Package ‘RcppHMM’

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Description Collection of functions to evaluate sequences, decode hidden states and estimate parameters from a single or multiple sequences of a discrete time Hidden Markov Model. The observed values can be modeled by a multinomial distribution for categorical/labeled emissions, a mixture of Gaussians for continuous data and also a mixture of Poissons for discrete values. It includes functions for random initialization, simulation, backward or forward sequence evaluation, Viterbi or forward-backward decoding and parameter estimation using an Expectation-Maximization approach.
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RcppHMM-package ................................................................. 2
Change Log ................................................................. 4
evaluation ................................................................. 5
forwardBackward ........................................................... 8
generateObservations .................................................... 12
initGHMM ................................................................. 15
initHMM ................................................................. 16
initPHMM ................................................................. 17
Overview of Package RcppHMM

Description

This package can model observations based on hidden Markov models. The observations can be considered to be emitted by a multinomial distribution, a mixture of Gaussians or a mixture of Poissons. It can be used for inference, parameter estimation and simulation.

Details

The package can be used to represent a discrete-time hidden Markov model. The states can generate categorical (labeled), continuous or discrete observations. The hidden state transition and observations can be randomly generated based on fixed parameters. The inference methods can be used to evaluate sequences or decode the hidden states that generated the observations. Finally, the model parameters can be estimated by a single or multiple observed sequences.

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References


Examples

# Multinominal case
# Set the model parameters to be estimated
n <- c("First","Second")
m <- c("A","T","C","G")
A <- matrix(c(0.8,0.2,
              0.1,0.9),
nrow = 2,
byrow = TRUE)

B <- matrix(c(0.2,0.2,0.3,0.3,
              0.4,0.4,0.1,0.1),
nrow = 2,
byrow = TRUE)

pi <- c(0.5, 0.5)

params <- list("Model" = "HMM",
                "StateNames" = n,
                "ObservationNames" = m,
                "A" = A,
                "B" = B,
                "Pi" = pi)

# Model parameters validation
HMM <- verifyModel(params)

# Data simulation
# Multiple sequences

set.seed(100)
length <- 100
seqs <- 100
observationsequences <- c()
for(i in 1:seqs){
  Y <- generateObservations(HMM, length)$Y
  observationsequences <- rbind(observationsequences, Y)
}

# New model random initialization

set.seed(1000)
newModel <- initHMM(2,4)
n = c("X1","X2")
m = c("A","T","C","G")

# Change model names
newModel <- setNames(newModel,
                     list("StateNames" = n,
"ObservationNames" = m)

# Model parameters estimation

newModel <- learnEM(newModel,
                   observationSequences,
                   iter=300,
                   delta = 1E-8,
                   pseudo = 0,
                   print = TRUE)

# New sequence simulation to compare the new model
# Data simulation

# Single sequence
Y <- generateObservations(HMM, length$Y

# Evaluation

evaluation(newModel, Y, "f")
evaluation(newModel, Y, "b")

# Hidden state decoding

hiddenStatesViterbi <- viterbi(newModel, Y)
hiddenStatesFB <- forwardBackward( newModel, Y)

---

## Change Log

### Changes Made to Package RcppHMM

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## Description

This page contains a listing of recent changes made to the package.

## Details

1. More examples were added to some functions. (November 2017)
2. Since there are different classes of HMMs and each of them with the same algorithms, a verification step was added to avoid memory leaks and variable compatibility. (May 2017)
3. The class of HMM with observations being modelled by a Gaussian Mixture Model (GHMM) was updated to have also a multivariate version (see `initGHMM`). (July 2017)
4. The emission matrix of the GHMM model was divided into two parameters: Mu and Sigma. Mu is now a 2D matrix with number of rows equal to the dimensionality of the observation vector and the number of columns equal to the number of hidden states. Sigma is now a 3D matrix with number of rows and columns equal to the the dimensionality of the observation vector and the number of slices equal to the number of hidden states (see `initGHMM`). (July 2017)
Observed sequence evaluation given a model

Description

This function computes the log-likelihood of an observed sequence being generated by a hidden Markov model with fixed parameters.

Usage

evaluation(hmm, sequence, method = "f")

Arguments

- `hmm`: a list with the necessary variables to define a hidden Markov model.
- `sequence`: sequence of observations to be evaluated. HMM and PHMM use a vector. GHMM uses a matrix.
- `method`: method specified to perform the evaluation

Details

The methods to be selected can be "f" for the forward algorithm or "b" for the backward algorithm. GHMM uses a matrix with the variables as rows and consecutive observations in the columns.

Value

A value that represents the log-likelihood of the sequence given the hidden Markov model.

References

Cited references are listed on the RcppHMM manual page.

See Also

generateObservations, verifyModel, loglikelihood

Examples

```r
## Values for a hidden Markov model with categorical observations
n <- c("First","Second")
m <- c("A","T","C","G")
A <- matrix(c(0.8,0.2,
             0.1,0.9),
            nrow = 2,
            byrow = TRUE)
B <- matrix(c(0.2, 0.2, 0.3, 0.3,
```
```r
0.4, 0.4, 0.1, 0.1),
nrow = 2,
byrow = TRUE)

Pi <- c(0.5, 0.5)

params <- list("Model" = "HMM",
    "StateNames" = n,
    "ObservationNames" = m,
    "A" = A,
    "B" = B,
    "Pi" = Pi)

HMM <- verifyModel(params)

# Data simulation
set.seed(100)
length <- 100
observationSequence <- generateObservations(HMM, length)

#Sequence evaluation

# It assumes that it will be evaluated using the forward algorithm
evaluation(HMM, observationSequence)

# The user sets the backward algorithm to evaluate the algorithm
evaluation(HMM, observationSequence, "b")

## Values for a hidden Markov model with discrete observations

n <- c("Low", "Normal", "High")

A <- matrix(c(0.5, 0.3, 0.2,
    0.2, 0.6, 0.2,
    0.1, 0.3, 0.6),
    ncol=length(n), byrow=TRUE)

B <- matrix(c(2600, # First distribution with mean 2600
    2700, # Second distribution with mean 2700
    2800) # Third distribution with mean 2800

Pi <- rep(1/length(n), length(n))

HMM.discrete <- verifyModel(list("Model"="PHMM", "StateNames" = n, "A" = A, "B" = B, "Pi" = Pi))

# Data simulation
set.seed(100)
length <- 100
observationSequence <- generateObservations(HMM.discrete, length)

#Sequence evaluation

# It assumes that it will be evaluated using the forward algorithm
```
evaluation(HMM.discrete, observationSequence$Y)

