Package 'drimmR'

February 24, 2021

Type Package

Title Estimation, Simulation and Reliability of drifting Markov Models

Version 1.0.0

Author Vlad Stefan Barbu,
Geoffray Brelurut,
Annthomy Gilles,
Arnaud Lefebvre,
Victor Mataigne,
Alexandre Seiller,
Nicolas Vergne

Maintainer Nicolas Vergne <Nicolas.Vergne@univ-rouen.fr>

Description This package introduces the drifting Markov models (DMMs) which are
non-homogeneous Markov models designed for modeling the heterogeneities of
sequences in a more flexible way than homogeneous Markov chains or even
hidden Markov models. In this context, we developed an R package dedicated to
the estimation, simulation and the exact computation of associated reliability
of drifting Markov models. The implemented methods are described in
Vergne, N. (2008), <doi:10.2202/1544-6115.1326> and
Barbu, V.S., Vergne, N. (2019) <doi:10.1007/s11009-018-9682-8> .

License GPL

Encoding UTF-8

LazyData true

Suggests utils,
knitr,
rmarkdown

Imports seqinr,
Biostrings,
testthat,
stats,
ggplot2,
parallel,
foreach,
future,
doParallel,
doSNOW,
tidyverse,
dplyr,

    reshape2,
    Rdpack

RdMacros Rdpack

RoxygenNote 7.1.1

VignetteBuilder knitr

Depends R (>= 2.10)

R topics documented:

---

aic   *Akaike Information Criterion (AIC)*

Description

Generic function computing the Akaike Information Criterion of the model x, with the list of sequences sequences.

Usage

```
aic(x, sequences)
```

Arguments

x	An object for which AIC of the DMM can be computed.
sequences	A vector of character or a list of vector of character representing the sequences for which the AIC criterion must be computed.

Value

A list of AIC (numeric)

Author(s)

Victor Mataigne, Alexandre Seiller

References

Barbu VS, Vergne N (2018). "Reliability and survival analysis for drifting Markov models: modelling and estimation." *Methodology and Computing in Applied Probability*, 1–33. doi: 10.1007/s1100901896828, https://doi.org/10.1007/s11009-018-9682-8. Vergne N (2008). "Drifting Markov models with polynomial drift and applications to DNA sequences." *Statistical Applications in Genetics Molecular Biology* , **7(1)** . doi: 10.2202/15446115.1326, https://doi.org/10.2202/1544-6115.1326.

---

aic.dmm   *Evaluate AIC*

Description

Evaluate AIC

Usage

```
## S3 method for class 'dmm'
aic(x, sequences)
```

Arguments

x	An object of class dmm
sequences	A character vector or a list of character vector representing the sequence

Value

A list of AIC (numeric)

Author(s)

Victor Mataigne, Alexandre Seiller

References

Barbu VS, Vergne N (2018). "Reliability and survival analysis for drifting Markov models: modelling and estimation." *Methodology and Computing in Applied Probability*, 1–33. doi: 10.1007/s1100901896828, https://doi.org/10.1007/s11009-018-9682-8. Vergne N (2008). "Drifting Markov models with polynomial drift and applications to DNA sequences." *Statistical Applications in Genetics Molecular Biology* , **7(1)** . doi: 10.2202/15446115.1326, https://doi.org/10.2202/1544-6115.1326.

See Also

fitdmm, getTransitionMatrix, loglik, aic

Examples

```
data(lambda, package = "drimmR")
sequence <- c("a","g","g","t","c","g","a","t","a","a","a")
dmm <- fitdmm(lambda, 1, 1, c('a','c','g','t'), init.estim = "freq", fit.method="sum")
aic(dmm,sequence)
```

---

availability   *Availability function*

Description

Pointwise (or instantaneous) availability of a system at time $l \in N$

Usage

```
availability(x, k1, k2, upstates, output_file = NULL, plot = FALSE)
```

Arguments

x	An object of class dmm
k1	Start position : a positive integer giving the start position along the sequence from which the availabilities of the DMM should be computed
k2	End position : a positive integer giving the end position along the sequence until which the availabilities of the DMM should be computed
upstates	Character vector of the subspace working states among the state space vector such that upstates< s
output_file	(Optional) A file containing matrix of availability probabilities (e.g, "C:/.../AVAL.txt")
plot	FALSE (no figure plot of availability by position); TRUE (figure plot)

Details

The pointwise (or instantaneous) availability is the probability that the system is in a working state at time l, independently of the fact that the system worked or not during the time interval $[0; l)$

Value

A matrix with positions and availability probabilities of states (and figure plot)

Author(s)

Alexandre Seiller

References

Barbu VS, Vergne N (2018). "Reliability and survival analysis for drifting Markov models: modelling and estimation." *Methodology and Computing in Applied Probability*, 1–33. doi: 10.1007/s1100901896828, https://doi.org/10.1007/s11009-018-9682-8.

See Also

fitdmm, getTransitionMatrix, reliability, maintainability

Examples

```
data(lambda, package = "drimmR")
dmm <- fitdmm(lambda, 1, 1, c('a','c','g','t'), init.estim = "freq", fit.method="sum")
k1 <- 1
k2 <- 200
upstates <- c("c","t")  # vector of working states
availability(dmm,k1,k2,upstates,plot=TRUE)
```

---

bic   *Bayesian Information Criterion (BIC)*

Description

Generic function computing the Bayesian Information Criterion of the model x, with the list of sequences sequences.

