

Package ‘drimmR’

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Type Package

Title Estimation, Simulation and Reliability of drifting Markov Models

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

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LazyData true

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knitr,
rmarkdown

Imports seqinr,
Biostrings,
testthat,
stats,
ggplot2,
utils,
parallel,
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future,
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RdMacros Rdpack

RoxygenNote 7.1.1

VignetteBuilder knitr

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aic	<i>Akaike Information Criterion (AIC) S3 generic function</i>
-----	---

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 of class "dmm" for which the loglikelihood 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 numeric value giving the value of the AIC.

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/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/10.2202/15446115.1326), <https://doi.org/10.2202/1544-6115.1326>.

aic.dmmsum

Evaluate AIC

Description

Evaluate AIC

Usage

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

Arguments

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

Value

A list of numeric, AIC

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/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/10.2202/15446115.1326), <https://doi.org/10.2202/1544-6115.1326>.

See Also

[dmmsum](#), [getTransitionMatrix](#), [loglik](#), [aic](#)

Examples

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

availability

Evaluate Availability

Description

Estimation of the pointwise (or instantaneous) availability for (ergodic) repairable systems at time $l \in N$

Usage

```
availability(x, k1, k2, s1, output_file = NULL, plot = FALSE)
```

Arguments

x	An object of class "dmm"
k1	start position (numeric)
k2	end position (numeric)
s1	Character vector of the subspace working states among the state space vector s.t. $s1 < s$
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 Availability score at each position

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/s11009-018-9682-8](https://doi.org/10.1007/s11009-018-9682-8), <https://doi.org/10.1007/s11009-018-9682-8>.

See Also

[dmmsum](#), [getTransitionMatrix](#), [reliability](#), [maintainability](#)

Examples

```
data(lambda, package = "drimmR")
dmm <- dmmsum(lambda, 1, 1, c('a','c','g','t'), init.estim = "freq")
k1 <- 1
k2 <- 200
s1 <- c("c","t") # vector of working states
availability(dmm,k1,k2,s1,plot=TRUE)
```

bic

Bayesian Information Criterion (BIC) S3 generic function

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 of class "dmm" for which the loglikelihood 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 numeric value giving the value of the BIC.

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/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/10.2202/15446115.1326), <https://doi.org/10.2202/1544-6115.1326>.

bic.dmmsum	<i>Evaluate BIC</i>
------------	---------------------

Description

Evaluate BIC

Usage

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

Arguments

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

Value

A numeric, BIC

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/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/10.2202/15446115.1326), <https://doi.org/10.2202/1544-6115.1326>.

See Also

[dmmsum](#), [getTransitionMatrix](#), [loglik](#), [bic](#)

Examples

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

Distribution_evol	<i>Plot distributions for a range of positions between <start> and <end></i>
-------------------	--

Description

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

Usage

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

Arguments

x	An object of class "dmm"
start	Start position (numeric)
end	End position (numeric)
step	A step (numeric)
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 of distributions with position and probability of states

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/s11009-018-9682-8](https://doi.org/10.1007/s11009-018-9682-8), <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: [10.2202/1544-6115.1326](https://doi.org/10.2202/1544-6115.1326), <https://doi.org/10.2202/1544-6115.1326>.

See Also

[dmmsum](#), [getDistribution](#), [getStationaryLaw](#)

Examples

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

dmmsum

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

```
dmmsum(
  sequences,
  order,
  degree,
  states,
  init.estim = c("mle", "freq", "prod", "stationary", "unif", ...)
)
```

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 frequencies of the words of length 'k' for all sequences. If 'init.estim' = "prod", then, 'init.estim' is estimated by using the product of the frequencies 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.

Details

The 'dmmsum' function creates a Drifting-Markov model object ('dmm').

Let $E = 1, \dots, s$, $s < \infty$ 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, \dots, X_n with state space $E = 1, 2, \dots, s$ 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 , $t = 1, \dots, n$, is defined by $P(X_t = v \mid X_{t-1} = u, X_{t-2}, \dots) = \Pi_{\frac{t}{n}}(u, v)$, $u, v \in E$, 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 $\Pi_{\frac{i}{d}} = (\Pi_{\frac{i}{d}}(u_1, \dots, u_k, v))_{u_1, \dots, u_k, v \in E}$ be d Markov transition matrices (of order k) over a state space E .