# The user sets the backward algorithm to evaluate the algorithm
evaluation(HMM.discrete, observationSequence$Y, "b")

## Values for a hidden Markov model with continuous observations
# Number of hidden states = 3
# Univariate gaussian mixture model

N = c("Low", "Normal", "High")
A <- matrix(c(0.5, 0.3, 0.2,
              0.2, 0.6, 0.2,
              0.1, 0.3, 0.6),
             ncol= length(N), byrow = TRUE)

Mu <- matrix(c(0, 50, 100), ncol = length(N))
Sigma <- array(c(144, 400, 100), dim = c(1,1,length(N)))
Pi <- rep(1/length(N), length(N))

HMM.cont.univariate <- verifyModel(list("Model"="GMMM",
                                      "StateNames" = N,
                                      "A" = A,
                                      "Mu" = Mu,
                                      "Sigma" = Sigma,
                                      "Pi" = Pi))

# Data simulation
set.seed(100)
length <- 100
observationSequence <- generateObservations(HMM.cont.univariate, length)

#Sequence evaluation

# It assumes that it will be evaluated using the forward algorithm
evaluation(HMM.cont.univariate, observationSequence$Y)

# The user sets the backward algorithm to evaluate the algorithm
evaluation(HMM.cont.univariate, observationSequence$Y, "b")

## Values for a hidden Markov model with continuous observations
# Number of hidden states = 2
# Multivariate gaussian mixture model
# Observed vector with dimensionality of 3
N = c("X1", "X2")
M <- 3

# Same number of dimensions
Sigma <- array(c(0, dim = c(M,M,length(N))))
Sigma[,1] <- matrix(c(1.0, 0.8, 0.8, 0.8, 1.0, 0.8, 0.8, 0.8, 1.0), ncol = M,
                    byrow = TRUE)
Sigma[,2] <- matrix(c(1.0, 0.4, 0.6, 0.4, 1.0, 0.6, 0.6, 0.6, 1.0), ncol = M,
                    byrow = TRUE)
forwardBackward

Forward-backward algorithm for hidden state decoding

Description

Function used to get the most likely hidden states at each observation in the provided sequence.

Usage

forwardBackward(hmm, sequence)
Arguments

- **hmm**: a list with the necessary variables to define a hidden Markov model.
- **sequence**: sequence of observations to be decoded. HMM and PHMM use a vector. GHMM uses a matrix.

Details

GHMM uses a matrix with the variables as rows and consecutive observations in the columns.

Value

A vector of hidden states in the traveled path of observations.

References

Cited references are listed on the RcppHMM manual page.

See Also

- `generateObservations`
- `verifyModel`
- `viterbi`

Examples

```r
## Values for a hidden Markov model with categorical observations
# Set the model parameters
n <- c("First", "Second")
m <- c("A", "T", "C", "G")
A <- matrix(c(0.8, 0.2,
              0.1, 0.9),
nrow = 2,
byrow = TRUE)

B <- matrix(c(0.2, 0.2, 0.3, 0.3,
              0.4, 0.4, 0.1, 0.1),
nrow = 2,
byrow = TRUE)

Pi <- c(0.5, 0.5)

params <- list("Model" = "HMM",
                "StateNames" = n,
                "ObservationNames" = m,
                "A" = A,
                "B" = B,
                "Pi" = Pi)

HMM <- verifyModel(params)

# Data simulation
set.seed(100)
length <- 100
```
observationSequence <- generateObservations(HMM, length)

# Sequence decoding
hiddenStates <- forwardBackward(HMM, observationSequence)
print(hiddenStates)

## Values for a hidden Markov model with discrete observations

n <- c("Low", "Normal", "High")

A <- matrix(c(0.5, 0.3, 0.2,
              0.2, 0.6, 0.2,
              0.1, 0.3, 0.6),
            ncol=length(n), byrow=TRUE)

B <- c(2000, 2700, 2800) # First distribution with mean 2000

Pi <- rep(1/length(n), length(n))

HMM.discrete <- verifyModel(list("Model"="PHMM", "StateNames" = n, "A" = A, "B" = B, "Pi" = Pi))

# Data simulation
set.seed(100)
length <- 100
observationSequence <- generateObservations(HMM.discrete, length)

# Sequence decoding
hiddenStates <- forwardBackward(HMM.discrete, observationSequence)
print(hiddenStates)

## Values for a hidden Markov model with continuous observations

# Number of hidden states = 3
# Univariate gaussian mixture model

N <- c("Low", "Normal", "High")

A <- matrix(c(0.5, 0.3, 0.2,
              0.2, 0.6, 0.2,
              0.1, 0.3, 0.6),
            ncol=length(N), byrow = TRUE)

Mu <- matrix(c(0, 50, 100), ncol = length(N))
Sigma <- array(c(144, 400, 100), dim = c(1,1,length(N)))
Pi <- rep(1/length(N), length(N))