Usage

```
bic(x, sequences)
```

Arguments

x	An object for which BIC of the DMM can be computed.
sequences	A vector or a list of vector of character representing the sequences for which the BIC criterion must be computed.

Value

A list of BIC (numeric)

Author(s)

Victor Mataigne, Alexandre Seiller

References

Barbu VS, Vergne N (2018). "Reliability and survival analysis for drifting Markov models: modelling and estimation." *Methodology and Computing in Applied Probability*, 1–33. doi: 10.1007/s1100901896828, https://doi.org/10.1007/s11009-018-9682-8. Vergne N (2008). "Drifting Markov models with polynomial drift and applications to DNA sequences." *Statistical Applications in Genetics Molecular Biology* , **7(1)** . doi: 10.2202/15446115.1326, https://doi.org/10.2202/1544-6115.1326.

---

bic.dmm   *Evaluate BIC*

Description

Evaluate BIC

Usage

```
## S3 method for class 'dmm'
bic(x, sequences)
```

Arguments

x	An object of class dmm
sequences	A character vector or a list of character vector representing the sequence

Value

A list of BIC (numeric)

Author(s)

Victor Mataigne, Alexandre Seiller

References

Barbu VS, Vergne N (2018). "Reliability and survival analysis for drifting Markov models: modelling and estimation." *Methodology and Computing in Applied Probability*, 1–33. doi: 10.1007/s1100901896828, https://doi.org/10.1007/s11009-018-9682-8. Vergne N (2008). "Drifting Markov models with polynomial drift and applications to DNA sequences." *Statistical Applications in Genetics Molecular Biology* , **7(1)** . doi: 10.2202/15446115.1326, https://doi.org/10.2202/1544-6115.1326.

See Also

fitdmm, getTransitionMatrix, loglik, bic

Examples

```
data(lambda, package = "drimmR")
sequence <- c("a","g","g","t","c","g","a","t","a","a","a")
dmm<- fitdmm(lambda, 1, 1, c('a','c','g','t'), init.estim = "freq", fit.method="sum")
bic(dmm,sequence)
```

---

distributions   *Plot distributions for a range of positions between <start> and <end>*

Description

Plot distributions for a range of positions between <start> and <end>

Usage

```
distributions(
  x,
  start = 1,
  end = NULL,
  step = NULL,
  output_file = NULL,
  plot = FALSE
)
```

Arguments

x	An object of class dmm
start	Start position : a positive integer giving the start position along the sequence from which the distributions of the DMM should be computed
end	End position : a positive integer giving the end position along the sequence until which the distributions of the DMM should be computed
step	A step (integer)
output_file	(Optional) A file containing matrix of distributions (e.g, "C:/.../DIST.txt")
plot	FALSE (no figure plot of dist evolution); TRUE (figure plot)

Value

A matrix with positions and distributions of states (and figure plot)

Author(s)

Alexandre Seiller

References

Barbu VS, Vergne N (2018). "Reliability and survival analysis for drifting Markov models: modelling and estimation." *Methodology and Computing in Applied Probability*, 1–33. doi: 10.1007/s1100901896828, https://doi.org/10.1007/s11009-018-9682-8. Vergne N (2008). "Drifting Markov models with polynomial drift and applications to DNA sequences." *Statistical Applications in Genetics Molecular Biology* , **7(1)** . doi: 10.2202/15446115.1326, https://doi.org/10.2202/1544-6115.1326.

See Also

fitdmm, getDistribution, getStationaryLaw

Examples

```
data(lambda, package = "drimmR")
dmm <- fitdmm(lambda, 1, 1, c('a','c','g','t'), init.estim = "freq", fit.method="sum")
distributions(dmm,start=1,end=1000,step=100, plot=TRUE)
```

---

failureRate	*Failure rates function*

Description

Estimation of two different definition of the failure rate : the BMP-failure rate and RG-failure rate.

As for BMP-failure rate, consider a system S starting to work at time $l = 0$. The BMP-failure rate at time $l \in N$ is the conditional probability that the failure of the system occurs at time l, given that the system has worked until time $l - 1$.

The RG-failure rate is a discrete-time adapted failure-rate proposed by D. Roy and R. Gupta. Classification of discrete lives. *Microelectronics Reliability*, 32(10):1459–1473, 1992.

Usage

```
failureRate(
  x,
  k1,
  k2,
  upstates,
  failure.rate = c("BMP", "RG"),
  output_file = NULL,
  plot = FALSE
)
```

Arguments

x	An object of class dmm
k1	Start position : a positive integer giving the start position along the sequence from which the failure rates of the DMM should be computed
k2	End position : a positive integer giving the end position along the sequence until which the failure rates of the DMM should be computed
upstates	Character vector of the subspace working states among the state space vector such that upstates < s
output_file	(Optional) A file containing matrix of failure rates at each position (e.g, "C:/.../ER.txt")
plot	FALSE (no figure plot of failure rates by position); TRUE (figure plot)
failure.rate	Default="BMP", then BMP-failure-rate is the method used to estimate the failure rate. If failure.rate= "RG", then RG-failure rate is the method used to estimate the failure rate.

