Package 'motifcounter'

November 6, 2025

Type Package

Title R package for analysing TFBSs in DNA sequences

Version 1.34.0

Date 2017

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Suggests knitr, rmarkdown, testthat, MotifDb, seqLogo, prettydoc

Imports Biostrings, methods

Depends R(>= 3.0)

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Description 'motifcounter' provides motif matching, motif counting
and motif enrichment functionality based on position
frequency matrices.
The main features of the packages include the utilization
of higher-order background models and accounting
for self-overlapping motif matches when determining motif enrichment.
The background model allows to capture dinucleotide
(or higher-order nucleotide) composition adequately
which may reduced model biases and misleading results compared
to using simple GC background models.
When conducting a motif enrichment analysis
based on the motif match count, the package
relies on a compound Poisson distribution or alternatively
a combinatorial model. These distribution account for self-overlapping
motif structures as exemplified by repeat-like or palindromic motifs,
and allow to determine the p-value and fold-enrichment for
a set of observed motif matches.

License GPL-2

biocViews Transcription,MotifAnnotation,SequenceMatching,Software

RoxygenNote 6.0.1

VignetteBuilder knitr

NeedsCompilation yes

Collate 'background_wrapper.R' 'comppoiss_wrapper.R'
'combinatorial_wrapper.R' 'score_wrapper.R' 'count_wrapper.R'
'enrichmentTest.R' 'forground_wrapper.R' 'markovmodel.R'
'motifcounter-package.R' 'observed_wrapper.R' 'option.R'
'overlap.R' 'simulate_wrapper.R' 'wrapper.R'

git_url https://git.bioconductor.org/packages/motifcounter

git_branch RELEASE_3_22

git_last_commit 64fa306

git_last_commit_date 2025-10-29

Repository Bioconductor 3.22

Date/Publication 2025-11-05

Contents

`motifcounter-package` *TFBSs analysis in DNA sequences*

Description

The package provides functions for determining the positions of motif hits as well as motif hit enrichment for a given position frequency matrix (PFM) in a DNA sequence of interest. The following examples guides you through the main functions of the 'motifcounter' package.

Details

For an analysis with 'motifcounter', the user is required to provide 1) a PFM, 2) a DNA sequence which is used to estimate a background model (see `link{readBackground}`), 3) a DNA sequence of interest that shall be scanned for motif hits (can be the same as the one used for point 2), and 4) (optionally) a desired false positive probability of motif hits in random DNA sequences (see `motifcounterOptions`).

Package:	motifcounter
Type:	Package
Version:	1.0
Date:	2016-11-04
License:	GPL-2

Author(s)

Wolfgang Kopp

Maintainer: Wolfgang Kopp <kopp@molgen.mpg.de>

Examples

```
# Load sequences
file = system.file("extdata", "seq.fasta", package = "motifcounter")
seqs = Biostrings::readDNAStringSet(file)

# Estimate an order-1 background model
order = 1
bg = readBackground(seqs, order)

# Load motif
motiffile = system.file("extdata", "x31.tab", package = "motifcounter")
motif = t(as.matrix(read.table(motiffile)))

# Normalize the motif
# Normalization is sometimes necessary to prevent zeros in
# the motif
```

```
motif = normalizeMotif(motif)

# Use subset of the sequences
seqs = seqs[1:10]

# Optionally, set the false positive probability
#alpha=0.001 # is also the default
#motifcounterOptions(alpha)

# Investigate the per-position and per-strand scores in a given sequence
scores = scoreSequence(seqs[[1]], motif, bg)

# Investigate the per-position and per-strand motif hits in a given sequence
hits = motifHits(seqs[[1]], motif, bg)

# Determine the average score profile across a set of sequences
scores = scoreProfile(seqs, motif, bg)

# Determine the average motif hit profile across a set of sequences
hits = motifHitProfile(seqs, motif, bg)

# Determine the empirical score distribution
scoreHistogram(seqs, motif, bg)

# Determine the theoretical score distribution in random sequences
scoreDist(motif, bg)


# Determine the motif hit enrichment in a set of DNA sequences
# 1. Use the compound Poisson approximation
#    and scan only a single strand for motif hits
result = motifEnrichment(seqs, motif, bg,
            singlestranded = TRUE, method = "compound")

# Determine the motif hit enrichment in a set of DNA sequences
# 2. Use the compound Poisson approximation
#    and scan both strands for motif hits
result = motifEnrichment(seqs, motif, bg,
            singlestranded = FALSE, method = "compound")

# Determine the motif hit enrichment in a set of DNA sequences
# 3. Use the combinatorial model
#    and scan both strands for motif hits
result = motifEnrichment(seqs, motif, bg, singlestranded = FALSE,
            method = "combinatorial")
```

`Background-class` *Background class definition*

Description

Objects of this class serve as a container that holds parameters for the Background model.

Details

A Background model is constructed via readBackground.

Slots

`station` Stationary probabilities

`trans` Transition probabilities

`counts` k-mer counts

`order` Background model order

---

clumpSizeDist *Clump size distribution*

Description

This function approximates the distribution of the clump sizes.

Usage

```
clumpSizeDist(maxclump, overlap, method = "kopp")
```

Arguments

`maxclump`	Maximal clump size
`overlap`	An Overlap object.
`method`	String that defines which method shall be invoked: 'pape' or 'kopp' (see description). Default: method = 'kopp'.

