

Package ‘hmma’

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Type Package

Title Constructs Asymmetric Hidden Markov Models

Version 1.0.0

Description Asymmetric hidden Markov model (HMM-A) learning.
HMM-As are similar to regular HMMs, but use Bayesian Networks (BNs) in their emission distribution. The HMM-As can therefore offer more problem insight [Bueno et al. 2017, <doi:10.1016/j.ijar.2017.05.011>].

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createHmma	<i>Create an asymmetric hidden Markov model.</i>
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Description

The createHmma method creates a HMM-A from the specifications provided. The amount of states are implicitly derived from the initial distribution. Bayesian networks can be created using the bnlearn package.

Usage

```
createHmma(init, trans, bns)
```

Arguments

init	This initial distribution as a vector.
trans	The transition distribution as a matrix.
bns	The Bayesian networks for the states.

See Also

[bnlearn](#) for more information regarding the creation of Bayesian networks

Examples

```
# Start by creating the initial and transition distribution
init <- c(0.3, 0.7)
trans <- c(0.4, 0.7, 0.6, 0.3)
dim(trans) <- c(2,2)

# Create a Bayesian network for each state using 'bnlearn'
library(bnlearn)
struc <- model2network("[X1][X2]")
cptX1 <- matrix(c(0.15, 0.85), ncol = 2, dimnames = list(NULL, c("TRUE", "FALSE")))
cptX2 <- matrix(c(0.7, 0.3), ncol = 2, dimnames = list(NULL, c("TRUE", "FALSE")))

bn1 <- custom.fit(struc, dist = list(X1 = cptX1,
```

```
                                X2 = cptX2))

struc <- model2network("[X2|X1][X1]")
cptX1 <- matrix(c(0.4, 0.6), ncol = 2, dimnames = list(NULL, c("TRUE", "FALSE")))
cptX2 <- matrix(c(0.9, 0.1, 0.5, 0.5), nrow = 2, ncol = 2)
dimnames(cptX2) <- list("X2" = c("TRUE", "FALSE"),
                        "X1" = c("TRUE", "FALSE"))

bn2 <- custom.fit(struc, dist = list(X1 = cptX1,
                                    X2 = cptX2))

bns <- list()
bns[[1]] <- bn1
bns[[2]] <- bn2

# Create the model
hmma <- createHmma(init = init, trans = trans, bns = bns)
```

hmma

hmma: A package for the construction of asymmetric hidden Markov models

Description

The hmma package is able to construct asymmetric hidden Markov models (HMM-As) from data. HMM-As are similar to regular HMMs, but use Bayesian Networks (BNs) in their emission distribution.

Details

HMMs have successfully been used in “speech recognition systems, in numerous applications in computational molecular biology, in data compression, and in other areas of artificial intelligence and pattern recognition”.

When limited data is available, HMMs may be unable to correctly capture these distributions. Bueno et al. show that HMMs can be enriched by employing state-specific Bayesian networks (BNs), i.e. BNs that may be different from state to state. This enables the model to better capture certain independencies, depending on the state. The resulting models are called asymmetric hidden Markov models (HMM-As). (see: <http://dx.doi.org/10.1016/j.ijar.2017.05.011> for more information)

hmmaExampleData	<i>An example dataset for use on HMM-As</i>
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Description

This dataset has been generated using a HMM-A with two different Bayesian networks. The observations consist of 100 sequences of length 20.

Usage

```
hmmaExampleData
```

Format

A list with the following items

x All observations.

N The length of the observation sequence.

Details

The sum of all observation lengths (`hmmaExampleData$N`) must be equal to the total number of observations (`hmmaExampleData$x`).

learnModel	<i>Learns a HMM-A from data</i>
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Description

The `learnModel` function, learns a HMM-A from the supplied data file. The function first creates a random model: the initial and transition distributions are initialized using a Dirichlet https://en.wikipedia.org/wiki/Dirichlet_distribution distribution. Thereafter the model is maximised for the datafile that is supplied.

