ance (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.

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)</pre>
```

extract.bestM

Selection of the best fitting model(s)

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).

r.HMM

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</pre>
```

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.
М	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.

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Value

A list containing the following elements:

Y An array with dimensions $p \times r \times num \times t$ containing the generated data.

obs. states An num x 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 \leftarrow array(NA, dim = c(p, r, k))
M[,,1] \leftarrow matrix(c(0,1,1,
                   -1,-1.5,-1),nrow = p, ncol = r, byrow = TRUE)
M[,,2] \leftarrow M[,,1] + 3
U \leftarrow array(NA, dim = c(p, p, k))
V \leftarrow array(NA, dim = c(r, r, k))
U[, , 1] \leftarrow U[, , 2] \leftarrow matrix(c(1.73, -0.59, -0.59, 2.52), nrow = p, ncol = p, byrow = TRUE)
V[, , 1] \leftarrow V[, , 2] \leftarrow 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,</pre>
                  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, num = 50 matrices, and t = 3 time points.
- 2) An num x t matrix containing the state memberships.

simData2

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 x t matrix containing the state memberships.
- 3) An num x t matrix identifying the atypical matrices, where atypical matrices are coded with a 1.

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