Details

The clump size distribution can be determined in two alternative ways:

1. A re-implemented version of the algorithm that was described in Pape et al. *Compound poisson approximation of the number of occurrences of a position frequency matrix (PFM) on both strands.* 2008 can be invoked using method='pape'.
2. An improved approximation of the clump size distribution uses more appropriate statistical assumptions concerning overlapping motif hits and that can be used with order-d background models as well. The improved version is used by default with method='kopp'.

Value

List containing

dist Distribution of the clump size

See Also

probOverlapHit

Examples

```
# Load sequences
seqfile = system.file("extdata", "seq.fasta", package = "motifcounter")
seqs = Biostrings::readDNAStringSet(seqfile)

# Load motif
motiffile = system.file("extdata", "x31.tab", package = "motifcounter")
motif = t(as.matrix(read.table(motiffile)))

# Load background model
bg = readBackground(seqs, 1)

# Use 100 individual sequences of length 150 bp each
seqlen = rep(150, 100)


# Compute overlapping probabilities
# for scanning the forward DNA strand only
op = motifcounter:::probOverlapHit(motif, bg, singlestranded = FALSE)

# Computes  the compound Poisson distribution
dist = motifcounter:::clumpSizeDist(20, op)
```

`combinatorialDist` *Combinatrial model approximation of the number of motif hits*

Description

This function approxmiates the distribution of the number of motif hits. To this end, it sums over all combinations of obtaining k hits in a random sequence of a given length using an efficient dynamic programming algorithm.

Usage

```
combinatorialDist(seqlen, overlap)
```

Arguments

`seqlen`	Integer-valued vector that defines the lengths of the individual sequences. For a given DNAStringSet, this information can be retrieved using `numMotifHits`.
`overlap`	An Overlap object.

Details

This function is an alternative to `compoundPoissonDist` which requires fixed-length sequences and currently only supports the computation of the distribution of the number of hits when both DNA strands are scanned for motif hits.

Value

List containing

dist Distribution of the number of hits

See Also

compoundPoissonDist

numMotifHits

probOverlapHit

Examples

```
# Load sequences
seqfile = system.file("extdata", "seq.fasta", package = "motifcounter")
seqs = Biostrings::readDNAStringSet(seqfile)

# Load motif
motiffile = system.file("extdata", "x31.tab", package = "motifcounter")
motif = t(as.matrix(read.table(motiffile)))

# Load background model
bg = readBackground(seqs, 1)

# Compute overlap probabilities
op = motifcounter:::probOverlapHit(motif, bg, singlestranded = FALSE)

# Use 2 sequences of length 100 bp each
seqlen = rep(100, 2)

# Computes the combinatorial distribution of the number of motif hits
dist = motifcounter:::combinatorialDist(seqlen, op)
```

---

compoundPoissonDist *Compound Poisson Approximation*

Description

This function approximates the distribution of the number of motif hits that emerges from a random DNA sequence of a given length.

Usage

```
compoundPoissonDist(seqlen, overlap, method = "kopp")
```

Arguments

seqlen	Integer-valued vector that defines the lengths of the individual sequences. For a given DNAStringSet, this information can be retrieved using numMotifHits.
overlap	An Overlap object.
method	String that defines which method shall be invoked: 'pape' or 'kopp' (see description). Default: method = 'kopp'.

Details

The distribution can be determined in two alternative ways:

1. A re-implemented version of the algorithm that was described in Pape et al. *Compound poisson approximation of the number of occurrences of a position frequency matrix (PFM) on both strands.* 2008 can be invoked using method='pape'. The main purpose of this implementation concerns benchmarking an improved approximation. In contrast to the original model, this implementation can be used with general order-d Markov models.
2. We provide an improved compound Poisson approximation that uses more appropriate statistical assumptions concerning overlapping motif hits and that can be used with order-d background models as well. The improved version is used by default with method='kopp'. Note: Only method='kopp' supports the computation of the distribution of the number of motif hits w.r.t. scanning a single DNA strand (see probOverlapHit).

Value

List containing

dist Distribution of the number of hits

See Also

combinatorialDist

probOverlapHit

numMotifHits

Examples

```
# Load sequences
seqfile = system.file("extdata", "seq.fasta", package = "motifcounter")
seqs = Biostrings::readDNAStringSet(seqfile)

# Load motif
motiffile = system.file("extdata", "x31.tab", package = "motifcounter")
motif = t(as.matrix(read.table(motiffile)))

# Load background model
bg = readBackground(seqs, 1)

# Use 100 individual sequences of length 150 bp each
seqlen = rep(150, 100)

# Compute overlapping probabilities
# for scanning the forward DNA strand only
op = motifcounter:::probOverlapHit(motif, bg, singlestranded = TRUE)

# Computes  the compound Poisson distribution
dist = motifcounter:::compoundPoissonDist(seqlen, op)
#plot(1:length(dist$dist)-1, dist$dist)

# Compute overlapping probabilities
# for scanning the forward DNA strand only
op = motifcounter:::probOverlapHit(motif, bg, singlestranded = FALSE)

# Computes  the compound Poisson distribution
```

```
dist = motifcounter:::compoundPoissonDist(seqlen, op)
#plot(1:length(dist$dist)-1, dist$dist)
```

`computeClumpStartProb` *Computes the Clump start probability based on a Markov model*

Description

This function leverages a Markov model in order to determine the clump start probability. The computation depends on the selected false positive probability for calling motif matches 'alpha' and the pre-determined overlapping match probabilities 'beta'.