HMM.cont.univariate <- verifyModel(list("Model"="GPHMM",
                                       "StateNames" = N,
                                       "A" = A,
                                       "Mu" = Mu,
                                       "Sigma" = Sigma,
                                       "Pi" = Pi))
# Data simulation
set.seed(100)
length <- 100
observationSequence <- generateObservations(HMM.cont.univariate, length)

# Sequence decoding
hiddenStates <- forwardBackward(HMM.cont.univariate, observationSequence$Y)
print(hiddenStates)

## Values for a hidden Markov model with continuous observations
## Number of hidden states = 2
## Multivariate gaussian mixture model
## Observed vector with dimensionality of 3
M = c("X1","X2")
M <- 3

## Same number of dimensions
Sigma <- array(0, dim =c(M,M,length(N)))
Sigma[,1] <- matrix(c(1,0,0.8,0.8,
                      0.8,1,0,0.8,
                      0.8,0.8,1,0), ncol = M,
                      byrow = TRUE)
Sigma[,2] <- matrix(c(1,0,0.4,0.6,
                      0.4,1,0,0.8,
                      0.6,0.8,1,0), ncol = M,
                      byrow = TRUE)

Mu <- matrix(c(0, 5,
               10, 0,
               5, 10),
              nrow = M,
              byrow = TRUE)

A <- matrix(c(0.6, 0.4,
              0.3, 0.7),
            ncol = length(N),
            byrow = TRUE)

Pi <- c(0.5, 0.5)

HMM.cont.multi <- verifyModel(list( "Model" = "GHHM",
                                   "StateNames" = N,
                                   "A" = A,
                                   "Mu" = Mu,
                                   "Sigma" = Sigma,
                                   "Pi" = Pi))

# Data simulation
set.seed(100)
length <- 100
observationSequence <- generateObservations(HMM.cont.multi, length)

# Sequence decoding
hiddenStates <- forwardBackward(HMM.cont.multi, observationSequence$Y)
print(hiddenStates)
generateObservations  Generate observations given a model

Description

Function used to generate simulated observations given a hidden Markov model.

Usage

generateObservations(hmm, length)

Arguments

- `hmm`: a list with the necessary variables to define a hidden Markov model.
- `length`: the number of observations will be generated.

Value

A list that contains the generated observations and the hidden state that generated it.

Values:

- `x`: a vector representing the path of hidden states.
- `y`: generated observations. HMM and PHMM return a vector. GHMM returns a matrix.

Examples

```r
## Values for a hidden Markov model with categorical observations
# Set the model parameters
n <- c("First", "Second")
m <- c("A", "T", "C", "G")
A <- matrix(c(0.8, 0.2,
             0.1, 0.9),
            nrow = 2,
            byrow = TRUE)
B <- matrix(c(0.2, 0.2, 0.3, 0.3,
             0.4, 0.1, 0.1, 0.1),
            nrow = 2,
            byrow = TRUE)
Pi <- c(0.5, 0.5)

params <- list("Model" = "HMM",
               "StateNames" = n,
               "ObservationNames" = m,
               "A" = A,
               "B" = B,
               "Pi" = Pi)
```

"Pi" = Pi)

HMM <- verifyModel(params)

# Data simulation
set.seed(100)
length <- 100
observationSequence <- generateObservations(HMM, length)
# Observed data
head(observationSequence$Y)
# Hidden states path
head(observationSequence$X)

## Values for a hidden Markov model with discrete observations
n <- c("Low","Normal","High")
A <- matrix(c(0.5, 0.3, 0.2,
             0.2, 0.6, 0.2,
             0.1, 0.3, 0.6),
nrow=length(n), byrow=TRUE)
B <- c(2600, 2700, 2800) # First distribution with mean 2600
Pi <- rep(1/length(n), length(n))

HMM.discrete <- verifyModel(list("Model"="PHMM", "StateNames" = n, "A" = A, "B" = B, "Pi" = Pi))

# Data simulation
set.seed(100)
length <- 100
observationSequence <- generateObservations(HMM.discrete, length)
# Observed data
head(observationSequence$Y)
# Hidden states path
head(observationSequence$X)

## Values for a hidden Markov model with continuous observations
# Number of hidden states = 3
# Univariate gaussian mixture model
N = c("Low","Normal","High")
A <- matrix(c(0.5, 0.3, 0.2,
             0.2, 0.6, 0.2,
             0.1, 0.3, 0.6),
nrow=length(N), byrow = TRUE)
Mu <- matrix(c(0, 50, 100), ncol = length(N))
Sigma <- array(c(144, 400, 100), dim = c(1,1,length(N)))
Pi <- rep(1/length(N), length(N))

HMM.cont.univariate <- verifyModel(list(  
"Model"="GHMM",  
"StateNames" = N,  
"A" = A,  
"Mu" = Mu,  
"Sigma" = Sigma,  
"Pi" = Pi))

# Data simulation
set.seed(100)
length <- 100
observationSequence <- generateObservations(HMM.cont.univariate, length)

# Observed data
observationSequence$Y[,1:6]
# Hidden states path
head(observationSequence$X)

## Values for a hidden Markov model with continuous observations
## Number of hidden states = 2
## Multivariate gaussian mixture model
## Observed vector with dimensionality of 3
N = c("X1","X2")
M <- 3

## Same number of dimensions
Sigma <- array(0, dim =c(M, M, length(N)))
Sigma[,,1] <- matrix(c(1.0,0.8,0.8,
                        0.8,1.0,0.8,
                        0.8,0.8,1.0), ncol = M,
                        byrow = TRUE)
Sigma[,,2] <- matrix(c(1.0,0.4,0.6,
                        0.4,1.0,0.8,
                        0.6,0.8,1.0), ncol = M,
                        byrow = TRUE)

Mu <- matrix(c(0, 5,
               10, 0,
               5, 10),
              nrow = M,
              byrow = TRUE)

A <- matrix(c(0.6, 0.4,
              0.3, 0.7),
             ncol = length(N),
             byrow = TRUE)

Pi <- c(0.5, 0.5)

HMM.cont.multi <- verifyModel(list(  
"Model" = "GHMM",  
"StateNames" = N,  
"A" = A,  
"Mu" = Mu,  
"Sigma" = Sigma,  
"Pi" = Pi))
initGHMM

Random Initialization for a Hidden Markov Model with emissions modeled as continuous variables

Description

Function used to generate a hidden Markov model with continuous variables and random parameters. This method allows using the univariate version of a Gaussian Mixture Model when setting m = 1. The code for the methods with categorical values or discrete data can be viewed in "initHMM" and "initPHMM", respectively.