Details

The BMP-failure rate denoted by $\lambda(l), l \in N$ is usually considered for continuous time systems.

The RG-failure rate denoted by $r(l), l \in N$ is adapted to work in discrete time systems.

Value

A matrix with positions and failure rate scores of states (and figure plot)

Author(s)

Alexandre Seiller

References

Barbu VS, Vergne N (2018). "Reliability and survival analysis for drifting Markov models: modelling and estimation." *Methodology and Computing in Applied Probability*, 1–33. doi: 10.1007/s1100901896828, https://doi.org/10.1007/s11009-018-9682-8. Roy D, Gupta R (1992). "Classification of discrete lives. Microelectronics Reliability." *Microelectronics Reliability*, 1459–1473. doi: 10.1016/00262714(92)90015D, https://doi.org/10.1016/0026-2714(92)90015-D.

See Also

fitdmm, getTransitionMatrix, reliability

Examples

```
data(lambda, package = "drimmR")
dmm <- fitdmm(lambda, 1, 1, c('a','c','g','t'), init.estim = "freq", fit.method="sum")
k1 <- 1
k2 <- 200
upstates <- c("c","t")  # vector of working states
failureRate(dmm,k1,k2,upstates,failure.rate="BMP",plot=TRUE)
```

---

fitdmm   *Point by point estimates of a k-th order drifting Markov Model*

Description

Estimation of d+1 points of support transition matrices and $|E|^k$ initial law of a k-th order drifting Markov Model starting from one or several sequences.

Usage

```
fitdmm(
  sequences,
  order,
  degree,
  states,
  init.estim = c("mle", "freq", "prod", "stationary", "unif"),
  fit.method = c("sum")
)
```

Arguments

sequences	A list of character vector(s) representing one (several) sequence(s)
order	Order of the Markov chain
degree	Degree of the polynomials (e.g., linear drifting if degree=1, etc.)
states	Vector of states space of length s > 1
init.estim	Default="mle". Method used to estimate the initial law. If init.estim = "mle", then the classical Maximum Likelihood Estimator is used, if init.estim = "freq", then, the initial distribution init.estim is estimated by taking the frequences of the words of length k for all sequences. If init.estim = "prod", then, init.estim is estimated by using the product of the frequences of each letter (for all the sequences) in the word of length k. If init.estim = "stationary", then init.estim is estimated by using the stationary law of the point of support transition matrices of each letter. If init.estim = "unif", then, init.estim of each letter is estimated by using $\frac{1}{s}$. Or 'init.estim'= customisable vector of length $|E|^k$. See Details for the formulas.
fit.method	If sequences is a list of several character vectors of the same length, the usual LSE over the sample paths is proposed when fit.method="sum" (a list of a single character vector is its special case).

Details

The fitdmm function creates a drifting Markov model object dmm.

Let $E = 1, \ldots, s$, $s < \infty$ be random system with finite state space, with a time evolution governed by discrete-time stochastic process of values in E. A sequence $X_0, X_1, \ldots, X_n$ with state space $E = 1, 2, \ldots, s$ is said to be a linear drifting Markov chain (of order 1) of length n between the Markov transition matrices Π_0 and Π_1 if the distribution of X_t, $t = 1, \ldots, n$, is defined by $P(X_t = v \mid X_{t-1} = u, X_{t-2}, \ldots) = \Pi_{\frac{t}{n}}(u, v)$, ; $u, v \in E$, where $\Pi_{\frac{t}{n}}(u, v) = (1 - \frac{t}{n})\Pi_0(u, v) + \frac{t}{n}\Pi_1(u, v)$, $u, v \in E$. The linear drifting Markov model of order 1 can be generalized to polynomial drifting Markov model of order k and degree d. Let $\Pi_{\frac{i}{d}} = (\Pi_{\frac{i}{d}}(u_1, \ldots, u_k, v))_{u_1, \ldots, u_k, v \in E}$ be d Markov transition matrices (of order k) over a state space E.

The estimation of DMMs is carried out for 4 different types of data :

One can observe one sample path : It is denoted by $H(m, n) := (X_0, X_1, \ldots, X_m)$, where m denotes the length of the sample path and n the length of the drifting Markov chain. Two cases can be considered:

1. m=n (a complete sample path),
2. m < n (an incomplete sample path).

One can also observe H i.i.d. sample paths : It is denoted by $H_i(m_i, n_i), i = 1, \ldots, H$. Two cases cases are considered :

1. $m_i = n_i = n \forall i = 1, \ldots, H$ (complete sample paths of drifting Markov chains of the same length),
2. $n_i = n \forall i = 1, \ldots, H$ (incomplete sample paths of drifting Markov chains of the same length). In this case, an usual LSE over the sample paths is used.

