Package ‘PWMEnrich’

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Imports seqLogo, gdata, evd
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Title PWM enrichment analysis
Type Package
LazyLoad yes
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Description A toolkit of high-level functions for DNA motif scanning
and enrichment analysis built upon Biostrings. The main
functionality is PWM enrichment analysis of already known PWMs
(e.g. from databases such as MotifDb), but the package also
implements high-level functions for PWM scanning and
visualisation. The package does not perform ”de novo” motif
discovery, but is instead focused on using motifs that are
either experimentally derived or computationally constructed by
other tools.
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as.data.frame,MotifEnrichmentReport-method

Convert a MotifEnrichmentReport into a data.frame object

Description

Convert a MotifEnrichmentReport into a data.frame object

Arguments

- **x**: the MotifEnrichmentReport object
- **row.names**: unused
- **optional**: unused
- **...**: unused

getBackgroundFrequencies

Get the four nucleotides background frequencies

Description

Estimate the background frequencies of A,C,G,T on a set of promoters from an organism

Usage

```
getBackgroundFrequencies(organism = "dm3",
                        pseudo.count = 1, quick = FALSE)
```

Arguments

- **organism**: either a name of the organisms for which the background should be compiled (supported names are "dm3", "mm9" and "hg19"), a BSgenome object, DNAStringSet, or list of DNAString objects
- **pseudo.count**: the number to which the frequencies sum up to, by default 1
- **quick**: if to preform fitting on a reduced set of 100 promoters. This will not give as good results but is much quicker than fitting to all the promoters (~10k). Usage of this parameter is recommended only for testing and rough estimates.

Author(s)

Robert Stojnic, Diego Diez

Examples

```r
## Not run:
getBackgroundFrequencies("dm3")
## End(Not run)
```
**groupReport,MotifEnrichmentResults-method**

Generate a motif enrichment report for the whole group of sequences together

**Description**

Generate a motif enrichment report for the whole group of sequences together

**Arguments**

- **obj**
  a MotifEnrichmentResults object

- **top**
  what proportion of top motifs should be examined in each individual sequence (by default 5%)

- **bg**
  if to use background corrected P-values to do the ranking (if available)

- **by.top.motifs**
  if to rank by the proportion of sequences where the motif is within 'top' percentage of motifs

... unused

**Value**

a MotifEnrichmentReport object containing a table with the following columns:

- 'rank' - The rank of the PWM's enrichment in the whole group of sequences together
- 'target' - The name of the PWM's target gene, transcript or protein complex.
- 'id' - The unique identifier of the PWM (if set during PWM creation).
- 'raw.score' - The raw score before P-value calculation
- 'p.value' - The P-value of motif enrichment (if available)
- 'top.motif.prop' - The proportion (between 0 and 1) of sequences where the motif is within top proportion of enrichment motifs.

**Examples**

```r
if(require("PWMEnrich.Dmelanogaster.background")){
  ###
  # load the pre-compiled lognormal background data(PWMLogn.dm3.MotifDb.Dmel)

  # scan two sequences for motif enrichment
  sequences = list(DNAString("GAAGTATCAAGTGACCAGTAAGTCCCAGATGA"), DNAString("AGGTAGATAGAACAGTAGGCAATGAAGCCGATG"))
  res = motifEnrichment(sequences, PWMLogn.dm3.MotifDb.Dmel)

  # produce a report for all sequences taken together
  r.default = groupReport(res)

  # produce a report where the last column takes top 1% motifs
  r = groupReport(res, top=0.01)

  # view the results
}```
r

# plot the top 10 most enriched motifs
plot(r[1:10])

makeBackground

Make a background for a set of position frequency matrices

Description

This is a convenience front-end function to compile new backgrounds for a set of PFMs. Currently only supports D. melanogaster, but in the future should support other common organisms as well.

Usage

makeBackground(motifs, organism = "dm3", type = "logn", quick = FALSE, bg.seq=NULL, ...)

Arguments

motifs  a list of position frequency matrices (4xL matrices)
organism either a name of the organisms for which the background should be compiled (currently supported names are "dm3", "mm9" and "hg19"), or a BSgenome object (see BSgenome package).
type  the type of background to be compiled. Possible types are:
    • "logn" - estimate a lognormal background
    • "cutoff" - estimate a Z-score background with fixed log-odds cutoff (in log2)
    • "pval" - estimate a Z-score background with a fixed P-value cutoff. Note that this may require a lot of memory since the P-value of motif hits is first estimated from the empirical distribution.
    • "empirical" - create an empirical P-value background. Note that this may require a lot of memory (up to 10GB in default "slow" mode (quick=FALSE) for 126 JASPAR motifs and 1000 D. melanogaster promoters).
    • "GEV" - estimate a generalized extreme value (GEV) distribution background by fitting linear regression to distribution parameters in log space
quick  if to preform fitting on a reduced set of 100 promoters. This will not give as good results but is much quicker than fitting to all the promoters (~10k). Usage of this parameter is recommended only for testing and rough estimates.
bg.seq  a set of background sequences to use. This parameter overrides the "organism" and "quick" parameters.
...  other named parameters that backend function makePWM***Background functions take.

Author(s)

Robert Stojnic, Diego Diez
Examples

# load in the two example de-novo motifs
motifs = readMotifs(system.file(package="PWMEnrich", dir="extdata", file="example.transfac"), remove.acc=TRUE)

## Not run:
# construct lognormal background
bg.logn = makeBackground(motifs, organism="dm3", type="logn")

# alternatively, any BSgenome object can also be used
if(require("BSgenome.Dmelanogaster.UCSC.dm3"))
    bg.logn = makeBackground(motifs, organism=Dmelanogaster, type="logn")

# construct a Z-score of hits with P-value background
bg.pval = makeBackground(motifs, organism="dm3", type="pval", p.value=1e-3)

# now we can use them to scan for enrichment in sequences (in this case there is a consensus Tin binding site)
motifEnrichment(DNAString("TGCATCAAGTGTGTAGTG"), bg.logn)
motifEnrichment(DNAString("TGCATCAAGTGTGTAGTG"), bg.pval)

## End(Not run)

makePriors

Make priors from background sequences

Description

These priors serve both as background nucleotide frequencies and pseudo-counts for PWMs.

Usage

makePriors(bg.seq, bg.pseudo.count)

Arguments

bg.seq a set of background sequences
bg.pseudo.count the total pseudocount shared between nucleotides

Examples

# some example sequences
sequences = list(DNAString("AAAGAGAGTGACCGATGAC"), DNAString("ACGTGAGGTAGTACG"))
# make priors with pseudo-count of 1 shared between them
makePriors(sequences, 1)
makePWM_cutoffBackground

*Make a cutoff background*

**Description**

Make a background based on number of motifs hits above a certain threshold.

**Usage**