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 be 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: $\hat{\mu}_i = \frac{N_{start_i}}{L}$, where N_{start_i} is the number of occurrences 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 frequencies of the words of length ' k ' for all sequences. The formula is $\hat{\mu}_i = \frac{N_i}{N}$, where N_i is the number of occurrences 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 frequencies of each state: The initial distribution is estimated by using the product of the frequencies 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", [dmmsum](#)

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/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/10.2202/15446115.1326), <https://doi.org/10.2202/1544-6115.1326>.

Examples

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

failureRate	<i>Evaluate failure rates</i>
-------------	-------------------------------

Description

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

Usage

```
failureRate(
  x,
  k1,
  k2,
  s1,
  error.rate = c("BMP", "RG"),
  output_file = NULL,
  plot = FALSE
)
```

Arguments

x	An object of class "dmm"
k1	start position (numeric)
k2	end position (numeric)
s1	Character vector of the subspace working states among the state space vector s.t. $s_1 < s$
error.rate	Default="BMP", then BMP-failure-rate is the method used to estimate the error rate. If error.rate= "RG", then RG-failure rate is the method used to estimate the error rate.
output_file	(Optional) A file containing matrix of error rates at each position (e.g, "C:/.../ER.txt")
plot	FALSE (no figure plot of error rates by position); TRUE (figure plot)

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 error rate score at each position

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/s11009-018-9682-8](https://doi.org/10.1007/s11009-018-9682-8), <https://doi.org/10.1007/s11009-018-9682-8>.

See Also

[dmmsum](#), [getTransitionMatrix](#), [reliability](#)

Examples

```
data(lambda, package = "drimmR")
dmm <- dmmsum(lambda, 1, 1, c('a','c','g','t'), init.estim = "freq")
k1 <- 1
k2 <- 200
s1 <- c("c","t") # vector of working states
failureRate(dmm,k1,k2,s1,error.rate="BMP",plot=TRUE)
```

getDistribution	<i>Get distribution S3 generic function</i>
-----------------	---

Description

Evaluate distribution at a given position or at every position

Usage

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

Arguments

x	An object of class "dmm"
pos	An integer, a position
all.pos	FALSE (evaluation at pos index) ; TRUE (evaluation for all pos indices)
internal	FALSE (default) ; TRUE (for internal use of distrib_evol 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/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: [10.2202/1544-6115.1326](https://doi.org/10.2202/1544-6115.1326), <https://doi.org/10.2202/1544-6115.1326>.

getDistribution.dmmsum

Get distribution

Description

Evaluate distribution at a given position or at every position

Usage

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

Arguments

x	An object of class "dmm", dmmsum
pos	An integer for position
all.pos	FALSE (default, evaluation at position index) ; TRUE (evaluation for all position indices)
internal	FALSE (default) ; TRUE (for internal use of distrib_evol 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/s11009-018-9682-8](https://doi.org/10.1007/s11009-018-9682-8), <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/10.2202/15446115.1326), <https://doi.org/10.2202/1544-6115.1326>.

See Also

[dmmsum](#), [getTransitionMatrix](#), [Distribution_evol](#), [getStationaryLaw](#)

Examples

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

getStationaryLaw	<i>Get stationary law S3 generic function</i>
------------------	---

Description

Evaluate stationary law at a given position or at every position

Usage

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

Arguments

x	An object of class "dmm"
pos	An integer, a position
all.pos	FALSE (default, evaluation at position index) ; TRUE (evaluation for all position indices)
internal	FALSE (default) ; TRUE (for internal use of dmmsum initial law)

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/s11009-018-9682-8](https://doi.org/10.1007/s11009-018-9682-8), <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: [10.2202/1544-6115.1326](https://doi.org/10.2202/1544-6115.1326), <https://doi.org/10.2202/1544-6115.1326>.

```
getStationaryLaw.dmmsum
```

Get stationary law

Description

Evaluate stationary law at a given position or at every position

Usage

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

Arguments

x	An object of class "dmm", dmmsum
pos	An integer for position
all.pos	FALSE (default, evaluation at position index) ; TRUE (evaluation for all position indices)
internal	FALSE (default) ; TRUE (for internal use of dmmsum initial law 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/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/10.2202/15446115.1326), <https://doi.org/10.2202/1544-6115.1326>.