The initial distribution of a k-th order drifting Markov Model is defined as $\mu_i = P(X_1 = i)$. The initial distribution of the k first letters is freely customisable by the user, but five methods are proposed for the estimation of the latter :

Estimation based on the Maximum Likelihood Estimator: The Maximum Likelihood Estimator for the initial distribution. The formula is: $\widehat{\mu_i} = \frac{Nstart_i}{L}$, where $Nstart_i$ is the number of occurences of the word i (of length k) at the beginning of each sequence and L is the number of sequences. This estimator is reliable when the number of sequences L is high.

Estimation based on the frequency: The initial distribution is estimated by taking the frequences of the words of length k for all sequences. The formula is $\widehat{\mu_i} = \frac{N_i}{N}$, where N_i is the number of occurences of the word i (of length k) in the sequences and N is the sum of the lengths of the sequences.

Estimation based on the product of the frequences of each state: The initial distribution is estimated by using the product of the frequences of each state (for all the sequences) in the word of length k.

Estimation based on the stationary law of point of support transition matrix for a word of length k : The initial distribution is estimated using $\mu(\Pi_{\frac{k-1}{n}})$

Estimation based on the uniform law : $\frac{1}{s}$

Value

An object of class dmm

Author(s)

Geoffray Brelurut, Alexandre Seiller

References

Barbu VS, Vergne N (2018). "Reliability and survival analysis for drifting Markov models: modelling and estimation." *Methodology and Computing in Applied Probability*, 1–33. doi: 10.1007/s1100901896828, https://doi.org/10.1007/s11009-018-9682-8. Vergne N (2008). "Drifting Markov models with polynomial drift and applications to DNA sequences." *Statistical Applications in Genetics Molecular Biology* , **7(1)** . doi: 10.2202/15446115.1326, https://doi.org/10.2202/1544-6115.1326.

Examples

```
data(lambda, package = "drimmR")
states <- c("a","c","g","t")
order <- 1
degree <- 1
fitdmm(lambda,order,degree,states, init.estim = "freq",fit.method="sum")
```

---

getDistribution   *Get the distributions of the DMM*

Description

Generic function evaluating the distribution of a model x at a given position code or at every position all.pos

Usage

```
getDistribution(x, pos, all.pos = FALSE, internal = FALSE)
```

Arguments

x	An object for which the distributions of the DMM can be computed.
pos	A positive integer giving the position along the sequence on which the distribution of the DMM should be computed
all.pos	'FALSE' (evaluation at position index) ; 'TRUE' (evaluation for all position indices)
internal	'FALSE' (default) ; 'TRUE' (for internal use of the distributions function)

Details

Distribution at position l is evaluated by $\mu_l = \mu_0 \prod_{t=k}^{l} \pi_{\frac{t}{n}}, \forall l \geq k, k \in N^*$ order of the DMM

Value

A vector or matrix of distribution probabilities

Author(s)

Alexandre Seiller

References

Barbu VS, Vergne N (2018). "Reliability and survival analysis for drifting Markov models: modelling and estimation." *Methodology and Computing in Applied Probability*, 1–33. doi: 10.1007/s1100901896828, https://doi.org/10.1007/s11009-018-9682-8. Vergne N (2008). "Drifting Markov models with polynomial drift and applications to DNA sequences." *Statistical Applications in Genetics Molecular Biology* , **7(1)** . doi: 10.2202/15446115.1326, https://doi.org/10.2202/1544-6115.1326.

---

getDistribution.dmm   *Get the distributions of the DMM*

Description

Evaluate the distribution of the DMM at a given position or at every position

Usage

```
## S3 method for class 'dmm'
getDistribution(x, pos, all.pos = FALSE, internal = FALSE)
```

Arguments

x	An object of class dmm
pos	A positive integer giving the position along the sequence on which the distribution of the DMM should be computed
all.pos	'FALSE' (default, evaluation at position index) ; 'TRUE' (evaluation for all position indices)
internal	'FALSE' (default) ; 'TRUE' (for internal use of distributions function)

Details

Distribution at position l is evaluated by $\mu_l = \mu_0 \prod_{t=k}^{l} \pi_{\frac{t}{n}}, \forall l \geq k, k \in N^*$ order of the DMM

Value

A vector or matrix of distribution probabilities

Author(s)

Alexandre Seiller

References

Barbu VS, Vergne N (2018). "Reliability and survival analysis for drifting Markov models: modelling and estimation." *Methodology and Computing in Applied Probability*, 1–33. doi: 10.1007/s1100901896828, https://doi.org/10.1007/s11009-018-9682-8. Vergne N (2008). "Drifting Markov models with polynomial drift and applications to DNA sequences." *Statistical Applications in Genetics Molecular Biology* , **7(1)** . doi: 10.2202/15446115.1326, https://doi.org/10.2202/1544-6115.1326.