```r
makePWM_cutoffBackground(bg.seq, motifs, 
cutoff = log2(exp(4)), bg.pseudo.count = 1, 
bg.source = "", verbose = TRUE)
```

**Arguments**

- `bg.seq`: a set of background sequences, either a list of DNAString object or DNAStringSet object.
- `motifs`: a set of motifs, either a list of frequency matrices, or a list of PWM objects. If frequency matrices are given, the background distribution is fitted from bg.seq.
- `cutoff`: the cutoff at which the background should be made, i.e. at which a motif hit is called significant.
- `bg.pseudo.count`: the pseudo count which is shared between nucleotides when frequency matrices are given.
- `bg.source`: a free-form textual description of how the background was generated.
- `verbose`: if to produce verbose output.

**Examples**

```r
## Not run:
if(require("PWMEnrich.Dmelanogaster.background")){
  data(MotifDb.Dmel.PFM)
  # make background for MotifDb motifs using 2kb promoters of all D. melanogaster transcripts using cutoff of 5
  if(require("BSgenome.Dmelanogaster.UCSC.dm3"))
    makePWM_cutoffBackground(Dmelanogaster$upstream2000, MotifDb.Dmel.PFM, cutoff=log2(exp(5)))
}

## End(Not run)
```
makePWMEmpiricalBackground

Make an empirical P-value background

Description

Make a background appropriate for empirical P-value calculation. The provided set of background sequences is concatenated into a single long sequence which is then scanned with the motifs and raw scores are saved. This object can be very large.

Usage

makePWMEmpiricalBackground(bg.seq, motifs, bg.pseudo.count = 1, bg.source = "", verbose = TRUE, ...)

Arguments

bg.seq a set of background sequences, either a list of DNAString object or DNAStringSet object
motifs a set of motifs, either a list of frequency matrices, or a list of PWM objects. If frequency matrices are given, the background distribution is fitted from bg.seq.
bg.pseudo.count the pseudo count which is shared between nucleotides when frequency matrices are given
bg.source a free-form textual description of how the background was generated
verbose if to produce verbose output
... currently unused (this is for convenience for makeBackground function)

Details

For reliable P-value calculation the size of the background set needs to be at least seq.len / min.P.value. For instance, to get P-values at a resolution of 0.001 for a single sequence of 500bp, we would need a background of at least 500/0.001 = 50kb. This ensures that we can make 1000 independent 500bp samples from this background to properly estimate the P-value. For a group of sequences, we would take seq.len to be the total length of all sequences in a group.

Examples

```r
### Not run:
if(require("PWMEnrich.Dmelanogaster.background")){
data(MotifDb.Dmel.PFM)

# make empirical background by saving raw scores for each bp in the sequence - this can be very large in memory
if(require("BSgenome.Dmelanogaster.UCSC.dm3"))
    makePWMEmpiricalBackground(Dmelanogaster$upstream2000[1:100], MotifDb.Dmel.PFM)
}

### End(Not run)
```
makePWMGEVBackground

Make a GEV background distribution

Description

Construct a lognormal background distribution for a set of sequences. Sequences concatenated are binned in ‘bg.len’ chunks and lognormal distribution fitted to them.

Usage

makePWMGEVBackground(bg.seq, motifs, bg.pseudo.count = 1,
bg.len = seq(200, 2000, 200), bg.source = "",
verbose = TRUE, fit.log = TRUE)

Arguments

bg.seq a set of background sequences, either a list of DNAString object or DNAStringSet object
motifs a set of motifs, either a list of frequency matrices, or a list of PWM objects. If frequency matrices are given, the background distribution is fitted from bg.seq.
bg.pseudo.count the pseudo count which is shared between nucleotides when frequency matrices are given
bg.len the length range of background chunks
bg.source a free-form textual description of how the background was generated
verbose if to produce verbose output
fit.log if to fit log odds (instead of odds)

Examples

## Not run:
if(require("PWMEnrich.Dmelanogaster.background")){
data(MotifDb.Dmel.PFM)

# make background for MotifDb motifs using 2kb promoters of all D. melanogaster transcripts
if(require("BSgenome.Dmelanogaster.UCSC.dm3"))
  makePWMGEVBackground(Dmelanogaster$upstream2000, MotifDb.Dmel.PFM)
}

## End(Not run)
makePWMLognBackground  
*Make a lognormal background distribution*

**Description**

Construct a lognormal background distribution for a set of sequences. Sequences concatenated are binned in `bg.len` chunks and lognormal distribution fitted to them.

**Usage**

```r
makePWMLognBackground(bg.seq, motifs, bg.pseudo.count = 1, bg.len = 250, 
  bg.len.sizes = 2^(0:4), bg.source = "", verbose = TRUE, 
  algorithm = "default")
```

**Arguments**

- **bg.seq**  
  a set of background sequences, either a list of DNAString object or DNAStringSet object

- **motifs**  
  a set of motifs, either a list of frequency matrices, or a list of PWM objects. If frequency matrices are given, the background distribution is fitted from bg.seq.

- **bg.pseudo.count**  
  the pseudo count which is shared between nucleotides when frequency matrices are given

- **bg.len**  
  background sequences will be split into tiles of this length (default: 250bp)

- **bg.len.sizes**  
  background tiles will be joined into bigger tiles containing this much smaller tiles. The default is $2^{(0:4)}$, which with bg.len translates into 250bp, 500bp, 1000bp, 1500bp, 2000bp, 4000bp. Note this is only used in the "human" algorithm.

- **bg.source**  
  a free-form textual description of how the background was generated

- **verbose**  
  if to produce verbose output

- **algorithm**  
  type of algorithm to use, valid values are: "default" and "human".

**Examples**