See Also

[dmmsum](#), [getTransitionMatrix](#), [stationaryLaw_evol](#), [getDistribution](#)

Examples

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

getTransitionMatrix	<i>Get transition S3 generic function</i>
---------------------	---

Description

Get transition S3 generic function

Usage

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

Arguments

x	An object of class "dmm"
pos	An integer, a position

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/s11009-018-9682-8](https://doi.org/10.1007/s11009-018-9682-8), <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: [10.2202/1544-6115.1326](https://doi.org/10.2202/1544-6115.1326), <https://doi.org/10.2202/1544-6115.1326>.

```
getTransitionMatrix.dmmsum
```

Get transition matrix at a given position

Description

Get transition matrix at a given position

Usage

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

Arguments

x	An object of class "dmm", dmmsum
pos	position along the sequence (integer)

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/s11009-018-9682-8](https://doi.org/10.1007/s11009-018-9682-8), <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: [10.2202/1544-6115.1326](https://doi.org/10.2202/1544-6115.1326), <https://doi.org/10.2202/1544-6115.1326>.

See Also

[dmmsum](#)

Examples

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

lambda	<i>lambda genome</i>
--------	----------------------

Description

Complete data from phage genome [WT71] of length 48502

Usage

```
data(lambda)
```

Format

A vector object of class "Rdata".

Examples

```
data(lambda)
```

length_probas	<i>Probability of occurrence of the Observed word of size n in a sequence at several positions</i>
---------------	--

Description

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

Usage

```
length_probas(n, sequence, pos, x, output_file = NULL, plot = FALSE)
```

Arguments

n	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/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/10.2202/15446115.1326), <https://doi.org/10.2202/1544-6115.1326>.

See Also

[dmmsum](#), [getTransitionMatrix](#), [word_proba](#)

Examples

```
data(lambda, package = "drimmR")
dmm <- dmmsum(lambda, 1, 1, c('a','c','g','t'), init.estim = "freq")
n <- 2
length_probas(n, lambda, c(1,length(lambda)-n+1), dmm,plot=TRUE)
```

loglik

Loglikelihood S3 generic function

Description

Generic function computing the loglikelihood of the model ‘x’, with the list of sequences ‘sequences’.

Usage

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

Arguments

x	An object of class "dmm" for which the loglikelihood 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 numeric, the log-likelihood

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/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/10.2202/15446115.1326), <https://doi.org/10.2202/1544-6115.1326>.

loglik.dmmsum	<i>Evaluate Log-likelihood</i>
---------------	--------------------------------

Description

Evaluate Log-likelihood

Usage

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

Arguments

x	An object of class "dmm", dmmsum
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/s11009-018-9682-8](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: [10.2202/1544-6115.1326](https://doi.org/10.2202/1544-6115.1326), <https://doi.org/10.2202/1544-6115.1326>.

See Also

[dmmsum](#), [getTransitionMatrix](#)

Examples

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

maintainability	<i>Evaluate Maintainability</i>
-----------------	---------------------------------

Description

Estimation of maintainability for (ergodic) repairable system at time $k \in N$.

Usage

```
maintainability(x, k1, k2, s1, output_file = NULL, plot = FALSE)
```

Arguments

x	An object of class "dmm"
k1	start position (numeric)
k2	end position (numeric)
s1	Character vector of the subspace working states among the state space vector s.t. $s1 < s$
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 repairable system is the probability that the system is repaired up to time l , given that it has failed at time $l = 0$.

Value

A matrix with Maintainability score at each position

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/s11009-018-9682-8](https://doi.org/10.1007/s11009-018-9682-8), <https://doi.org/10.1007/s11009-018-9682-8>.