See Also

fitdmm, getTransitionMatrix, distributions, getStationaryLaw

Examples

```
data(lambda, package = "drimmR")
dmm <- fitdmm(lambda, 1, 1, c('a','c','g','t'), init.estim = "freq", fit.method="sum")
t <- 10
getDistribution(dmm,pos=t)
```

---

getStationaryLaw   *Get the stationary laws of the DMM*

Description

Generic function evaluating the stationary law of a model x at a given position pos or at every position all.pos

Usage

```
getStationaryLaw(x, pos, all.pos = FALSE, internal = FALSE)
```

Arguments

x	An object for which the stationary laws of the DMM can be computed.
pos	A positive integer giving the position along the sequence on which the stationary law of the DMM should be computed
all.pos	'FALSE' (default, evaluation at position index) ; 'TRUE' (evaluation for all position indices)
internal	'FALSE' (default) ; 'TRUE' (for internal use of the initial law computation)

Details

Stationary law at position t is evaluated by solving $\mu_t \, \pi_{\frac{t}{n}} = \mu$

Value

A vector or matrix of stationary law probabilities

Author(s)

Alexandre Seiller

References

Barbu VS, Vergne N (2018). "Reliability and survival analysis for drifting Markov models: modelling and estimation." *Methodology and Computing in Applied Probability*, 1–33. doi: 10.1007/s1100901896828, https://doi.org/10.1007/s11009-018-9682-8. Vergne N (2008). "Drifting Markov models with polynomial drift and applications to DNA sequences." *Statistical Applications in Genetics Molecular Biology* , **7(1)** . doi: 10.2202/15446115.1326, https://doi.org/10.2202/1544-6115.1326.

---

getStationaryLaw.dmm   *Get the stationary laws of the DMM*

Description

Evaluate the stationary law of the DMM at a given position or at every position

Usage

```
## S3 method for class 'dmm'
getStationaryLaw(x, pos, all.pos = FALSE, internal = FALSE)
```

Arguments

x	An object of class dmm
pos	A positive integer giving the position along the sequence on which the stationary law of the DMM should be computed
all.pos	'FALSE' (default, evaluation at position index) ; 'TRUE' (evaluation for all position indices)
internal	'FALSE' (default) ; 'TRUE' (for internal use of th initial law of fitdmm and word applications)

Details

Stationary law at position t is evaluated by solving $\mu_t \, \pi_{\frac{t}{n}} = \mu$

Value

A vector or matrix of stationary law probabilities

Author(s)

Alexandre Seiller

References

Barbu VS, Vergne N (2018). "Reliability and survival analysis for drifting Markov models: modelling and estimation." *Methodology and Computing in Applied Probability*, 1–33. doi: 10.1007/s1100901896828, https://doi.org/10.1007/s11009-018-9682-8. Vergne N (2008). "Drifting Markov models with polynomial drift and applications to DNA sequences." *Statistical Applications in Genetics Molecular Biology* , **7(1)** . doi: 10.2202/15446115.1326, https://doi.org/10.2202/1544-6115.1326.

See Also

fitdmm, getTransitionMatrix, stationary_distributions, getDistribution

Examples

```
data(lambda, package = "drimmR")
dmm <- fitdmm(lambda, 1, 1, c('a','c','g','t'), init.estim = "freq", fit.method="sum")
t <- 10
getStationaryLaw(dmm,pos=t)
```

---

getTransitionMatrix   *Get transition matrix of the drifting Markov Model*

Description

Generic function evaluating the transition matrix of a model x at a given position pos

Usage

```
getTransitionMatrix(x, pos)
```

Arguments

x	An object for which the transition matrices of the DMM can be computed.
pos	A positive integer giving the position along the sequence on which the transition matrix of the DMM should be computed

Value

A transition matrix at a given position

Author(s)

Victor Mataigne, Alexandre Seiller

References

Barbu VS, Vergne N (2018). "Reliability and survival analysis for drifting Markov models: modelling and estimation." *Methodology and Computing in Applied Probability*, 1–33. doi: 10.1007/s1100901896828, https://doi.org/10.1007/s11009-018-9682-8. Vergne N (2008). "Drifting Markov models with polynomial drift and applications to DNA sequences." *Statistical Applications in Genetics Molecular Biology* , **7(1)** . doi: 10.2202/15446115.1326, https://doi.org/10.2202/1544-6115.1326.

---

getTransitionMatrix.dmm

Get transition matrix of the drifting Markov Model

Description

Evaluate the transition matrix of the DMM at a given position

Usage

```
## S3 method for class 'dmm'
getTransitionMatrix(x, pos)
```

Arguments

x	An object of class dmm
pos	A positive integer giving the position along the sequence on which the transition matrix of the DMM should be computed

Value

A transition matrix at a given position

Author(s)

Victor Mataigne, Alexandre Seiller

References

Barbu VS, Vergne N (2018). "Reliability and survival analysis for drifting Markov models: modelling and estimation." *Methodology and Computing in Applied Probability*, 1–33. doi: 10.1007/s1100901896828, https://doi.org/10.1007/s11009-018-9682-8. Vergne N (2008). "Drifting Markov models with polynomial drift and applications to DNA sequences." *Statistical Applications in Genetics Molecular Biology* , **7(1)** . doi: 10.2202/15446115.1326, https://doi.org/10.2202/1544-6115.1326.

See Also

fitdmm

Examples

```
data(lambda, package = "drimmR")
dmm <- fitdmm(lambda, 1, 1, c('a','c','g','t'),init.estim = "freq", fit.method="sum")
t <- 10
getTransitionMatrix(dmm,pos=t)
```

lambda	*lambda genome*

Description

Complete data from phage genome [WT71] of length 48502

Usage

```
data(lambda)
```

Format

A vector object of class "Rdata".