```r
## Not run:
if(require("PWMEnrich.Dmelanogaster.background")){
  data(MotifDb.Dmel.PFM)
  # make background for MotifDb motifs using 2kb promoters of all D. melanogaster transcripts
  if(require("BSgenome.Dmelanogaster.UCSC.dm3"))
    makePWMLognBackground(Dmelanogaster$upstream2000, MotifDb.Dmel.PFM)
}
## End(Not run)
```
makePWMPvalCutoffBackground

Construct a cutoff background from empirical background

Description

This function takes already calculated empirical background distribution and chooses cutoff for each motif based on P-value cutoff for individual sites.

Usage

makePWMPvalCutoffBackground(bg.p, p.value = 0.001, bg.source = "")

Arguments

bg.p an object of class PWMEmpiricalBackground
p.value the P-value used to find cutoffs for each of the motifs
bg.source textual description of background source

Value

an object of type PWMCutoffBackground

Examples

## Not run:
if(require("PWMEnrich.Dmelanogaster.background")){
  data(MotifDb.Dmel.PFM)
  # make empirical background - here we use only 100 sequences for illustrative purposes
  if(require("BSgenome.Dmelanogaster.UCSC.dm3"))
    bg.p = makePWMEmpiricalBackground(Dmelanogaster$upstream2000[1:100], MotifDb.Dmel.PFM)
    # use the empirical background to pick a threshold and make cutoff background
    makePWMPvalCutoffBackground(bg.p, 0.001)
}
## End(Not run)

makePWMPvalCutoffBackgroundFromSeq

Construct a P-value cutoff background from a set of sequences

Description

This function creates a P-value cutoff background for motif enrichment.
motifDiffEnrichment

**Usage**

```
makePWMValCutoffBackgroundFromSeq(bg.seq, motifs,
p.value = 0.001, bg.pseudo.count = 1, bg.source = "",
verbose = TRUE)
```

**Arguments**

- `bg.seq`: a set of background sequences, either a list of DNAString object or DNAStringSet object
- `motifs`: a set of motifs, either a list of frequency matrices, or a list of PWM objects. If frequency matrices are given, the background distribution is fitted from `bg.seq`
- `p.value`: the P-value used to find cutoffs for each of the motifs
- `bg.pseudo.count`: the pseudo count which is shared between nucleotides when frequency matrices are given
- `bg.source`: textual description of background source
- `verbose`: if to print verbose output

**Value**

an object of type PWMcutoffBackground

**Examples**

```r
## Not run:
if(require("PWMEnrich.Dmelanogaster.background")){
  data(MotifDb.Dmel.PFM)
  # use the empirical background to pick a threshold and make cutoff background
  makePWMValCutoffBackground(Dmelanogaster$upstream2000, 0.001)
}
## End(Not run)
```

motifDiffEnrichment

**Differential motif enrichment**

**Description**

Test for differential enrichment between two groups of sequences

**Usage**

```
motifDiffEnrichment(sequences1, sequences2, pwms,
  score = "autodetect", bg = "autodetect",
  cutoff = log2(exp(4)), verbose = TRUE, res1 = NULL, res2 = NULL)
```
motifDiffEnrichment

Arguments

sequences1  First set of sequences. Can be either a single sequence (an object of class DNAString), or a list of DNAString objects, or a DNAStringSet object.

sequences2  Second set of sequences. Can be either a single sequence (an object of class DNAString), or a list of DNAString objects, or a DNAStringSet object.

pwms  this parameter can take multiple values depending on the scoring scheme and background correction used. When the method parameter is set to "autodetect", the following default algorithms are going to be used:

  • if pwms is a list containing either frequency matrices or a list of PWM objects then the "affinity" algorithm is selected. If frequency matrices are given, they are converted to PWMS using uniform background. For best performance, convert frequency matrices to PWMS before calling this function using realistic genomic background.
  • Otherwise, appropriate scoring scheme and background correction are selected based on the class of the object (see below).

score  this parameter determines which scoring scheme to use. Following scheme as available:

  • "autodetect" - default value. Scoring method is determined based on the type of pwms parameter.
  • "affinity" - use threshold-free affinity scores without a background. The pwms parameter can either be a list of frequency matrices, PWM objects, or a PWMLognBackground object.
  • "cutoff" - use number of motif hits above a score cutoff as a measure of enrichment. No background correction is performed. The pwms parameter can either be a list of frequency matrices, PWM objects, or a PWMCutoffBackground object.

bg  this parameter determines which background correction to use, if any.

  • "autodetect" - default value. Background correction is determined based on the type of the pwms parameter.
  • "logn" - use a lognormal distribution background pre-computed for a set of PWMS. This requires pwms to be of class PWMLognBackground.
  • "z" - use a z-score for the number of significant motif hits compared to background number of hits. This requires pwms to be of class PWMCutoffBackground.
  • "none" - no background correction

cutoff  the score cutoff for a significant motif hit if scoring scheme "cutoff" is selected.

res1  the output of motifEnrichment if already calculated for sequences1

res2  the output of motifEnrichment if already calculated for sequences2

verbose  if to produce verbose output

Details

This function calls motifEnrichment on two groups of sequences and calculates the difference statistics when possible.

Examples

if(require("PWMEnrich.Dmelanogaster.background")){
  # load the background file for drosophila and lognormal correction
data(PWMLogn.dm3.MotifDb.Dmel)

# get the differential enrichment
diff = motifDiffEnrichment(DNAString("TGCATCAAGTGTGTAGTGTGAGATTAGT"), DNAString("TGAACGAGTAGGACGATGAGAGATTGATG"), PWMLogn.dm3.MotifDb.Dmel, verbose=FALSE)

# motifs differentially enriched in the first sequence (with lognormal background correction)
head(sort(diff$group.bg, decreasing=TRUE))

# motifs differentially enriched in the second sequence (with lognormal background correction)
head(sort(diff$group.bg))

motifEcdf

Calculate the empirical distribution score distribution for a set of motifs

Description

Calculate the empirical distribution score distribution for a set of motifs

Usage

motifEcdf(motifs, organism = NULL, bg.seq = NULL, quick = FALSE, pseudo.count = 1)

Arguments

motifs a set of motifs, either a list of frequency matrices, or a list of PWM objects. If frequency matrices are given, the background distribution is fitted from bg.seq.
organism either a name of the organisms for which the background should be compiled (supported names are "dm3", "mm9" and "hg19"), or a BSgenome object (see BSgenome package).
bg.seq a set of background sequence (either this or organism needs to be specified!). Can be a DNAString or DNAStringSet object.
quick if to do the fitting only on a small subset of the data (only in combination with organism). Useful only for code testing!
pseudo.count the pseudo count which is shared between nucleotides when frequency matrices are given

Value

a list of ecdf objects (see help page for ecdf for usage).
motifEnrichment

**Description**

Calculate motif enrichment using one of available scoring algorithms and background corrections.

**Usage**