Usage

initGHMM(n,m)

Arguments

n the number of hidden states to use.
m the number of variables generated by the hidden states (Dimensionality of the observed vector).

Value

A "list" that contains the required values to specify the model.

Model it specifies that the observed values are to be modeled as a Gaussian mixture model.

StateNames the set of hidden state names.

A the transition probabilities matrix.

Mu a matrix of means of the observed variables (rows) in each states (columns).

Sigma a 3D matrix that has the covariance matrix of each state. The number of slices is equal to the maximum number of hidden states.

Pi the initial probability vector.
**initHMM**

*Random Initialization for a Hidden Markov Model with emissions modeled as categorical variables*

**Description**

Function used to generate a hidden Markov model with categorical variables and random parameters. The code for the methods with continuous values or discrete data can be viewed in "initGPHMM" and "initPHMM", respectively.

**Usage**

```r
initHMM(n, m)
```

**Arguments**

- `n` the number of hidden states to use.
- `m` the number of possible categories (labels) generated by the hidden states.

**Value**

A "*list*" that contains the required values to specify the model.

- **Model** it specifies that the observed values are to be modeled as a multinomial distribution.
- **StateNames** the set of hidden state names.
- **ObservationNames** the set of possible observed values.
- **A** the transition probabilities matrix.
- **B** the emission probabilities matrix.
- **Pi** the initial probability vector.

**References**

Cited references are listed on the RcppHMM manual page.
**initPHMM**

Random Initialization for a Hidden Markov Model with emissions modeled as discrete variables

**Description**

Function used to generate a hidden Markov model with discrete observations and random parameters. This model is used when the observed data are counts that can be modelled with a mixture of Poissons. The code for the methods with categorical values or continuous data can be viewed in "initHMM" and "initGHMM", respectively.

**Usage**

`initPHMM(n)`

**Arguments**

- `n` the number of hidden states to use.

**Value**

A "list" that contains all the required values to specify the model.

- **Model**: it specifies that the observed values are to be modeled as a Poisson mixture model.
- **StateNames**: the set of hidden state names.
- **A**: the transition probabilities matrix.
- **B**: a vector with the lambda parameter for each Poisson distribution.
- **Pi**: the initial probability vector.

**References**

Cited references are listed on the RcppHMM manual page.

**Examples**

```r
n <- 2
m <- 2
model <- initPHMM(n,m)
print(model)
```
learnEM

*Expectation-Maximization algorithm to estimate the model parameters*

**Description**

Expectation-Maximization algorithm to estimate the model parameters based on a single or multiple observed sequences.

**Usage**

```r
learnEM(hmm, sequences, iter = 100, delta = 1e-05, pseudo = 0, print = TRUE)
```

**Arguments**

- `hmm`: a list with the necessary variables to define a hidden Markov model.
- `sequences`: sequences of observations to be used as training set. HMM and PHMM use a matrix. GHMM uses a 3D array.
- `iter`: a value that sets the maximum number of iterations to run.
- `delta`: a value set to be the minimum error considered as a convergence criteria.
- `pseudo`: a value set to consider pseudo-counts.
- `print`: a logical value to print the error at each iteration.

**Details**

This function can be used for univariate or multivariate distributions. HMM and PHMM use a matrix with different sequences as rows and consecutive observations in the columns. GHMM uses an array with the variables as rows, consecutive observations in the columns and different sequences as slices.

**Value**

A "list" that contains the estimated hidden Markov model parameters.

**References**

Cited references are listed on the RcppHMM manual page.

**See Also**

`generateObservations`, `verifyModel`
Examples

```r
## Values for a hidden Markov model with categorical observations
# Set the model parameters
n <- c("First","Second")
m <- c("A","T","C","G")
A <- matrix(c(0.8,0.2,
      0.1,0.9),
    nrow = 2,
    byrow = TRUE)
B <- matrix(c(0.2, 0.2, 0.3, 0.3,
      0.4, 0.4, 0.1, 0.1),
    nrow = 2,
    byrow = TRUE)

pi <- c(0.5, 0.5)

params <- list("Model" = "HMM",
    "StateNames" = n,
    "ObservationNames" = m,
    "A" = A,
    "B" = B,
    "Pi" = pi)

HMM <- verifyModel(params)

# Data simulation
set.seed(100)
length <- 100
segs <- 10

# Multiple sequences to be used as training set
observationSequences <- c()
for(i in 1:segs){
  Y <- generateObservations(HMM, length)$Y
  observationSequences <- rbind(observationSequences, Y)
}

# New model random initialization
# Model to be trained
set.seed(1000)
newModel <- initHMM(2,4)
n = c("X1","X2")
m = c("A","T","C","G")
newModel <- setNames(newModel,
    list("StateNames" = n,
    "ObservationNames" = m))

newModel <- learnEM(newModel,
    observationSequences,
    iter= 50,
    ..
```
delta = 1E-5,
pseudo = 3,
print = TRUE)

println(newModel)