Usage

```
computeClumpStartProb(overlap)
```

Arguments

`overlap`	An Overlap object.

Details

The general idea of the method relies on the fact that for the stationary distribution of the Markov model, motif matches must be observed with probability 'alpha'. Hence, the clump start probability 'tau' is optimized to achieve that goal.

The R interface is only used for the purpose of testing the correctness of the model.

Value

Clump start probability 'tau'

See Also

`compoundPoissonDist`

`numMotifHits`

`probOverlapHit`

Examples

```
# Load sequences
seqfile = system.file("extdata", "seq.fasta", package = "motifcounter")
seqs = Biostrings::readDNAStringSet(seqfile)

# Load motif
motiffile = system.file("extdata", "x31.tab", package = "motifcounter")
motif = t(as.matrix(read.table(motiffile)))

# Load background model
bg = readBackground(seqs, 1)

# Compute overlap probabilities
```

```
op = motifcounter:::probOverlapHit(motif, bg, singlestranded = FALSE)


# Computes the clump start probability
dist = motifcounter:::computeClumpStartProb(op)
```

`generateDNAString` *Generate DNAString*

Description

This function generates a random DNAString of a given length by sampling from the background model.

Usage

```
generateDNAString(len, bg)
```

Arguments

`len`	Integer length of the sequence
`bg`	A Background object

Value

A DNAString object

See Also

`generateDNAStringSet`

Examples

```
# Load sequences
seqfile = system.file("extdata", "seq.fasta", package = "motifcounter")
seqs = Biostrings::readDNAStringSet(seqfile)

# Load background
bg = readBackground(seqs, 1)

# Generate a 1 kb random sequence
motifcounter:::generateDNAString(1000, bg)
```

generateDNAStringSet *Generate DNAStringSet*

Description

This function generates a DNAStringSet-object of the given individual sequence lengths by sampling from the background model.

Usage

```
generateDNAStringSet(seqlen, bg)
```

Arguments

seqlen	Integer-valued vector that defines the lengths of the individual sequences. For a given DNAStringSet, this information can be retrieved using numMotifHits.
bg	A Background object

Value

A DNAStringSet object

See Also

generateDNAStringSet

Examples

```
# Load sequences
seqfile = system.file("extdata", "seq.fasta", package = "motifcounter")
seqs = Biostrings::readDNAStringSet(seqfile)

# Load background
bg = readBackground(seqs, 1)

# Generate random sequences of various lengths
motifcounter:::generateDNAStringSet(10:50, bg)
```

getAlpha *Accessor to slot alpha*

Description

Accessor to slot alpha

Usage

```
getAlpha(obj)
```

Arguments

obj	An Overlap object

Value

alpha slot

---

getBeta *Accessor to slot beta*

Description

Accessor to slot beta

Usage

```
getBeta(obj)
```

Arguments

obj	An Overlap object

Value

beta slot

---

getBeta3p *Accessor to slot beta3p*

Description

Accessor to slot beta3p

Usage

```
getBeta3p(obj)
```

Arguments

obj	An Overlap object

Value

beta3p slot

getBeta5p *Accessor to slot beta*

Description

Accessor to slot beta

Usage

```
getBeta5p(obj)
```

Arguments

obj	An Overlap object

Value

beta5p slot

getCounts *Accessor to slot counts*

Description

Accessor to slot counts

Usage

```
getCounts(obj)
```

Arguments

obj	A Background object

Value

counts slot

getGamma *Accessor to slot gamma*

Description

Accessor to slot gamma

Usage

```
getGamma(obj)
```

Arguments

obj	An Overlap object

Value

gamma slot

getOrder *Accessor to slot order*

Description

Accessor to slot order

Usage

```
getOrder(obj)
```

Arguments

obj	A Background object

Value

order slot

getSinglestranded *Accessor to slot singlestranded*

Description

Accessor to slot singlestranded

Usage

```
getSinglestranded(obj)
```

Arguments

obj	An Overlap object

Value

singlestranded slot

getStation *Accessor to slot station*

Description

Accessor to slot station

Usage

```
getStation(obj)
```

Arguments

obj	A Background object

Value

station slot

getTrans *Accessor to slot trans*

Description

Accessor to slot trans

Usage

```
getTrans(obj)
```

Arguments

obj	A Background object

Value

trans slot

hitStrand *Hit strand*

Description

This function computes the per-position motif matches in a given DNA strand.

Usage

```
hitStrand(seq, pfm, bg, threshold = NULL)
```

Arguments

seq	A DNAString object
pfm	An R matrix that represents a position frequency matrix
bg	A Background object
threshold	Score threshold for calling motif matches. If NULL, the threshold will determined from alpha.

Details

The function returns the per-position scores for the given strand. If the sequence is too short, it contains an empty vector.