```r
motifEnrichment(sequences, pwms, score = "autodetect", bg = "autodetect", cutoff = NULL, verbose = TRUE, motif.shuffles = 30, B = 1000, group.only = FALSE)
```

**Arguments**

- `sequences`: the sequences to be scanned for enrichment. Can be either a single sequence (an object of class DNAString), or a list of DNAString objects, or a DNAStringSet object.

- `pwms`: this parameter can take multiple values depending on the scoring scheme and background correction used. When the `method` parameter is set to "autodetect", the following default algorithms are going to be used:
  - if `pwms` is a list containing either frequency matrices or a list of PWM objects then the "affinity" algorithm is selected. If frequency matrices are given, they are converted to PWMs using uniform background. For best performance, convert frequency matrices to PWMs before calling this function using realistic genomic background.
  - Otherwise, appropriate scoring scheme and background correction are selected based on the class of the object (see below).

- `score`: this parameter determines which scoring scheme to use. Following scheme as available:
  - "autodetect" - default value. Scoring method is determined based on the type of `pwms` parameter.
  - "affinity" - use threshold-free affinity scores without a background. The `pwms` parameter can either be a list of frequency matrices, PWM objects, or a PWMLognBackground object.
  - "cutoff" - use number of motif hits above a score cutoff as a measure of enrichment. No background correction is performed. The `pwms` parameter can either be a list of frequency matrices, PWM objects, or a PWMCutoffBackground object.
  - "clover" - use the Clover algorithm (Frith et al, 2004). The Clover score of a single sequence is identical to the affinity score, while for a group of sequences is an average of products of affinities over all sequence subsets.

- `bg`: this parameter determines which background correction to use, if any.
  - "autodetect" - default value. Background correction is determined based on the type of the `pwms` parameter.
  - "logn" - use a lognormal distribution background pre-computed for a set of PWMs. This requires `pwms` to be of class PWMLognBackground.
* "z" - use a z-score for the number of significant motif hits compared to background number of hits. This requires `pwms` to be of class `PWMCutoffBackground`.

* "pval" - use empirical P-value based on a set of background sequences. This requires `pwms` to be of class `PWMEmpiricalBackground`. Note that `PWMEmpiricalBackground` objects tend to be very large so that the empirical P-value can be calculated in reasonable time.

* "ms" - shuffle columns of motif matrices and use that as basis for P-value calculation. Note that since the sequences need to rescanmed with all of the new shuffled motifs this can be very slow. Also, this also works only on *individual* sequences, not groups.

* "none" - no background correction

cutoff
the score cutoff for a significant motif hit if scoring scheme "cutoff" is selected.

verbose
if to print verbose output

motif.shuffles
number of times to shuffle motifs if using "ms" background correction

B
number of replicates when calculating empirical P-value

group.only
if to return statistics only for the group of sequences, not individual sequences.

In the case of empirical background the P-values for individual sequences are not calculated (thus saving time), for other backgrounds they are calculated but not returned.

Details

This function provides an interface to all algorithms available in PWMEnrich to find motif enrichment in a single or a group of sequences with/without background correction.

Since for all algorithms the first step involves calculating raw scores without background correction, the output always contains the scores without background correction together with (optional) background-corrected scores.

Unless otherwise specified the scores are returned both separately for each sequence (without/with background) and for the whole group of sequences (without/with background).

To use a background correction you need to supply a set of PWMs with precompiled background distribution parameters (see function `makeBackground`). When such an object is supplied as the `pwm` parameter, the scoring scheme and background correction are automatically determined.

There are additional packages with already pre-computed background (e.g. see package `PWMEnrich.Dmelanogaster.background`). Please refer to (Stojnic & Adryan, 2012) for more details on the algorithms.

Value

a `MotifEnrichmentResults` object containing a subset following elements:

* "score" - scoring scheme used

* "bg" - background correction used

* "params" - any additional parameters

* "sequences" - the set of sequences used

* "pwms" - the set of pwms used

* "sequence.nobg" - per-sequence scores without any background correction. For "affinity" and "clover" a matrix of mean affinity scores; for "cutoff" number of significant hits above a cutoff

* "sequence.bg" - per-sequence scores after background correction. For "logn" and "pval" the P-value (smaller is better); for "z" and "ms" background corrections the z-scores (bigger is better).
motifEnrichment

- "group.nobg" - aggregate scores for the whole group of sequences without background correction. For "affinity" and "clover" the mean affinity over all sequences in the set; for "cutoff" the total number of hits in all sequences.
- "group.bg" - aggregate scores for the whole group of sequences with background correction. For "logn" and "pval", the P-value for the whole group (smaller is better); for "z" and "ms" the z-score for the whole set (bigger is better).
- "sequence.norm" - (only for "logn") the length-normalized scores for each of the sequences. Currently only implemented for "logn", where it returns the values normalized from LogN(0,1) distribution
- "group.norm" - (only for "logn") similar to sequence.norm, but for the whole group of sequences

References


Examples