## Values for a hidden Markov model with discrete observations

n <- c("Low", "Normal", "High")
A <- matrix(c(0.5, 0.3, 0.2,
                 0.2, 0.6, 0.2,
                 0.1, 0.3, 0.6),
               ncol=length(n), byrow=TRUE)
B <- c(2000, # First distribution with mean 2000
       2700, # Second distribution with mean 2700
       2800) # Third distribution with mean 2800
Pi <- rep(1/length(n), length(n))
HMM.discrete <- verifyModel(list("Model"="PHMM", "StateNames" = n, "A" = A, "B" = B, "Pi" = Pi))

# Data simulation
set.seed(100)
length <- 100
segs <- 50

# Multiple sequences to be evaluated
observationSequences<- c()
for(i in 1:segs){
    Y <- generateObservations(HMM.discrete, length)$Y
    observationSequences <- rbind(observationSequences , Y)
}

println(observationSequences)
# New model random initialization
# Model to be trained
set.seed(1000)
newModel <- initPHMM(3)

newModel <- learnEM(newModel,
                     observationSequences,
                     iter= 50,
                     delta = 1E-5,
                     print = FALSE)

println(newModel)

## Values for a hidden Markov model with continuous observations
# Number of hidden states = 3
# Univariate gaussian mixture model

N = c("Low", "Normal", "High")
A <- matrix(c(0.5, 0.3, 0.2,
              0.2, 0.6, 0.2,
              0.1, 0.3, 0.6),
             ncol = length(N), byrow = TRUE)

Mu <- matrix(c(0, 50, 100), ncol = length(N))
Sigma <- array(c(144, 400, 100), dim = c(1, 1, length(N)))
Pi <- rep(1/length(N), length(N))

HMM.cont.univariate <- verifyModel(list("Model"="GHMM",
                                      "StateNames" = N,
                                      "A" = A,
                                      "Mu" = Mu,
                                      "Sigma" = Sigma,
                                      "Pi" = Pi))

# Data simulation
set.seed(100)
length <- 100
segs <- 50

# Multiple sequences to be evaluated
observationSequences <- array(0, dim = c(1, length, seqs))
for(i in 1:segs){
  Y <- generateObservations(HMM.cont.univariate, length)
  observationSequences[, , i] <- Y
}
dim(observationSequences)

# New model random initialization
# Model to be trained
set.seed(10000)
newModel <- initGHMM(3)

newModel <- learnEM(newModel, observationSequences,
                     iter = 50,
                     delta = 1E-5,
                     print = FALSE)

print(newModel)

## Values for a hidden Markov model with continuous observations
# Number of hidden states = 2
# Multivariate gaussian mixture model
# Observed vector with dimensionality of 3
N = c("X1","X2")
M <- 3

# Same number of dimensions
Sigma <- array(0, dim=c(M,M,length(N)))
Sigma[,1] <- matrix(c(1.0,0.8,0.8,
                      0.8,1.0,0.8,
                      0.8,0.8,1.0), ncol = M,
                      byrow = TRUE)
Sigma[,2] <- matrix(c(1.0,0.4,0.6,
                      0.4,1.0,0.8,
                      0.6,0.8,1.0), ncol = M,
                      byrow = TRUE)
Mu <- matrix(c(0, 5,
              10, 0,
              5, 10),
             nrow = M,
             byrow = TRUE)
A <- matrix(c(0.6,0.4,
            0.3, 0.7),
           ncol = length(N),
           byrow = TRUE)
Pi <- c(0.5, 0.5)

HMM.cont.multi <- verifyModel(list("Model" = "GHMM",
                                  "StateNames" = N,
                                  "A" = A,
                                  "Mu" = Mu,
                                  "Sigma" = Sigma,
                                  "Pi" = Pi))

# Data simulation
set.seed(100)
length <- 100
seqs <- 50

# Multiple sequences to be evaluated
observationSequences<- array(0, dim = c(M, length, seqs))
for(i in 1:seqs){
  Y <- generateObservations(HMM.cont.multi, length)$Y
  observationSequences[,,,i] <- Y
}
dim(observationSequences)

# New model random initialization
# Model to be trained
set.seed(1000)
newModel <- initGMMM(2, M)

newModel <- learnEM(newModel,
                     observationSequences,
loglikelihood

iter = 50,
delta = 1E-5,
print = FALSE)

print(newModel)

loglikelihood Evaluation of multiple observed sequences given a model

Description
This function computes the log-likelihood of multiple observed sequences generated by a hidden
Markov model with fixed parameters.

Usage
loglikelihood(hmm, sequences)

Arguments
hmm a list with the necessary variables to define a hidden Markov model.
sequences sequences of observations to be evaluated. HMM and PHMM use a matrix.

GHMM uses a 3D array.

Value
A value that represents the log-likelihood of the multiple observed sequences given the hidden
Markov model. HMM and PHMM use a matrix with different sequences as rows and consecutive
observations in the columns. GHMM uses an array with the variables as rows, consecutive
observations in the columns and different sequences as slices.

References
Cited references are listed on the RcppHMM manual page.