Examples

```
data(lambda)
```

lengthWord_probabilities	
	Probability of occurrence of the observed word of size n in a sequence at several positions

Description

Probability of occurrence of the observed word of size n in a sequence at several positions

Usage

```
lengthWord_probabilities(m, sequence, pos, x, output_file = NULL, plot = FALSE)
```

Arguments

m	An integer, the length word
sequence	A vector of characters
pos	A vector of integer positions
x	An object of class dmm
output_file	(Optional) A file containing the vector of probabilities (e.g,"C:/.../PROB.txt")
plot	FALSE (no figure plot of words probabilities); TRUE (figure plot)

Value

A dataframe of probability by position (and probability plots)

Author(s)

Victor Mataigne, Alexandre Seiller

References

Barbu VS, Vergne N (2018). "Reliability and survival analysis for drifting Markov models: modelling and estimation." *Methodology and Computing in Applied Probability*, 1–33. doi: 10.1007/s1100901896828, https://doi.org/10.1007/s11009-018-9682-8. Vergne N (2008). "Drifting Markov models with polynomial drift and applications to DNA sequences." *Statistical Applications in Genetics Molecular Biology* , **7(1)** . doi: 10.2202/15446115.1326, https://doi.org/10.2202/1544-6115.1326.

See Also

fitdmm, getTransitionMatrix, word_probability

Examples

```
data(lambda, package = "drimmR")
dmm <- fitdmm(lambda, 1, 1, c('a','c','g','t'), init.estim = "freq")
m <- 2
lengthWord_probabilities(m, lambda, c(1,length(lambda)-m+1), dmm,plot=TRUE, fit.method="sum")
```

---

loglik   *Log-likelihood*

Description

Generic function computing the log-likelihood of the model x, with the list of sequences sequences.

Usage

```
loglik(x, sequences)
```

Arguments

x	An object for which the log-likelihood of the DMM can be computed.
sequences	A vector of character or list of vectors representing the sequences for which the log-likelihood of the model must be computed.

Value

A list of loglikelihood (numeric)

Author(s)

Annthomy Gilles, Alexandre Seiller

References

Barbu VS, Vergne N (2018). "Reliability and survival analysis for drifting Markov models: modelling and estimation." *Methodology and Computing in Applied Probability*, 1–33. doi: 10.1007/s1100901896828, https://doi.org/10.1007/s11009-018-9682-8. Vergne N (2008). "Drifting Markov models with polynomial drift and applications to DNA sequences." *Statistical Applications in Genetics Molecular Biology* , **7(1)** . doi: 10.2202/15446115.1326, https://doi.org/10.2202/1544-6115.1326.

---

loglik.dmm	*Evaluate Log-likelihood*

Description

Evaluate Log-likelihood

Usage

```
## S3 method for class 'dmm'
loglik(x, sequences)
```

Arguments

x	An object of class dmm
sequences	A character vector or a list of character vectors representing the sequence

Value

A list of log-likelihood (numeric)

Author(s)

Annthomy Gilles, Alexandre Seiller

References

Barbu VS, Vergne N (2018). "Reliability and survival analysis for drifting Markov models: modelling and estimation." *Methodology and Computing in Applied Probability*, 1–33. doi: 10.1007/s1100901896828, https://doi.org/10.1007/s11009-018-9682-8. Vergne N (2008). "Drifting Markov models with polynomial drift and applications to DNA sequences." *Statistical Applications in Genetics Molecular Biology* , **7(1)** . doi: 10.2202/15446115.1326, https://doi.org/10.2202/1544-6115.1326.

See Also

fitdmm, getTransitionMatrix

Examples

```
data(lambda, package = "drimmR")
sequence <- c("a","g","g","t","c","g","a","t","a","a","a")
dmm <- fitdmm(lambda, 1, 1, c('a','c','g','t'), init.estim = "freq", fit.method="sum")
loglik(dmm,sequence)
```

maintainability	*Maintainability function*

Description

Maintainability of a system at time $k \in N$.

Usage

```
maintainability(x, k1, k2, upstates, output_file = NULL, plot = FALSE)
```

Arguments

x	An object of class dmm
k1	Start position : a positive integer giving the start position along the sequence from which the maintainabilities of the DMM should be computed
k2	End position : a positive integer giving the end position along the sequence until which the maintainabilities of the DMM should be computed
upstates	Character vector of the subspace working states among the state space vector such that upstates < s
output_file	(Optional) A file containing matrix of maintainability probabilities (e.g, "C:/.../MAIN.txt")
plot	FALSE (no figure plot of maintainability by position); TRUE (figure plot)

Details

The maintainability at time $k \in N$ of a system is the probability that the system is repaired up to time l, given that is has failed at time $l = 0$.

Value

A matrix with positions and maintainability probabilities of states (and figure plot)

Author(s)

Alexandre Seiller

References

Barbu VS, Vergne N (2018). "Reliability and survival analysis for drifting Markov models: modelling and estimation." *Methodology and Computing in Applied Probability*, 1–33. doi: 10.1007/s1100901896828, https://doi.org/10.1007/s11009-018-9682-8.