```r
if(require("PWMEnrich.Dmelanogaster.background")){
  ###
  # load the pre-compiled lognormal background
  data(PWMLogn.dm3.MotifDb.Dmel)
  # scan two sequences for motif enrichment
  sequences = list(DNAString("GAAGTATCAAGTGACCAGTAGATTGAAGTAGACCAGTC"), DNAString("AGGTAGATAGAACAGTAGGCAATGGGGGAAATTGAGAGTC"))
  res = motifEnrichment(sequences, PWMLogn.dm3.MotifDb.Dmel)
  # most enriched in both sequences (lognormal background P-value)
  head(motifRankingForGroup(res))
  # most enriched in both sequences (raw affinity, no background)
  head(motifRankingForGroup(res, bg=FALSE))
  # most enriched in the first sequence (lognormal background P-value)
  head(motifRankingForSequence(res, 1))
  # most enriched in the first sequence (raw affinity, no background)
  head(motifRankingForSequence(res, 1, bg=FALSE))

  ###
  # Load the pre-compiled background for hit-based motif counts with cutoff of P-value = 0.001
  data(PWMValueCutoff1e3.dm3.MotifDb.Dmel)
  res.count = motifEnrichment(sequences, PWMValueCutoff1e3.dm3.MotifDb.Dmel)
  # Enrichment in the whole group, z-score for the number of motif hits
  head(motifRankingForGroup(res))
  # First sequence, sorted by number of motif hits with P-value < 0.001
  head(motifRankingForSequence(res, 1, bg=FALSE))
}
```
MotifEnrichmentReport  A report class with formatted results of motif enrichment

Description

The columns stored in this object will depend on the type of the report (either for group of sequences, or individual sequences).

Slots

- `d`: a DataFrame object that contains the main tabular report data
- `pwms`: a list of PWM objects corresponding to rows of `d`

MotifEnrichmentResults  A wrapper class for results of motifEnrichment() that should make it easier to access the results.

Description

Note that this is only a wrapper around a list which is the return value in PWMEnrich 1.3 and as such it provides the same interface as a list (for backward compatibility), with some additional methods.

Slots

- `res`: a list of old results with elements such as: sequence.bg, sequence.nobg, group.bg, group.nobg

motifIC  Information content for a PWM or PFM

Description

Information content for a PWM or PFM

Usage

```r
motifIC(motif,
prior.params = c(A = 0.25, C = 0.25, G = 0.25, T = 0.25),
bycol = FALSE)
```

Arguments

- `motif`: a matrix of frequencies, or a PWM object
- `prior.params`: the prior parameters to use when a matrix is given (ignored if motif is already a PWM)
- `bycol`: if to return values separately for each column
motifRankingForGroup, MotifEnrichmentResults-method

Value
information content in bits (i.e. log2)

Examples

if(require("PWMEnrich.Dmelanogaster.background")){
  data(MotifDb.Dmel)
  data(MotifDb.Dmel.PFM)

  # the nucleotide distribution is taken from the PWM (in this case genomic background)
  motifIC(MotifDb.Dmel["ttk"])
  # information content with default uniform background because the input is a matrix, not PWM object
  motifIC(MotifDb.Dmel.PFM["ttk"])
}

motifRankingForGroup, MotifEnrichmentResults-method

Get a ranking of motifs by their enrichment in the whole set of sequences

Description

Get a ranking of motifs by their enrichment in the whole set of sequences

Arguments

obj a MotifEnrichmentResults object
bg if to use background corrected P-values to do the ranking (if available)
id if to show PWM IDs instead of target TF names
order if to output the ordering of PWMs instead of actual P-values or raw values
rank if the output should be rank of a PWM instead of actual P-values or raw values
unique if TRUE, only the best rank is taken for each TF (only when id = FALSE, order = FALSE)
... currently unused

Value

a vector of log(P-values), P-values or raw enrichments sorted such that the first motif is most enriched

Examples

if(require("PWMEnrich.Dmelanogaster.background")){
  ###
  # load the pre-compiled lognormal background
  data(PWMLogn.dm3MotifDb.Dmel)

  # scan two sequences for motif enrichment
  sequences = list(DNAString("GAAGTATCAAGTGACCAGTAAGTCCCAGATGA"), DNAString("AGGTAGATAGAAGTAGGCAATGAAGCCGATG"))
  res = motifEnrichment(sequences, PWMLogn.dm3MotifDb.Dmel)
motifRankingForSequence,MotifEnrichmentResults-method

Get a ranking of motifs by their enrichment in one specific sequence

Description

Get a ranking of motifs by their enrichment in one specific sequence

Arguments

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>obj</td>
<td>a MotifEnrichmentResults object</td>
</tr>
<tr>
<td>seq.id</td>
<td>either the sequence number or sequence name</td>
</tr>
<tr>
<td>bg</td>
<td>if to use background corrected P-values to do the ranking (if available)</td>
</tr>
<tr>
<td>id</td>
<td>if to show PWM IDs instead of target TF names</td>
</tr>
<tr>
<td>order</td>
<td>if to output the ordering of PWMs instead of actual P-values or raw values</td>
</tr>
<tr>
<td>rank</td>
<td>if the output should be rank of a PWM instead of actual P-values or raw values</td>
</tr>
<tr>
<td>unique</td>
<td>if TRUE, only the best rank is taken for each TF (only when id = FALSE, order = FALSE)</td>
</tr>
<tr>
<td>...</td>
<td>currently unused</td>
</tr>
</tbody>
</table>

Value

a vector of P-values or raw enrichments sorted such that the first motif is most enriched

Examples