See Also

[dmmsum](#), [getTransitionMatrix](#)

Examples

```
data(lambda, package = "drimmR")
dmm <- dmmsum(lambda, 1, 1, c('a','c','g','t'), init.estim = "freq")
k1 <- 1
k2 <- 200
s1 <- c("c","t") # vector of working states
maintainability(dmm,k1,k2,s1,plot=TRUE)
```

reliability	<i>Evaluate Reliability</i>
-------------	-----------------------------

Description

Estimation of reliability for (ergodic) repairable or (non-ergodic) non-repairable systems at time $l \in N$

Usage

```
reliability(x, k1, k2, s1, output_file = NULL, plot = FALSE)
```

Arguments

x	An object of class "dmm"
k1	start position (numeric)
k2	end position (numeric)
s1	Character vector of the subspace working states among the state space vector s.t. $s1 < s$
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 thaht the system has functioned without failure in the period $[0, l]$

Value

A matrix with Reliability score at each position

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/s11009-018-9682-8](https://doi.org/10.1007/s11009-018-9682-8), <https://doi.org/10.1007/s11009-018-9682-8>.

See Also

[dmmsum](#), [getTransitionMatrix](#)

Examples

```
data(lambda, package = "drimmR")
dmm <- dmmsum(lambda, 1, 1, c('a','c','g','t'), init.estim = "freq")
k1 <- 1
k2 <- 200
s1 <- c("c","t") # vector of working states
reliability(dmm,k1,k2,s1,plot=TRUE)
```

simulate	<i>Simulate S3 generic function</i>
----------	-------------------------------------

Description

Simulate S3 generic function

Usage

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

Arguments

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

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/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/10.2202/15446115.1326), <https://doi.org/10.2202/1544-6115.1326>.

simulate.dmmsum	<i>Simulate a sequence with the Drifting Markov Model</i>
-----------------	---

Description

Simulate a sequence with the Drifting Markov Model

Usage

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

Arguments

x	An object of class "dmm", dmmsum
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/s11009-018-9682-8](https://doi.org/10.1007/s11009-018-9682-8), <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: [10.2202/1544-6115.1326](https://doi.org/10.2202/1544-6115.1326), <https://doi.org/10.2202/1544-6115.1326>.

See Also

[dmmsum](#), [getTransitionMatrix](#), [getStationaryLaw](#)

Examples

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

stationaryLaw_evol	<i>Plot stationary laws for a range of positions between <start> and <end></i>
--------------------	--

Description

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

Usage

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

Arguments

x	An object of class "dmm"
start	Start position (numeric)
end	End position (numeric)
step	A step (numeric)
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 of probabilities with position and probability 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/s11009-018-9682-8](https://doi.org/10.1007/s11009-018-9682-8), <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: [10.2202/1544-6115.1326](https://doi.org/10.2202/1544-6115.1326), <https://doi.org/10.2202/1544-6115.1326>.

See Also

[dmmsum](#), [getStationaryLaw](#)

Examples

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

words_probas	<i>Probability of several words at several positions of a DMM</i>
--------------	---

Description

Probability of several words at several positions of a DMM

Usage

```
words_probas(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/s11009-018-9682-8](https://doi.org/10.1007/s11009-018-9682-8), <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/10.2202/15446115.1326), <https://doi.org/10.2202/1544-6115.1326>.

See Also

[dmmsum](#), [getTransitionMatrix](#), [word_proba](#), [word_probas](#)

Examples

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

word_proba

*Probability of a word at a position t of a DMM***Description**

Probability of a word at a position t of a DMM

Usage

```
word_proba(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/s11009-018-9682-8](https://doi.org/10.1007/s11009-018-9682-8), <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: [10.2202/1544-6115.1326](https://doi.org/10.2202/1544-6115.1326), <https://doi.org/10.2202/1544-6115.1326>.

See Also

[dmmsum](#), [getTransitionMatrix](#), [word_probab](#), [words_probab](#)

Examples

```
data(lambda, package = "drimmR")
dmm <- dmmsum(lambda, 1, 1, c('a','c','g','t'), init.estim = "freq")
word_proba("aggctga",4,dmm)
```

word_probas	<i>Probabilities of a word at several positions of a DMM</i>
-------------	--

Description

Probabilities of a word at several positions of a DMM

Usage

```
word_probas(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/s11009-018-9682-8](https://doi.org/10.1007/s11009-018-9682-8), <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: [10.2202/1544-6115.1326](https://doi.org/10.2202/1544-6115.1326), <https://doi.org/10.2202/1544-6115.1326>.

See Also

[dmmsum](#), [getTransitionMatrix](#), [word_proba](#), [words_probas](#)

Examples

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

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