Value

hits Vector of motif hits on the given strand

Examples

```
# Load sequences
seqfile = system.file("extdata", "seq.fasta", package = "motifcounter")
seqs = Biostrings::readDNAStringSet(seqfile)

# Load background
bg = readBackground(seqs, 1)

# Load motif
motiffile = system.file("extdata", "x31.tab", package = "motifcounter")
motif = t(as.matrix(read.table(motiffile)))

# Compute the per-position and per-strand scores
motifcounter:::hitStrand(seqs[[1]], motif, bg)
```

`lenSequences` *Length of sequences in a given fasta file*

Description

The function returns a vector containing the lengths of each sequence contained in a set of sequences. Sequences containing 'N' or 'n' are skipped from the analysis and are set to length zero.

Usage

```
lenSequences(seqs)
```

Arguments

seqs	A DNAStringSet object

Value

A vector containing the lengths of each individual sequences

Examples

```
# Load sequences
file = system.file("extdata", "seq.fasta", package = "motifcounter")
seqs = Biostrings::readDNAStringSet(file)

# Retrieve sequence lengths
motifcounter:::lenSequences(seqs)
```

markovModel *Markov model for generating Y_1Y_2_Y3 ...*

Description

This function implements the Markov model for producing motif matches. The function takes a state probability vector and uses the transition probabilities in order to obtain the state probability at the next time point. This function is used used to determine the stationary distribution of the states.

Usage

```
markovModel(overlap, nsteps = 1)
```

Arguments

overlap	An Overlap object.
nsteps	Number of state transitions to perform

Details

The R interface is only used for the purpose of testing the correctness of the model.

Value

List containing

dist State probability distribution after the given number of steps

See Also

compoundPoissonDist

numMotifHits

probOverlapHit

Examples

```
# Load sequences
seqfile = system.file("extdata", "seq.fasta", package = "motifcounter")
seqs = Biostrings::readDNAStringSet(seqfile)

# Load motif
motiffile = system.file("extdata", "x31.tab", package = "motifcounter")
motif = t(as.matrix(read.table(motiffile)))

# Load background model
bg = readBackground(seqs, 1)

# Compute overlap probabilities
op = motifcounter:::probOverlapHit(motif, bg, singlestranded = FALSE)


# Computes the state probabilities of the Markov model
# (default: after one step)
```

```
dist = motifcounter:::markovModel(op)
```

`motifAndBackgroundValid` *Check valididity of PFM with background*

Description

This function checks if the PFM x background combination is valid. The function throws an error if this is not the case.

Usage

```
motifAndBackgroundValid(pfm, bg)
```

Arguments

`pfm`	An R matrix that represents a position frequency matrix
`bg`	A Background object

Value

None

Examples

```
# Load sequences
seqfile = system.file("extdata", "seq.fasta", package = "motifcounter")
seqs = Biostrings::readDNAStringSet(seqfile)

# Load background
bg = readBackground(seqs, 1)

# Load motif
motiffile = system.file("extdata", "x1.tab", package = "motifcounter")
motif = t(as.matrix(read.table(motiffile)))

# Check validity
motifcounter:::motifAndBackgroundValid(motif, bg)
```

motifcounterOptions *Set parameters for the enrichment analysis*

Description

This function sets some global parameters for the ‘motifcounter‘ package.

Usage

```
motifcounterOptions(alpha = 0.001, gran = 0.1, ncores = 1)
```

Arguments

alpha	Numeric False positive probabililty for calling motif hits by chance. Default: alpha = 0.001
gran	Numeric score granularity which is used for discretizing the score range. Default: gran = 0.1
ncores	Interger number of cores used for parallel processing, if openMP is available. Default: ncores = 1

Details

alpha=0.001 amounts to calling one motif hit per strand by chance in a sequence of length 1000 bp. Decreasing gran will increase number of discrete bins that represent the real-valued score range. This will yield more a accurate score distribution due to less discretization noise, however, it incurs an increase of the computational burden.

Value

None

Examples

```
# Prescribe motifcounter Options
motifcounterOptions(alpha = 0.001, gran = 0.1, ncores = 1)
```

motifEnrichment *Enrichment of motif hits*

Description

This function determines whether a given motif is enriched in a given DNA sequences.

Usage

```
motifEnrichment(seqs, pfm, bg, singlestranded = FALSE, method = "compound")
```

Arguments

seqs	A DNAStringSet or DNAString object
pfm	An R matrix that represents a position frequency matrix
bg	A Background object
singlestranded	Boolean that indicates whether a single strand or both strands shall be scanned for motif hits. Default: singlestranded = FALSE.
method	String that defines whether to use the 'compound' Poisson approximation' or the 'combinatorial' model. Default: method='compound'.