```r
if(require("PWMEnrich.Dmelanogaster.background")){
  ###
  # load the pre-compiled lognormal background
data(PWMLogn.dm3.MotifDb.Dmel)

  # scan two sequences for motif enrichment
  sequences = list(DNAString("GAAGTATCAAGTGACCAGTAAGTCCCAGATGA"), DNAString("AGGTAGATAGAACAGTAGGCAATGAAGCCGATG"))
  res = motifEnrichment(sequences, PWMLogn.dm3.MotifDb.Dmel)
```
# most enriched in the second sequences (sorted by lognormal background P-value)
head(motifRankingForSequence(res, 2))

# return unique TFs enriched in sequence 2
head(motifRankingForSequence(res, 2, unique=TRUE))

# sorted by raw affinity instead of P-value
head(motifRankingForSequence(res, 2, bg=FALSE))

# show IDs instead of target TF names
head(motifRankingForSequence(res, 2, id=TRUE))

# output the rank instead of P-value
head(motifRankingForSequence(res, 2, rank=TRUE))

---

**motifScores**

**Motif affinity of number of hits over a threshold**

**Description**

Scan a number of sequences either to find overall affinity, or a number of hits over a score threshold.

**Usage**

```r
motifScores(sequences, motifs, raw.scores = FALSE, verbose = TRUE, cutoff = NULL)
```

**Arguments**

- `sequences` a set of sequences to be scanned, a list of DNAString or other scannable objects
- `motifs` a list of motifs either as frequency matrices (PFM) or as PWM objects. If PFMs are specified they are converted to PWMs using uniform background.
- `raw.scores` if to return raw scores (odds) for each position in the sequence. Note that scores for forward and reverse strand are concatenated into a single long vector of scores (twice the length of the sequence)
- `verbose` if to print verbose output
- `cutoff` if not NULL, will count number of matches with score above value specified (instead of returning the average affinity). Can either be one value, or a vector of values for each of the motifs.

**Value**

if raw.scores=FALSE, returns a matrix of mean scores (after cutoff if any), where columns are motifs. The returned values are either mean odd scores (not log-odd), or number of hits above a threshold; otherwise if raw.scores=TRUE, returns a list of raw score values (before cutoff)
motifSimilarity

**Examples**

```r
if(require("PWMEnrich.Dmelanogaster.background")){
  data(MotifDb.Dmel)
  affinity = motifScores(DNAString("CGTAGGATAAAAGTAACCTAGTTGATGAAAG"), MotifDb.Dmel) # affinity scores
  counts = motifScores(DNAString("CGTAGGATAAAAGTAACCTAGTTGATGAAAG"), MotifDb.Dmel, cutoff=log2(exp(4))) # motif hit count with Patser score of 4
  print(affinity)
  print(counts)

  # scanning multiple sequences
  sequences = list(DNAString("CGTAGGATAAAAGTAACCTAGTTGATGAAAG"), DNAString("TGAGACGAAGGGGATGAGATGCGGAAGAGTGAAA"))
  affinity2 = motifScores(sequences, MotifDb.Dmel)
  print(affinity2)
}
```

**motifSimilarity**

Calculates similarity between two PFMs.

**Description**

This function calculates the normalized motif correlation as a measure of motif frequency matrix similarity.

**Usage**

```r
motifSimilarity(m1, m2, trim = 0.4, self.sim = FALSE)
```

**Arguments**

- **m1**: matrix with four rows representing the frequency matrix of first motif
- **m2**: matrix with four rows representing the frequency matrix of second motif
- **trim**: bases with information content smaller than this value will be trimmed off both motif ends
- **self.sim**: if to calculate self similarity (i.e. without including offset=0 in alignment)

**Details**

This score is essentially a normalized version of the sum of column correlations as proposed by Pietrokovski (1996). The sum is normalized by the average motif length of m1 and m2, i.e. \((\text{ncol}(m1)+\text{ncol}(m2))/2\). Thus, for two identical motifs this score is going to be 1. For unrelated motifs the score is going to be typically around 0.

Motifs need to aligned for this score to be calculated. The current implementation tries all possible ungapped alignment with a minimal of two basepair matching, and the maximal score over all alignments is returned.

Motif 1 is aligned both to Motif 2 and its reverse complement. Thus, the motif similarities are the same if the reverse complement of any of the two motifs is given.

**References**

Examples

```r
if(require("PWMEnrich.Dmelanogaster.background")){
  data(MotifDb.Dmel.PFM)

  # calculate the similarity of tin and vnd motifs (which are almost identical)
  motifSimilarity(MotifDb.Dmel.PFM["tin"], MotifDb.Dmel.PFM["vnd"])