See Also
generateObservations, verifyModel, evaluation

Examples
## Values for a hidden Markov model with categorical observations
# Set the model parameters
n <- c("First","Second")
m <- c("A", "T", "C", "G")
A <- matrix(c(0.8,0.2,
 0.1,0.9),
nrow = 2,
byrow = TRUE)

B <- matrix(c(0.2, 0.2, 0.3, 0.3,
              0.4, 0.4, 0.1, 0.1),
              nrow = 2,
              byrow = TRUE)

Pi <- c(0.5, 0.5)

params <- list(
    "Model" = "HMM",
    "StateNames" = n,
    "ObservationNames" = m,
    "A" = A,
    "B" = B,
    "Pi" = Pi)

HMM <- verifyModel(params)

# Data simulation
set.seed(100)
length <- 100
seqs <- 10

# Multiple sequences to be evaluated
observationSequences <- c()
for(i in 1:seqs){
    Y <- generateObservations(HMM, length)$Y
    observationSequences <- rbind(observationSequences, Y)
}
dim(observationSequences)

# Sequences evaluation
loglikelihood(HMM, observationSequences)

## Values for a hidden Markov model with discrete observations

n <- c("Low","Normal","High")

A <- matrix(c(0.5, 0.3, 0.2,
              0.2, 0.6, 0.2,
              0.1, 0.3, 0.6),
             ncol=length(n), byrow=TRUE)

B <- c(2600, 2700, 2800) # First distribution with mean 2600 2700, # Second distribution with mean 2700 2800 # Third distribution with mean 2800

Pi <- rep(1/length(n), length(n))

# Data simulation
set.seed(100)
length <- 100
seqs <- 10

# Multiple sequences to be evaluated
observationSequences <- c()
for(i in 1:seqs){
    Y <- generateObservations(HMM.discrete, length)$Y
    observationSequences <- rbind(observationSequences, Y)
}
dim(observationSequences)

# Sequences evaluation
loglikelihood(HMM.discrete, observationSequences)

## Values for a hidden Markov model with continuous observations
# Number of hidden states = 3
# Univariate gaussian mixture model
N = c("Low", "Normal", "High")
A <- matrix(c(0.5, 0.3, 0.2,
              0.2, 0.6, 0.2,
              0.1, 0.3, 0.6),
             ncol = length(N), byrow = TRUE)
Mu <- matrix(c(0, 50, 100), ncol = length(N))
Sigma <- array(c(144, 400, 100), dim = c(1, 1, length(N)))
Pi <- rep(1/length(N), length(N))

HMM.cont.univariate <- verifyModel(list("Model"="GHMM",
                                       "StateNames" = N,
                                       "A" = A,
                                       "Mu" = Mu,
                                       "Sigma" = Sigma,
                                       "Pi" = Pi))

# Data simulation
set.seed(100)
length <- 100
seqs <- 10

# Multiple sequences to be evaluated
observationSequences <- array(0, dim = c(1, length, seqs))
for(i in 1:seqs){
    Y <- generateObservations(HMM.cont.univariate, length)$Y
    observationSequences[,,i] <- Y
}
dim(observationSequences)

# Sequences evaluation
loglikelihood(HMM\_cont.univariate, observationSequences)

```r
## Values for a hidden Markov model with continuous observations
# Number of hidden states = 2
# Multivariate gaussian mixture model
# Observed vector with dimensionality of 3
N = c("X1", "X2")
M <- 3

# Same number of dimensions
Sigma <- array(0, dim = c(M, M, length(N)))
Sigma[,1] <- matrix(c(1.0, 0.8, 0.8,
                      0.8, 1.0, 0.8,
                      0.8, 0.8, 1.0), ncol = M,
                      byrow = TRUE)
Sigma[,2] <- matrix(c(1.0, 0.4, 0.6,
                      0.4, 1.0, 0.8,
                      0.6, 0.8, 1.0), ncol = M,
                      byrow = TRUE)
Mu <- matrix(c(0, 5,
               10, 0,
               5, 10),
              nrow = M,
              byrow = TRUE)
A <- matrix(c(0.6, 0.4,
              0.3, 0.7),
             ncol = length(N),
             byrow = TRUE)
Pi <- c(0.5, 0.5)

HMM\_cont.multi <- verifyModel(list("Model" = "GHM\_M",
                                   "StateNames" = N,
                                   "A" = A,
                                   "Mu" = Mu,
                                   "Sigma" = Sigma,
                                   "Pi" = Pi))

# Data simulation
set.seed(100)
length <- 100
seqs <- 10

# Multiple sequences to be evaluated
observationSequences <- array(0, dim = c(M, length, seqs))
for(i in 1:seqs){
  Y <- generateObservations(HMM\_cont.multi, length)$Y
  observationSequences[,i] <- Y
}

dim(observationSequences)
```
setNames 27

#Sequences evaluation
loglikelihood(HMM.cont.multi, observationSequences)

setNames  Set the names of the model

Description
Function used to set new hidden state names to the model. If it is a categorical model, it also sets
the labels for the observations. This function verifies that all the parameters and new names agree
in size.

Usage
setNames(hmm, names)

Arguments
  hmm  a list with the necessary variables to define a hidden Markov model.
  names a list with the new names to be set in the model.

Value
A "list" that contains the verified hidden Markov model parameters.

Examples
## Values for a hidden Markov model with categorical observations

set.seed(1000)
newModel <- initHMM(2, 4)
n <- c("First", "Second")
m <- c("A", "T", "C", "G")
newModel <- setNames(newModel,
  list( "StateNames" = n,
        "ObservationNames" = m ) )

## Values for a hidden Markov model with continuous observations

set.seed(1000)
newModel <- initGPHM(3)
n <- c("Low", "Normal", "High")
newModel <- setNames(newModel,
  list( "StateNames" = n ))

## Values for a hidden Markov model with discrete observations

set.seed(1000)
setParameters

newModel <- initHMM(3)
n <- c("Low", "Normal", "High")
newModel <- setNames(newModel,
  list("StateNames" = n))

Description

Function used to set the model parameters. This function verifies that parameters and names correspond.

Usage

setParameters(hmm, params)

Arguments

hmm a list with the necessary variables to define a hidden Markov model.
params a list with the new parameters to be set in the model.

Value

A "list" that contains the verified hidden Markov model parameters.