Details

Enrichment is tested by comparing the observed number of motif hits against a theoretical distribution of the number of motif hits in random DNA sequences. Optionally, the theoretical distribution of the number of motif hits can be evaluated by either a 'compound Poisson model' or the 'combinatorial model'. Additionally, the enrichment test can be conducted with respect to scanning only the forward strand or both strands of the DNA sequences. The latter option is only available for the 'compound Poisson model'

Value

List that contains

pvalue P-value for the enrichment test

fold Fold-enrichment with respect to the expected number of hits

See Also

compoundPoissonDist, combinatorialDist

Examples

```
# Load sequences
seqfile = system.file("extdata", "seq.fasta", package = "motifcounter")
seqs = Biostrings::readDNAStringSet(seqfile)

# Load background
bg = readBackground(seqs, 1)

# Load motif
motiffile = system.file("extdata", "x31.tab", package = "motifcounter")
motif = t(as.matrix(read.table(motiffile)))

# 1 ) Motif enrichment test w.r.t. scanning a *single* DNA strand
# based on the 'Compound Poisson model'

result = motifEnrichment(seqs, motif, bg,
            singlestranded = TRUE, method = "compound")

# 2 ) Motif enrichment test w.r.t. scanning *both* DNA strand
# based on the 'Compound Poisson model'

result = motifEnrichment(seqs, motif, bg, method = "compound")
```

```
# 3 ) Motif enrichment test w.r.t. scanning *both* DNA strand
# based on the *combinatorial model*

result = motifEnrichment(seqs, motif, bg, singlestranded = FALSE,
            method = "combinatorial")
```

`motifHitProfile` *Motif hit profile across multiple sequences*

Description

This function computes the per-position average motif hit profile across a set of fixed-length DNA sequences. It can be used to reveal positional constraints of TFBSs.

Usage

```
motifHitProfile(seqs, pfm, bg)
```

Arguments

`seqs`	A DNAStringSet or DNAString object
`pfm`	An R matrix that represents a position frequency matrix
`bg`	A Background object

Value

List containing

fscores Per-position average forward strand motif hits

rscores Per-position average reverse strand motif hits

Examples

```
# Load sequences
seqfile = system.file("extdata", "seq.fasta", package = "motifcounter")
seqs = Biostrings::readDNAStringSet(seqfile)
seqs = seqs[1:10]

# Load background
bg = readBackground(seqs, 1)

# Load motif
motiffile = system.file("extdata", "x31.tab", package = "motifcounter")
motif = t(as.matrix(read.table(motiffile)))

# Compute the motif hit profile
motifHitProfile(seqs, motif, bg)
```

motifHits *Motif hit observations*

Description

This function determines per-position motif hits in a given DNA sequence.

Usage

```
motifHits(seq, pfm, bg, threshold = NULL)
```

Arguments

seq	A DNAString object
pfm	An R matrix that represents a position frequency matrix
bg	A Background object
threshold	Score threshold for calling motif matches. If NULL, the threshold will determined from alpha.

Value

List containing

fhits Per-position motif hits on the forward strand

rhits Per-position motif hits on the reverse strand

Examples

```
# Load sequences
seqfile = system.file("extdata", "seq.fasta", package = "motifcounter")
seq = Biostrings::readDNAStringSet(seqfile)

# Load background
bg = readBackground(seq, 1)

# Load motif
motiffile = system.file("extdata", "x31.tab", package = "motifcounter")
motif = t(as.matrix(read.table(motiffile)))

# Determine the motif hits
motifHits(seq[[1]], motif, bg)
```

`motifValid` *Check valididity of PFM*

Description

This function checks if the PFM is valid. The function throws an error if the R matrix does not represent a PFM.

Usage

```
motifValid(pfm)
```

Arguments

`pfm`	An R matrix that represents a position frequency matrix

Value

None

Examples

```
# Load motif
motiffile = system.file("extdata", "x1.tab", package = "motifcounter")
motif = t(as.matrix(read.table(motiffile)))

# Check validity
motifcounter:::motifValid(motif)
```

`normalizeMotif` *Normalizes a PFM*

Description

This function normalizes a PFM and optionally adds pseudo-evidence to each entry of the matrix.

Usage

```
normalizeMotif(pfm, pseudo = 0.01)
```

Arguments

`pfm`	An R matrix that represents a position frequency matrix
`pseudo`	Small numeric pseudo-value that is added to each entry in the PFM in order to ensure strictly positive entries. Default: pseudo = 0.01

Value

A normalized PFM

Examples

```
# Load motif
motiffile = system.file("extdata", "x1.tab", package = "motifcounter")
motif = t(as.matrix(read.table(motiffile)))

# Normalize motif
new_motif = normalizeMotif(motif)
```

---

numMotifHits *Number of motif hits in a set of DNA sequences*

Description

This function counts the number of motif hits that are found in a given set of DNA sequences.

Usage

```
numMotifHits(seqs, pfm, bg, singlestranded = FALSE)
```

Arguments

seqs	A DNAStringSet or DNAString object
pfm	An R matrix that represents a position frequency matrix
bg	A Background object
singlestranded	Boolean that indicates whether a single strand or both strands shall be scanned for motif hits. Default: singlestranded = FALSE.

Details

Optionally, it can be used to count motif hits on one or both strands, respectively.

Value

A list containing

nseq Number of individual sequences

lseq Vector of individual sequence lengths

numofhits Vector of the number of hits in each individual sequence

Examples

```
# Load sequences
seqfile = system.file("extdata", "seq.fasta", package = "motifcounter")
seqs = Biostrings::readDNAStringSet(seqfile)

# Load background
bg = readBackground(seqs, 1)

# Load motif
motiffile = system.file("extdata", "x31.tab", package = "motifcounter")
```

```
motif = t(as.matrix(read.table(motiffile)))

# Count motif hits both strands
noc = motifcounter:::numMotifHits(seqs, motif, bg)
noc$numofhits

# Count motif hits on a single strand
noc = motifcounter:::numMotifHits(seqs, motif, bg, singlestranded = TRUE)
noc$numofhits
```

`Overlap-class` *Overlap class definition*

Description

Objects of this class serve as a container that holds parameters for the overlapping hit probabilities.