See Also

fitdmm, getTransitionMatrix

Examples

```
data(lambda, package = "drimmR")
dmm <- fitdmm(lambda, 1, 1, c('a','c','g','t'), init.estim = "freq", fit.method="sum")
k1 <- 1
k2 <- 200
upstates <- c("c","t")  # vector of working states
maintainability(dmm,k1,k2,upstates,plot=TRUE)
```

---

reliability	*Reliability function*

Description

Reliability or the survival function of a system at time $l \in N$

Usage

```
reliability(x, k1, k2, upstates, output_file = NULL, plot = FALSE)
```

Arguments

x	An object of class dmm
k1	Start position : a positive integer giving the start position along the sequence from which the reliabilities of the DMM should be computed
k2	End position : a positive integer giving the end position along the sequence until which the reliabilities of the DMM should be computed
upstates	Character vector of the subspace working states among the state space vector such that upstates < s
output_file	(Optional) A file containing matrix of reliability probabilities (e.g, "C:/.../REL.txt")
plot	FALSE (no figure plot of reliability by position); TRUE (figure plot)

Details

The reliability at time $l \in N$ is the probability that the system has functioned without failure in the period $[0, l]$

Value

A matrix with positions and reliability probabilities of states (and figure plot)

Author(s)

Alexandre Seiller

References

Barbu VS, Vergne N (2018). "Reliability and survival analysis for drifting Markov models: modelling and estimation." *Methodology and Computing in Applied Probability*, 1–33. doi: 10.1007/s1100901896828, https://doi.org/10.1007/s11009-018-9682-8.

See Also

[fitdmm](#), [getTransitionMatrix](#)

Examples

```
data(lambda, package = "drimmR")
dmm <- fitdmm(lambda, 1, 1, c('a','c','g','t'), init.estim = "freq", fit.method="sum")
k1 <- 1
k2 <- 200
upstates <- c("c","t")  # vector of working states
reliability(dmm,k1,k2,upstates,plot=TRUE)
```

---

simulate   *Simulate a sequence under a drifting Markov model*

Description

Generic function simulating a sequence of length `model_size` under a model `x`

Usage

```
simulate(x, output_file, model_size = 1e+05)
```

Arguments

x	An object for which simulated sequences of the DMM can be computed.
output_file	(Optional) File containing the simulated sequence (e.g, "C:/.../SIM.txt")
model_size	Size of the model

Value

the vector of simulated sequence

Author(s)

Annthomy Gilles, Alexandre Seiller

References

Barbu VS, Vergne N (2018). "Reliability and survival analysis for drifting Markov models: modelling and estimation." *Methodology and Computing in Applied Probability*, 1–33. doi: [10.1007/s1100901896828](#), <https://doi.org/10.1007/s11009-018-9682-8>. Vergne N (2008). "Drifting Markov models with polynomial drift and applications to DNA sequences." *Statistical Applications in Genetics Molecular Biology* , **7(1)** . doi: [10.2202/15446115.1326](#), <https://doi.org/10.2202/1544-6115.1326>.

---

simulate.dmm   *Simulate a sequence under a drifting Markov model*

Description

Simulate a sequence under a k-th order DMM.

Usage

```
## S3 method for class 'dmm'
simulate(x, output_file = NULL, model_size = NULL)
```

Arguments

x	An object of class dmm
output_file	(Optional) File containing the simulated sequence (e.g, "C:/.../SIM.txt")
model_size	Size of the model

Value

the vector of simulated sequence

Author(s)

Annthomy Gilles, Alexandre Seiller

References

Barbu VS, Vergne N (2018). "Reliability and survival analysis for drifting Markov models: modelling and estimation." *Methodology and Computing in Applied Probability*, 1–33. doi: 10.1007/s1100901896828, https://doi.org/10.1007/s11009-018-9682-8. Vergne N (2008). "Drifting Markov models with polynomial drift and applications to DNA sequences." *Statistical Applications in Genetics Molecular Biology* , **7(1)** . doi: 10.2202/15446115.1326, https://doi.org/10.2202/1544-6115.1326.

See Also

fitdmm, getTransitionMatrix, getStationaryLaw

Examples

```
data(lambda, package = "drimmR")
dmm <- fitdmm(lambda, 1, 1, c('a','c','g','t'), init.estim = "freq", fit.method="sum")
simulate(dmm, model_size=100)
```

---

stationary_distributions

Plot stationary laws for a range of positions between <start> and <end>

Description

Plot stationary laws for a range of positions between <start> and <end>

Usage

```
stationary_distributions(
  x,
  start = 1,
  end = NULL,
  step = NULL,
  output_file = NULL,
  plot = FALSE
)
```

Arguments

x	An object of class dmm
start	Start position : a positive integer giving the start position along the sequence from which the stationary laws of the DMM should be computed
end	End position : a positive integer giving the end position along the sequence until which the stationary laws of the DMM should be computed
step	A step (integer)
output_file	(Optional) A file containing matrix of stationary laws (e.g, "C:/.../SL.txt")
plot	FALSE (no figure plot of SL evolution); TRUE (figure plot)

Value

A matrix with positions and stationary laws of states (and figure plot)

Author(s)

Alexandre Seiller

References

Barbu VS, Vergne N (2018). "Reliability and survival analysis for drifting Markov models: modelling and estimation." *Methodology and Computing in Applied Probability*, 1–33. doi: 10.1007/s1100901896828, https://doi.org/10.1007/s11009-018-9682-8. Vergne N (2008). "Drifting Markov models with polynomial drift and applications to DNA sequences." *Statistical Applications in Genetics Molecular Biology* , **7(1)** . doi: 10.2202/15446115.1326, https://doi.org/10.2202/1544-6115.1326.