Examples

## Values for a hidden Markov model with categorical observations

set.seed(1000)
newModel <- initHMM(2,4)

A <- matrix(c(0.378286, 0.621714,
              0.830970, 0.169030),
            nrow = 2,
            byrow = TRUE)

B <- matrix(c(0.1930795, 0.2753869, 0.3463100, 0.1852237,
             0.2871577, 0.1848870, 0.1614925, 0.3664628),
            nrow = 2,
            byrow = TRUE)

Pi <- c(0.4757797, 0.5242203)

ewModel <- setParameters(newModel,
                           list("A" = A,
                                "B" = B,
"Pi" = Pi )

## Values for a hidden Markov model with discrete observations

set.seed(1000)
n <- 3
newModel <- initPHMM(n)
A <- matrix(c(0.5, 0.3, 0.2,
            0.2, 0.6, 0.2,
            0.1, 0.3, 0.6),
            ncol=n, byrow=TRUE)
B <- c(2600, # First distribution with mean 2600
      2700, # Second distribution with mean 2700
      2800) # Third distribution with mean 2800
Pi <- rep(1/n, n)

newModel <- setParameters(newModel,
   list( "A" = A,
        "B" = B,
        "Pi" = Pi) )

## Values for a hidden Markov model with continuous observations
# Number of hidden states = 3
# Univariate gaussian mixture model
N <- 3
newModel <- initGHM(N)
A <- matrix(c(0.5, 0.3, 0.2,
            0.2, 0.6, 0.2,
            0.1, 0.3, 0.6),
            ncol= N, byrow = TRUE)
Mu <- matrix(c(0, 50, 100), ncol = N)
Sigma <- array(c(144, 400, 100), dim = c(1,1,N))
Pi <- rep(1/N, N)

newModel <- setParameters(newModel,
   list( "A" = A,
        "Mu" = Mu,
        "Sigma" = Sigma,
        "Pi" = Pi))

## Values for a hidden Markov model with continuous observations
# Number of hidden states = 2
# Multivariate gaussian mixture model
# Observed vector with dimensionality of 3
N <- 2
M <- 3
verifyModel

Description

Function used to verify that all the parameters satisfy the model constraints.

Usage

verifyModel(model)

Arguments

model a list with the necessary parameters to set a hidden Markov model with fixed values.
Details

The model must have a stochastic transition matrix and a stochastic initial probability vector, also the row and column sizes must coincide with the number of provided state names. If the model uses categorical values, the emission matrix also must be stochastic and must have a column for each observation label and a row for each state name. And if the model uses discrete data, all the values must be positive assuming that they are counts.

Value

A "list" that contains the verified hidden Markov model parameters.

Examples

```r
## Values for a hidden Markov model with categorical observations

n <- c("First","Second")
m <- c("A","T","C","G")
A <- matrix(c(0.378286,0.621714,
              0.830970,0.169030),
           nrow = 2,
           byrow = TRUE)

B <- matrix(c(0.1930795, 0.2753869, 0.3463100, 0.1852237,
              0.2871577, 0.1848870, 0.1614925, 0.3664628),
           nrow = 2,
           byrow = TRUE)

pi <- c(0.4757797, 0.5242203)

params <- list(  "Model" = "HMM",
                "StateNames" = n,
                "ObservationNames" = m,
                "A" = A,
                "B" = B,
                "Pi" = pi)

verifiedModel <- verifyModel(params)
print(verifiedModel)

## Values for a hidden Markov model with discrete observations

n <- c("Low","Normal","High")

A <- matrix(c(0.5, 0.3, 0.2,
              0.2, 0.6, 0.2,
              0.1, 0.3, 0.6),
           ncol=length(n), byrow=TRUE)

B <- c(2600, # First distribution with mean 2600
       2700,  # Second distribution with mean 2700
       2800) # Third distribution with mean 2800)
```
Pi <- rep(1/length(n), length(n))

HMM.discrete <- verifyModel(list("Model"="PHMM", "StateNames" = n, "A" = A, "B" = B, "Pi" = Pi))
print(HMM.discrete)

### Values for a hidden Markov model with continuous observations
# Number of hidden states = 3
# Univariate gaussian mixture model

N = c("Low", "Normal", "High")
A <- matrix(c(0.5, 0.3, 0.2,
              0.2, 0.6, 0.2,
              0.1, 0.3, 0.6),
             ncol= length(N), byrow = TRUE)
Mu <- matrix(c(0, 50, 100), ncol = length(N))
Sigma <- array(c(144, 400, 100), dim = c(1,1,length(N)))
Pi <- rep(1/length(N), length(N))

newModel <- verifyModel(list(  "Model"="GMM",
                              "StateNames" = N,
                              "A" = A,
                              "Mu" = Mu,
                              "Sigma" = Sigma,
                              "Pi" = Pi))

### Values for a hidden Markov model with continuous observations
# Number of hidden states = 2
# Multivariate gaussian mixture model
# Observed vector with dimensionality of 3
N = c("X1", "X2")
M <- 3

# Same number of dimensions
Sigma <- array(0, dim =c(M,M,length(N)))
Sigma[,,1] <- matrix(c(1.0, 0.8, 0.8,
                       0.8, 1.0, 0.8,
                       0.8, 0.8, 1.0), ncol = M)
Sigma[,,2] <- matrix(c(1.0, 0.4, 0.6,
                       0.4, 1.0, 0.8,
                       0.6, 0.8, 1.0), ncol = M)
Mu <- matrix(c(0, 5, 10, 0,
               5, 10, nrow = M)
A <- matrix(c(0.6, 0.3,
             0.4, 0.7), ncol = length(N))
Pi <- c(0.5, 0.5)

newModel <- verifyModel(list(  "Model" = "GHMM",
                               "StateNames" = N,
viterbi

Viterbi algorithm for hidden state decoding

**Description**

Function used to get the most likely path of hidden states generated by the observed sequence.

**Usage**

`viterbi(hmm, sequence)`

**Arguments**

- `hmm`: a list with the necessary variables to define a hidden Markov model.
- `sequence`: sequence of observations to be decoded. HMM and PHMM use a vector. GHMM uses a matrix.