Details

An Overlap object is constructed via the `probOverlapHit`

Slots

`alpha` Scalar numeric significance level to call motif matches

`beta` Numeric vector of principal overlapping hit probabilities on the same strand.

`beta3p` Numeric vector of principal overlapping hit probabilities with 3'-overlap.

`beta5p` Numeric vector of principal overlapping hit probabilities with 5'-overlap.

`gamma` Numeric vector of marginal overlapping hit probabilities.

`singlestranded` logical flag to indicate whether one or both strands are scanned for motif matches.

`probOverlapHit` *Overlapping motif hit probabilities*

Description

This function computes a set of self-overlapping probabilites for a motif and background model.

Usage

```
probOverlapHit(pfm, bg, singlestranded = FALSE)
```

Arguments

`pfm`	An R matrix that represents a position frequency matrix
`bg`	A Background object
`singlestranded`	Boolean that indicates whether a single strand or both strands shall be scanned for motif hits. Default: singlestranded = FALSE.

Details

The ‘gamma‘s are determined based on two-dimensional score distributions (similar as described in Pape et al. 2008), however, they are computed based on an order-d background model. On the other hand, the ‘beta‘s represent overlapping hit probabilities that were corrected for intermediate hits.

Value

An Overlap object

Examples

```
# Load sequences
seqfile = system.file("extdata", "seq.fasta", package = "motifcounter")
seqs = Biostrings::readDNAStringSet(seqfile)

# Load background
bg = readBackground(seqs, 1)

# Load motif
motiffile = system.file("extdata", "x31.tab", package = "motifcounter")
motif = t(as.matrix(read.table(motiffile)))

# Compute overlapping hit probabilities for scanning both DNA strands
op = motifcounter:::probOverlapHit(motif, bg, singlestranded = FALSE)

# Compute overlapping hit probabilities for scanning a single DNA strand
op = motifcounter:::probOverlapHit(motif, bg, singlestranded = TRUE)
```

---

readBackground *Estimates a background model from a set of DNA sequences*

Description

Given a set of DNA sequences and an order, this function estimates an order-d Markov model which is used to characterize random DNA sequences.

Usage

```
readBackground(seqs, order = 1)
```

Arguments

seqs	A DNAStringSet object
order	Order of the Markov models that shall be used as the background model. Default: order = 1.

Value

A Background object

Examples

```
# Load sequences
file = system.file("extdata", "seq.fasta", package = "motifcounter")
seqs = Biostrings::readDNAStringSet(file)

# Estimate an order-1 Markov model
bg = readBackground(seqs, 1)
```

`revcompMotif` *Reverse complements a PFM*

Description

This function computes the reverse complement of a given PFM.

Usage

```
revcompMotif(pfm)
```

Arguments

`pfm`	An R matrix that represents a position frequency matrix

Value

Reverse complemented PFM

Examples

```
# Load motif
motiffile = system.file("extdata", "x1.tab", package = "motifcounter")
motif = t(as.matrix(read.table(motiffile)))

# Reverse complement motif
revcompmotif = motifcounter:::revcompMotif(motif)
```

`scoreDist` *Score distribution*

Description

This function computes the score distribution for the given PFM and background. The Score distribution is computed based on an efficient dynamic programming algorithm.

Usage

```
scoreDist(pfm, bg)
```

Arguments

pfm	An R matrix that represents a position frequency matrix
bg	A Background object

Value

List that contains

scores Vector of scores

dist Score distribution

Examples

```
# Load sequences
seqfile = system.file("extdata", "seq.fasta", package = "motifcounter")
seqs = Biostrings::readDNAStringSet(seqfile)

# Load background
bg = readBackground(seqs, 1)

# Load motif
motiffile = system.file("extdata", "x31.tab", package = "motifcounter")
motif = t(as.matrix(read.table(motiffile)))

# Compute the score distribution
dp = scoreDist(motif, bg)
```

---

scoreDistBf *Score distribution*

Description

This function computes the score distribution for a given PFM and a background model.

Usage

```
scoreDistBf(pfm, bg)
```

Arguments

pfm	An R matrix that represents a position frequency matrix
bg	A Background object

Details

The result of this function is identical to scoreDist, however, the method employs a less efficient algorithm that enumerates all DNA sequences of the length of the motif. This function is only used for debugging and testing purposes and might require substantial computational resources for long motifs.

Value

List containing

scores Vector of scores

dist Score distribution

See Also

scoreDist

Examples

```
# Load sequences
seqfile = system.file("extdata", "seq.fasta", package = "motifcounter")
seqs = Biostrings::readDNAStringSet(seqfile)

# Load background
bg = readBackground(seqs, 1)

# Load motif
motiffile = system.file("extdata", "x31.tab", package = "motifcounter")
motif = t(as.matrix(read.table(motiffile)))

# Compute the score distribution
dp = motifcounter:::scoreDistBf(motif, bg)
```

---

scoreDistEmpirical *Empirical score distribution*

Description

This function estimates the empirical score distribution on a set of randomly generated DNA sequences based on the background model. This function is only used for benchmarking analysis.