  # similarity of two unrelated motifs
  motifSimilarity(MotifDb.Dmel.PFM["tin"], MotifDb.Dmel.PFM["ttk"])
}
```

names,MotifEnrichmentReport

<table>
<thead>
<tr>
<th>Names of variables</th>
</tr>
</thead>
</table>

Description

Columns stored in the motif enrichment report

Access a column by name

Subset the report

Arguments

- `x` the MotifEnrichmentReport object
- `x` the MotifEnrichmentReport object
- `name` the variable name
- `i` the row selector
- `j` unused
- `...` unused
- `drop` unused (always FALSE)

Value

the names of the variables

names,MotifEnrichmentResults

<table>
<thead>
<tr>
<th>Names of variables</th>
</tr>
</thead>
</table>

Description

Name of different pieces of information associated with MotifEnrichmentResults

Access a property by name
Arguments

- `x` the MotifEnrichmentResults object
- `x` the MotifEnrichmentResults object
- `name` the variable name

Value

the names of the variables

---

### names, PWM

**Names of variables**

**Description**

Name of different pieces of information associated with PWM

Access a property by name

Returns the motif length, i.e. the number of columns in the PWM.

**Arguments**

- `x` the PWM object
- `x` the PWM object
- `name` the variable name
- `x` the PWM object

**Value**

the names of the variables

---

### names, PWMcutoffBackground

**Names of variables**

**Description**

Name of different pieces of information associated with PWMcutoffBackground

Access a property by name

**Arguments**

- `x` the PWMcutoffBackground object
- `x` the PWMcutoffBackground object
- `name` the variable name

**Value**

the names of the variables
**names,PWMEmpiricalBackground**

*Names of variables*

**Description**

Name of different pieces of information associated with PWMEmpiricalBackground

Access a property by name

**Arguments**

- `x` the PWMEmpiricalBackground object
- `x` the PWMEmpiricalBackground object
- `name` the variable name

**Value**

the names of the variables

---

**names,PWMGEVBackground**

*Names of variables*

**Description**

Name of different pieces of information associated with PWMGEVBackground

Access a property by name

**Arguments**

- `x` the PWMGEVBackground object
- `x` the PWMGEVBackground object
- `name` the variable name

**Value**

the names of the variables
names,PWMLognBackground

Names of variables

Description
Name of different pieces of information associated with PWMLognBackground
Access a property by name

Arguments
x the PWMLognBackground object
x the PWMLognBackground object
name the variable name

Value
the names of the variables

PFMtoPWM

Convert frequencies into motifs using PWMUnscaled

Description
Convert frequencies into motifs using PWMUnscaled

Usage
PFMtoPWM(motifs, id = names(motifs),
name = names(motifs), seq.count = NULL, ...)

Arguments

motifs a list of motifs represented as matrices of frequencies (PFM)
id the set of IDs for the motifs (defaults to names of the 'motifs' list)
name the set of names for the motifs (defaults to names of the 'motifs' list)
seq.count if frequencies in the motifs are normalized to 1, provides a vector of sequence
counts (e.g. for MotifDb motifs)
... other parameters to PWMUnscaled

Examples
if(require("PWMEnrich.Dmelanogaster.background")){
data(MotifDb.Dmel.PFM)

PFMtoPWM(MotifDb.Dmel.PFM) # convert to PWM with uniform background

prior = getBackgroundFrequencies("dm3", quick=TRUE) # get background for drosophila (quick mode on a reduced
PFMtoPWM(MotifDb.Dmel.PFM, prior.params=prior) # convert with genomic background
}
Description

This function produces a sequence logo (via package seqLogo).
Plots a graphical version of the motif enrichment report. Note that all values are plotted, if you want to plot only a subset of a report, first select this subset (see examples).

Arguments

- `x`: the PWM object
- `y`: unused
- `...`: other parameters to pass to seqLogo’s `plot` function
- `x`: a MotifEnrichmentReport object
- `y`: unused
- `fontsize`: font size to use in the plot
- `header.fontsize`: font size of the header
- `widths`: the relative widths of columns
- `...`: unused if(require("PWMEnrich.Dmelanogaster.background")) ### # load the pre-compiled lognormal background data(PWMLogn.dm3.MotifDb.Dmel)
# scan two sequences for motif enrichment sequences = list(DNAString("GAAGTATCAAGTGACCAGTAAGTCCCAGATGA"), DNAString("AGGTAGATAGAACAGTAGGCAATGAAGCCGATG"))
res = motifEnrichment(sequences, PWMLogn.dm3.MotifDb.Dmel)
# produce a report for all sequences taken together r = groupReport(res)
# plot the top 10 most enriched motifs plot(r[1:10])

Examples

```
if(require("PWMEnrich.Dmelanogaster.background")){
data(MotifDb.Dmel)

  # plot the tinman motif from MotifDb
  plot(MotifDb.Dmel["tin"])
}
```

plotMotifScores

Plot the raw motifs scores as returned by motifScores()

Description

This function visualises the motif scores for one or more sequences. Sequences are drawn as lines, and scores are plotted as triangles at both sides of the line (corresponding to the two strands). The width of the base of the triangle corresponds to motif width and the height to the motif $\log(score)$ that is positive and greater than the cutoff parameter (if specified). All scores have the same y-axis, so the heights of bars are comparable between sequences and motifs.
Usage

plotMotifScores(scores, sel.motifs = NULL,
seq.names = NULL, cols = NULL, cutoff = NULL,
log.fun = log2, main = "", legend.space = 0.3,
max.score = NULL, trans = 0.5, text.cex = 0.9,
legend.cex = 0.9, motif.names = NULL,
seq.len.spacing = 8, shape="rectangle")

Arguments

scores the list of motifs scores. Each element of the list is a matrix of scores for one sequences. The columns in the matrix correspond to different motifs. Each column contains the odds (not log-odds!) scores over both strands. For example, for a sequence of length 5, scores for a 3 bp motifs could be: c(0.1, 1, 4, NA, NA, 1, 0.3, 2, NA, NA).
The first 3 numbers are odds scores starting at first three bases, and the second lot of 3 numbers is the scores starting at the same positions but with the reverse complement of the motif. The last two values are NA on both strands because we do not support partial motif hits.

sel.motifs a vector of motif names. Use this parameter to show the motif hits to only a subset of motifs for which the scores are available.

seq.names a vector of sequence names to show in the graph. If none specified, the sequences will be named Sequence 1, Sequence 2, ...

cols a vector of colours to use to colour code motif hits. If none are specified, the current palette will be used.

cutoff either a single value, or a vector of values. The values are PWM cutoffs after log.fun (see below). Only motif scores above these cutoffs will be shown. If a single values is specified, it will be used for all PWMs, otherwise the vector needs to specify one cutoff per PWM.

log.fun the logarithm function to use to calculate log-odds. By default log2 is used for consistency with Biostrings.

main the main title

legend.space the proportion of horizontal space to reserve for the legend. The default is 30%.

max.score the maximal log-odds score used to scale all other scores. By default this values is automatically determined, but it can also be set manually to make multiple plots comparable.

trans the level of transparency. By default 50% transparency to be able to see overlapping binding sites

text.cex the scaling factor for sequence names

legend.cex the scaling factor for the legend

motif.names optional vector of motif names to show instead of those present as column names in scores

seq.len.spacing the spacing (in bp units) between the end of the sequence line and the text showing the length in bp

shape the shape to use to draw motif occurrences, valid values are "rectangle" (default), "line" and "triangle"
Examples