See Also

fitdmm, getStationaryLaw

Examples

```
data(lambda, package = "drimmR")
dmm <- fitdmm(lambda, 1, 1, c('a','c','g','t'), init.estim = "freq", fit.method="sum")
stationary_distributions(dmm,start=1,end=1000,step=100, plot=TRUE)
```

---

words_probabilities	*Probability of appearance of several words at several positions of a DMM*

Description

Probability of appearance of several words at several positions of a DMM

Usage

```
words_probabilities(words, pos, x, output_file = NULL, plot = FALSE)
```

Arguments

words	A vector of characters containing words
pos	A vector of integer positions
x	An object of class dmm
output_file	(Optional) A file containing the matrix of probabilities (e.g,"C:/.../PROB.txt")
plot	FALSE (no figure plot of words probabilities); TRUE (figure plot)

Value

A dataframe of word probabilities along the positions of the sequence

Author(s)

Victor Mataigne, Alexandre Seiller

References

Barbu VS, Vergne N (2018). "Reliability and survival analysis for drifting Markov models: modelling and estimation." *Methodology and Computing in Applied Probability*, 1–33. doi: 10.1007/s1100901896828, https://doi.org/10.1007/s11009-018-9682-8. Vergne N (2008). "Drifting Markov models with polynomial drift and applications to DNA sequences." *Statistical Applications in Genetics Molecular Biology* , **7(1)** . doi: 10.2202/15446115.1326, https://doi.org/10.2202/1544-6115.1326.

See Also

fitdmm, getTransitionMatrix, word_probability, word_probabilities

Examples

```
data(lambda, package = "drimmR")
dmm <- fitdmm(lambda, 1, 1, c('a','c','g','t'), init.estim = "freq", fit.method="sum")
words_probabilities(c("atcgattc", "taggct", "ggatcgg"),c(100,300),dmm, plot=TRUE)
```

word_probabilities   *Probabilities of a word at several positions of a DMM*

Description

Probabilities of a word at several positions of a DMM

Usage

```
word_probabilities(word, pos, x, output_file = NULL, plot = FALSE)
```

Arguments

word	A subsequence (string of characters)
pos	A vector of integer positions
x	An object of class dmm
output_file	(Optional) A file containing the vector of probabilities (e.g,"C:/.../PROB.txt")
plot	FALSE (no figure plot of word probabilities); TRUE (figure plot)

Value

A numeric vector, probabilities of word

Author(s)

Victor Mataigne, Alexandre Seiller

References

Barbu VS, Vergne N (2018). "Reliability and survival analysis for drifting Markov models: modelling and estimation." *Methodology and Computing in Applied Probability*, 1–33. doi: 10.1007/s1100901896828, https://doi.org/10.1007/s11009-018-9682-8. Vergne N (2008). "Drifting Markov models with polynomial drift and applications to DNA sequences." *Statistical Applications in Genetics Molecular Biology* , **7(1)** . doi: 10.2202/15446115.1326, https://doi.org/10.2202/1544-6115.1326.

See Also

fitdmm, getTransitionMatrix, word_probability, words_probabilities

Examples

```
data(lambda, package = "drimmR")
dmm <- fitdmm(lambda, 1, 1, c('a','c','g','t'), init.estim = "freq", fit.method="sum")
word_probabilities("aggctga",c(100,300),dmm, plot=TRUE)
```

Description

Probability of a word at a position t of a DMM

Usage

```
word_probability(word, pos, x, output_file = NULL, internal = FALSE)
```

Arguments

word	A subsequence (string of characters)
pos	A position (numeric)
x	An object of class dmm
output_file	(Optional) A file containing the probability (e.g,"C:/.../PROB.txt")
internal	FALSE (default) ; TRUE (for internal use of word applications)

Value

A numeric, probability of word

Author(s)

Victor Mataigne, Alexandre Seiller

References

Barbu VS, Vergne N (2018). "Reliability and survival analysis for drifting Markov models: modelling and estimation." *Methodology and Computing in Applied Probability*, 1–33. doi: 10.1007/s1100901896828, https://doi.org/10.1007/s11009-018-9682-8. Vergne N (2008). "Drifting Markov models with polynomial drift and applications to DNA sequences." *Statistical Applications in Genetics Molecular Biology* , **7(1)** . doi: 10.2202/15446115.1326, https://doi.org/10.2202/1544-6115.1326.

See Also

fitdmm, getTransitionMatrix, word_probabilities, words_probabilities

Examples

```
data(lambda, package = "drimmR")
dmm <- fitdmm(lambda, 1, 1, c('a','c','g','t'), init.estim = "freq", fit.method="sum")
word_probability("aggctga",4,dmm)
```

Index