Usage

```
scoreDistEmpirical(pfm, bg, seqlen, nsim)
```

Arguments

pfm	An R matrix that represents a position frequency matrix
bg	A Background object
seqlen	Integer-valued vector that defines the lengths of the individual sequences. For a given DNAStringSet, this information can be retrieved using numMotifHits.
nsim	Integer number of random samples.

Value

List containing

scores Vector of scores

dist Score distribution

See Also

scoreDist

Examples

```
# Load sequences
seqfile = system.file("extdata", "seq.fasta", package = "motifcounter")
seqs = Biostrings::readDNAStringSet(seqfile)

# Load background
bg = readBackground(seqs, 1)

# Load motif
motiffile = system.file("extdata", "x31.tab", package = "motifcounter")
motif = t(as.matrix(read.table(motiffile)))


# Compoute the empirical score distribution in
# sequences of length 1kb using 1000 samples
motifcounter:::scoreDistEmpirical(motif, bg, seqlen = 1000, nsim = 1000)
```

---

scoreHistogram *Score histogram*

Description

This function computes the empirical score distribution for a given set of DNA sequences.

Usage

```
scoreHistogram(seqs, pfm, bg)
```

Arguments

seqs	A DNAStringSet or DNAString object
pfm	An R matrix that represents a position frequency matrix
bg	A Background object

Details

It can be used to compare the empirical score distribution against the theoretical one (see scoreDist).

Value

List containing

scores Vector of scores

dist Score distribution

See Also

scoreDist

Examples

```
# Load sequences
seqfile = system.file("extdata", "seq.fasta", package = "motifcounter")
seqs = Biostrings::readDNAStringSet(seqfile)

# Load background
bg = readBackground(seqs, 1)

# Load motif
motiffile = system.file("extdata", "x31.tab", package = "motifcounter")
motif = t(as.matrix(read.table(motiffile)))

# Compute the empirical score histogram
scoreHistogram(seqs, motif, bg)
```

`scoreHistogramSingleSeq` *Score histogram on a single sequence*

Description

This function computes the empirical score distribution by normalizing the observed score histogram for a given sequence.

Usage

```
scoreHistogramSingleSeq(seq, pfm, bg)
```

Arguments

`seq`	A DNAString object
`pfm`	An R matrix that represents a position frequency matrix
`bg`	A Background object

Value

List containing

scores Vector of scores

dist Score distribution

Examples

```
# Load sequences
seqfile = system.file("extdata", "seq.fasta", package = "motifcounter")
seqs = Biostrings::readDNAStringSet(seqfile)

# Load background
bg = readBackground(seqs, 1)

# Load motif
```

```
motiffile = system.file("extdata", "x31.tab", package = "motifcounter")
motif = t(as.matrix(read.table(motiffile)))

# Compute the per-position and per-strand scores
motifcounter:::scoreHistogramSingleSeq(seqs[[1]], motif, bg)
```

`scoreProfile` *Score profile across multiple sequences*

Description

This function computes the per-position and per-strand average score profiles across a set of DNA sequences. It can be used to reveal positional constraints of TFBSs.

Usage

```
scoreProfile(seqs, pfm, bg)
```

Arguments

`seqs`	A DNAStringSet or DNAString object
`pfm`	An R matrix that represents a position frequency matrix
`bg`	A Background object

Value

List containing

fscores Vector of per-position average forward strand scores

rscores Vector of per-position average reverse strand scores

Examples

```
# Load sequences
seqfile = system.file("extdata", "seq.fasta", package = "motifcounter")
seqs = Biostrings::readDNAStringSet(seqfile)

# Load background
bg = readBackground(seqs, 1)

# Load motif
motiffile = system.file("extdata", "x31.tab", package = "motifcounter")
motif = t(as.matrix(read.table(motiffile)))

# Compute the score profile
scoreProfile(seqs, motif, bg)
```

scoreSequence *Score observations*

Description

This function computes the per-position and per-strand score in a given DNA sequence.

Usage

```
scoreSequence(seq, pfm, bg)
```

Arguments

seq	A DNAString object
pfm	An R matrix that represents a position frequency matrix
bg	A Background object

Value

List containing

fscores Vector of scores on the forward strand

rscores Vector of scores on the reverse strand

Examples

```
# Load sequences
seqfile = system.file("extdata", "seq.fasta", package = "motifcounter")
seqs = Biostrings::readDNAStringSet(seqfile)

# Load background
bg = readBackground(seqs, 1)

# Load motif
motiffile = system.file("extdata", "x31.tab", package = "motifcounter")
motif = t(as.matrix(read.table(motiffile)))

# Compute the per-position and per-strand scores
scoreSequence(seqs[[1]], motif, bg)
```

scoreStrand *Score strand*

Description

This function computes the per-position score in a given DNA strand.

Usage

```
scoreStrand(seq, pfm, bg)
```

Arguments

seq	A DNAString object
pfm	An R matrix that represents a position frequency matrix
bg	A Background object

Details

The function returns the per-position scores for the given strand. If the sequence is too short, it contains an empty vector.