Usage

```
learnModel(  
  data,  
  amountOfStates = 2,  
  maxit = 50,  
  seed,  
  iss = 1e-04,  
  debug = FALSE  
)
```

Arguments

data	The datafile. The datafile should be a list containing a dataframe with the data as its \$x component and contain the lengths of the observations a the \$N component (see details).
amountOfStates	The amount of states.
maxit	The maximum amount of iterations.
seed	Seed (optional).
iss	The Imaginary Sample Size (iss), also called priors, to add data.
debug	Debugmode.

Details

The learnModel makes use of the mhsmm [hmmfit](#) function. An example of the structure of the datafile can be found in [hmmaExampleData](#).

Value

The output of the function is an asymmetric hidden Markov model. This model contains the amount of states, the initial distribution, the transition distribution and the emission distribution (Bayesian networks in the different states).

The model can quickly be visualised with the [visualise](#) method. The [visualise](#) method does not show the Bayesian networks within the states as this would result in unreadable graphs. Instead, the bnlearn [graphviz.plot](#) method can be used (see the examples below).

Examples

```
fit <- learnModel(data = hmmaExampleData, amountOfStates = 3, seed = 1234)
visualise(fit)

# See bn in first state
library(bnlearn)
graphviz.plot(fit$params.emission[[1]])
```

predict.hmma

Predict sequence of data on HMMA

Description

predict.hmma is simply a wrapper function for the mhsmm [predict.hmmspec](#) function. It generates the predicted state sequence for data, given the model.

Usage

```
## S3 method for class 'hmma'
predict(object, data, method = "viterbi", ...)
```

Arguments

object	The HMMA
data	The data file
method	The prediction method (viterbi or smoothed, see details)
...	Futher arguments.

Details

From the mhsmm documentation: If method="viterbi", this technique applies the Viterbi algorithm for HMMs, producing the most likely sequence of states given the observed data. If method="smoothed", then the individually most likely (or smoothed) state sequence is produced, along with a matrix with the respective probabilities for each state. This function differs from predict.hmm in that it takes the output from hmmspec ie. this is useful when users already know their parameters and wish to make predictions.

Value

The return object contains the data, a vector 's' with the reconstructed state sequence, the vector N with the lengths of the sequences, a matrix p with the probabilities of the states (only with smoothed). For more details see [predict.hmmspec](#).

The loglikelihood is returned as the \$loglik component.

See Also

[predict.hmmspec](#) for more information.

simulate.hmma	<i>Simulates a HMM-A.</i>
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Description

simulate.hmma simulates a HMM-A. The only difference between simulate.hmma and simulate.hmmspec is that this function adds the names of the nodes of the Bayesian networks to the results. The simulate.hmmspec function only uses numbers, instead of names.

Usage

```
## S3 method for class 'hmma'
simulate(object, nsim, seed = NULL, ...)
```

Arguments

object	A hmma object
nsim	An integer or vector of integers (for multiple sequences) specifying the length of the sequence(s)
seed	seed for the random number generator
...	Further arguments passed to or from other methods.

Value

A simulation with the following values

- *s* The states of the model.
- *x* The observations.
- *n* The length of the observation.

Examples

```
# Get a HMM-A (e.g. from learnModel or createHmma)
model <- learnModel(data = hmmaExampleData, amountOfStates = 2, seed = 1234)

# Simulate the data, results in 100 observation sequences of length 20.
data <- simulate(model, nsim = c(rep(20, 100)))
```

visualise

Visualise the HMM-A

Description

The function *visualise* shows a graphical representation of the found HMM-A. Only the initial distribution and transition distribution are shown. Each state contains a Bayesian network, these would be unreadable when displayed within each state. The bnlearn [graphviz.plot](#) method is used to display the bayesian networks.

Usage

```
visualise(model, numDigitsRound = 2)
```

Arguments

model The model.
numDigitsRound The amount of decimals that should be presented in the graph.

Examples

```
# First, we need a model that we want to visualise, we create
# one using the learnModel function.
fit <- learnModel(data = hmmaExampleData, amountOfStates = 3)

# To visualise the states and transitions, we use the visualise method
visualise(fit)

# To visualise the BNs within the states, use the code below
library(bnlearn)
graphviz.plot(fit$params.emission[[1]])
```

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