**Details**

The Viterbi algorithm is based on a greedy approach, therefore it would only give the most probable path. GHMM uses a matrix with the variables as rows and consecutive observations in the columns.

**Value**

A vector with the path of hidden states that generated the observed sequence.

**References**

Cited references are listed on the RcppHMM manual page.

**See Also**

`generateObservations`, `verifyModel`, `forwardBackward`
Examples

```r
## Values for a hidden Markov model with categorical observations
# Set the model parameters
n <- c("First", "Second")
m <- c("A", "T", "C", "G")
A <- matrix(c(0.8, 0.2, 0.1, 0.9),
nrow = 2,
byrow = TRUE)

B <- matrix(c(0.2, 0.2, 0.3, 0.3, 0.4, 0.4, 0.1, 0.1),
nrow = 2,
byrow = TRUE)

Pi <- c(0.5, 0.5)

params <- list("Model" = "HMM",
  "StateNames" = n,
  "ObservationNames" = m,
  "A" = A,
  "B" = B,
  "Pi" = Pi)

HMM <- verifyModel(params)

# Data simulation
set.seed(100)
length <- 100
observationSequence <- generateObservations(HMM, length)

# Sequence decoding
hiddenStates <- viterbi(HMM, observationSequence$Y)
print(hiddenStates)

## Values for a hidden Markov model with discrete observations
n <- c("Low", "Normal", "High")

A <- matrix(c(0.5, 0.3, 0.2, 0.2, 0.6, 0.2, 0.1, 0.3, 0.6),
  ncol=length(n), byrow=TRUE)

B <- c(2000, 2700, 2800) # First distribution with mean 2000
     # Second distribution with mean 2700
     # Third distribution with mean 2800

Pi <- rep(1/length(n), length(n))

HMM.discrete <- verifyModel(list("Model"="PHMM", "StateNames" = n, "A" = A, "B" = B, "Pi" = Pi))
```
```r
# Data simulation
set.seed(100)
length <- 100
observationSequence <- generateObservations(HMM.discrete, length)

# Sequence decoding
hiddenStates <- viterbi(HMM.discrete, observationSequence$Y)
print(hiddenStates)

## Values for a hidden Markov model with continuous observations
## Number of hidden states = 3
## Univariate gaussian mixture model

N = c("Low", "Normal", "High")
A <- matrix(c(0.5, 0.3, 0.2,
              0.2, 0.6, 0.2,
              0.1, 0.3, 0.6),
             ncol= length(N), byrow = TRUE)
Mu <- matrix(c(0, 50, 100), ncol = length(N))
Sigma <- array(c(144, 400, 100), dim = c(1,1,length(N)))
Pi <- rep(1/length(N), length(N))

HMM.cont.univariate <- verifyModel(list(
"Model"="GHMM",
"StateNames" = N,
"A" = A,
"Mu" = Mu,
"Sigma" = Sigma,
"Pi" = Pi))

# Data simulation
set.seed(100)
length <- 100
observationSequence <- generateObservations(HMM.cont.univariate, length)

# Sequence decoding
hiddenStates <- viterbi(HMM.cont.univariate, observationSequence$Y)
print(hiddenStates)

## Values for a hidden Markov model with continuous observations
## Number of hidden states = 2
## Multivariate gaussian mixture model
## Observed vector with dimensionality of 3
N = c("X1","X2")
M <- 3

## Same number of dimensions
Sigma <- array(0, dim =c(M,M,length(N)))
Sigma[,1] <- matrix(c(1,0,0,0,8,0,8,
                      0,8,0,0,8,0,8,
                      0,8,0,8,1,0), ncol = M,
                      byrow = TRUE)
Sigma[,2] <- matrix(c(1,0,0,0,4,0,6,
                      0,4,0,0,4,0,4,
                      0,4,0,4,1,0), ncol = M,
                      byrow = TRUE)
```


0.4, 1.0, 0.8,
0.6, 0.8, 1.0), ncol = M,
byrow = TRUE)

Mu <- matrix(c(0, 5,
10, 0,
5, 10),
nrow = M,
byrow = TRUE)

A <- matrix(c(0.6, 0.4,
0.3, 0.7),
ncol = length(N),
byrow = TRUE)

Pi <- c(0.5, 0.5)

HMM.cont.multi <- verifyModel(list("Model" = "GHHM",
"StateNames" = N,
"A" = A,
"Mu" = Mu,
"Sigma" = Sigma,
"Pi" = Pi))

# Data simulation
set.seed(100)
length <- 100
observationSequence <- generateObservations(HMM.cont.multi, length)

# Sequence decoding
hiddenStates <- viterbi(HMM.cont.multi, observationSequence$Y)
print(hiddenStates)
Index

*Topic documentation
  Change Log, 4

*Topic initialization
  initGHMM, 15
  initHMM, 16
  initPHMM, 17

*Topic methods
  evaluation, 5
  forwardBackward, 8
  generateObservations, 12
  loglikelihood, 23
  setNames, 27
  setParameters, 28
  verifyModel, 5, 9, 18, 23, 30, 33
  viterbi, 9, 33

*Topic optimize
  learnEM, 18
  viterbi, 33

Change Log, 4
Changes (Change Log), 4

evaluation, 5, 23

forwardBackward, 8, 33

generateObservations, 5, 9, 12, 18, 23, 33

initGHMM, 4, 15, 16, 17
initHMM, 15, 16, 17
initPHMM, 15, 16, 17

learnEM, 18
list, 12, 15–18, 27, 28, 31
loglikelihood, 5, 23

RcppHMM, 5, 9, 16–18, 23, 33
RcppHMM (RcppHMM-package), 2
RcppHMM-package, 2

setNames, 27