Value

scores Vector of scores on the given strand

Examples

```
# Load sequences
seqfile = system.file("extdata", "seq.fasta", package = "motifcounter")
seqs = Biostrings::readDNAStringSet(seqfile)

# Load background
bg = readBackground(seqs, 1)

# Load motif
motiffile = system.file("extdata", "x31.tab", package = "motifcounter")
motif = t(as.matrix(read.table(motiffile)))

# Compute the per-position and per-strand scores
motifcounter:::scoreStrand(seqs[[1]], motif, bg)
```

scoreThreshold *Score threshold*

Description

This function computes the score threshold for a desired false positive probability ‘alpha‘.

Usage

```
scoreThreshold(pfm, bg)
```

Arguments

pfm	An R matrix that represents a position frequency matrix
bg	A Background object

Details

Note that the returned alpha usually differs slightly from the one that is prescribed using motifcounterOptions, because of the discrete nature of the sequences.

Value

List containing

threshold Score threshold

alpha False positive probability

Examples

```
# Load sequences
seqfile = system.file("extdata", "seq.fasta", package = "motifcounter")
seqs = Biostrings::readDNAStringSet(seqfile)

# Load background
bg = readBackground(seqs, 1)

# Load motif
motiffile = system.file("extdata", "x31.tab", package = "motifcounter")
motif = t(as.matrix(read.table(motiffile)))

# Compute the score threshold
motifcounter:::scoreThreshold(motif, bg)
```

sigLevel *Retrieve the false positive probability*

Description

This function returns the current false positive level for calling motif hits in random sequences.

Usage

```
sigLevel()
```

Details

The returned value is usually slightly smaller than the prescribed ‘alpha‘ in ‘motifcounterOptions‘, because of the discrete nature of sequences.

Value

False positive probability

Examples

```
motifcounter:::sigLevel()
```

simulateClumpSizeDist *Empirical clump size distribution*

Description

This function repeatedly simulates random DNA sequences according to the background model and subsequently counts the number of k-clump occurrences, where denotes the clump size. This function is only used for benchmarking analysis.

Usage

```
simulateClumpSizeDist(pfm, bg, seqlen, nsim = 10, singlestranded = FALSE)
```

Arguments

pfm	An R matrix that represents a position frequency matrix
bg	A Background object
seqlen	Integer-valued vector that defines the lengths of the individual sequences. For a given DNAStringSet, this information can be retrieved using numMotifHits.
nsim	Integer number of random samples.
singlestranded	Boolean that indicates whether a single strand or both strands shall be scanned for motif hits. Default: singlestranded = FALSE.

Value

A List that contains

dist Empirical distribution of the clump sizes

See Also

compoundPoissonDist,combinatorialDist

Examples

```
# Load sequences
seqfile = system.file("extdata", "seq.fasta", package = "motifcounter")
seqs = Biostrings::readDNAStringSet(seqfile)

# Load background
bg = readBackground(seqs, 1)

# Load motif
motiffile = system.file("extdata", "x31.tab", package = "motifcounter")
motif = t(as.matrix(read.table(motiffile)))

# Study the clump size frequencies in one sequence of length 1 Mb
seqlen = 1000000

# scan both strands
simc = motifcounter:::simulateClumpSizeDist(motif, bg, seqlen)

# scan a single strand
simc = motifcounter:::simulateClumpSizeDist(motif, bg,
    seqlen, singlestranded = TRUE)
```

---

simulateNumHitsDist *Empirical number of motif hits distribution*

Description

This function repeatedly simulates random DNA sequences according to the background model and subsequently counts how many motif hits occur in them. Thus, this function gives rise to the empirical distribution of the number of motif hits. This function is only used for benchmarking analysis.

Usage

```
simulateNumHitsDist(pfm, bg, seqlen, nsim, singlestranded = FALSE)
```

Arguments

pfm	An R matrix that represents a position frequency matrix
bg	A Background object
seqlen	Integer-valued vector that defines the lengths of the individual sequences. For a given DNAStringSet, this information can be retrieved using numMotifHits.
nsim	Integer number of random samples.
singlestranded	Boolean that indicates whether a single strand or both strands shall be scanned for motif hits. Default: singlestranded = FALSE.

Value

A List that contains

dist Empirical distribution of the number of motif hits

See Also

compoundPoissonDist,combinatorialDist

Examples

```
# Load sequences
seqfile = system.file("extdata", "seq.fasta", package = "motifcounter")
seqs = Biostrings::readDNAStringSet(seqfile)

# Load background
bg = readBackground(seqs, 1)

# Load motif
motiffile = system.file("extdata", "x31.tab", package = "motifcounter")
motif = t(as.matrix(read.table(motiffile)))

# Study the counts in one sequence of length 150 bp
seqlen = rep(150, 1)

# Compute empirical distribution of the number of motif hits
# by scanning both strands using 100 samples
simc = motifcounter:::simulateNumHitsDist(motif, bg,
    seqlen, nsim = 100, singlestranded = FALSE)

# Compute empirical distribution of the number of motif hits
# by scanning a single strand using 100 samples
simc = motifcounter:::simulateNumHitsDist(motif, bg,
    seqlen, nsim = 100, singlestranded = TRUE)
```

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