```r
if(require("PWMEnrich.Dmelanogaster.background")){
    # Load Drosophila PWMs
    data(MotifDb.Dmel)

    # two sequences of interest
    sequences = list(DNAString("GAAGTATCAAGTGACCAGGTGAAGTCCCAGATGA"), DNAString("AGGTAGATAGAACAGTAGGCAATGAAGCCGATG"))

    # select the tinman and snail motifs
    pwms = MotifDb.Dmel[c("tin", "sna")]

    # get the raw score that will be plotted
    scores = motifScores(sequences, pwms, raw.scores=TRUE)

    # plot the scores in both sequences, green for tin and blue for sna
    plotMotifScores(scores, cols=c("green", "blue"))
}
```

plotMultipleMotifs  Plot multiple motifs in a single plot

Description

Individual motif logos are plotted on a rows x cols grid. This function is a convenience interface for the seqLogoGrid function that deals with viewpoint placement in a matrix-like grid layout.

Usage

```r
plotMultipleMotifs(pwms, titles = names(pwms),
    rows = ceiling(sqrt(length(pwms)));
    cols = ceiling(sqrt(length(pwms)));
    xmargin.scale = 0.4, ymargin.scale = 0.4, ...)```

Arguments

- **pwms**: a list of PWM objects or frequency matrices
- **titles**: a character vector of titles for each of the plots
- **rows**: number of rows in the grid
- **cols**: number or cols in the grid
- **xmargin.scale**: the scaling parameter for the X-axis margin. Useful when plotting more than one logo on a page
- **ymargin.scale**: the scaling parameter for the Y-axis margin. Useful when plotting more than one logo on a page
- **...**: other parameters passed to seqLogoGrid()

Details

By default will try to make a square grid plot that would fit all the motifs and use list names as captions.
**plotTopMotifsGroup, MotifEnrichmentResults-method**

*Plot the top N enrichment motifs in a group of sequences*

**Description**

Plot the top N enrichment motifs in a group of sequences

**Arguments**

- **obj**: a `MotifEnrichmentResults` object
- **n**: the number of top ranked motifs to plot
- **bg**: if to use background corrected P-values to do the ranking (if available)
- **id**: if to show PWM IDs instead of target TF names
- **...**: other parameters passed to `plotMultipleMotifs()`

**Examples**

```r
if(require("PWMEnrich.Dmelanogaster.background")){
    ###
    # load the pre-compiled lognormal background
data(PWMLogn.dm3.MotifDb.Dmel)

    # scan two sequences for motif enrichmentsequences = list(DNAString("GAAGTATCAAGTGACCAGTAAGTCCCAGATGA"), DNAString("AGGTAGATAGAACAGTAGGCAATGAAGCCGATG"))
res = motifEnrichment(sequences, PWMLogn.dm3.MotifDb.Dmel)

    # plot the top 4 motifs in a 2x2 grid
plotTopMotifsGroup(res, 4)

    # plot top 3 motifs in a single row
plotTopMotifsGroup(res, 3, row=1, cols=3)
}
```

**plotTopMotifsSequence, MotifEnrichmentResults-method**

*Plot the top N enrichment motifs in a single sequence*

**Description**

Plot the top N enrichment motifs in a single sequence

**Arguments**

- **obj**: a `MotifEnrichmentResults` object
- **seq.id**: either the sequence number or sequence name
- **n**: the number of top ranked motifs to plot
- **bg**: if to use background corrected P-values to do the ranking (if available)
- **id**: if to show PWM IDs instead of target TF names
- **...**: other parameters passed to `plotMultipleMotifs()`
Examples

```r
if (require("PWMEnrich.Dmelanogaster.background")){
##
# load the pre-compiled lognormal background
data(PWMLogn.dm3.MotifDb.Dmel)

# scan two sequences for motif enrichment
sequences = list(DNAString("GAAGTATCAAGTGACCAGTAAGTCCCAGATGA"),
                 DNAString("AGGTAGATAGAACAGTAGGCAATGAAGCCGATG"))
res = motifEnrichment(sequences, PWMLogn.dm3.MotifDb.Dmel)

# plot the top 4 motifs in a 2x2 grid
plotTopMotifsSequence(res, 1, 4)

# plot top 3 motifs in a single row
plotTopMotifsSequence(res, 1, 3, row=1, cols=3)
}
```

PWM

A class that represents a Position Weight Matrix (PWM)

Description

A class that represents a Position Weight Matrix (PWM)

Slots

- **id**: a systematic ID given to this PWM, could include the source, version, etc
- **name**: the name of the transcription factor (TF) to which the PWM corresponds to
- **pfm**: Position Frequency Matrix (PFM) from which the PWM is derived
- **prior.params**: Defines prior frequencies of the four bases (A,C,G,T), a named vector. These will be added to individual values for the PFM and at the same time used as background probabilities
- **pwm**: Final Position Weight Matrix (PWM) constructed using prior.params with logarithm base 2

PWM.CutoffBackground

Hit count background distribution for a set of PWMs

Description

Hit count background distribution for a set of PWMs

Slots

- **bg.source**: textual description of where the background distribution is derived from
- **bg.cutoff**: the cutoff score used to find significant motif hits (in log2 odds), either a single value or a vector of values
- **bg.P**: the density of significant motif hits per nucleotide in background
- **pwms**: the pwms for which the background has been compiled
**PWMEmpiricalBackground**  
*Background for calculating empirical P-values*

**Description**

This object contains raw scores for one very long sequence, thus it can be very large.

**Slots**

- **bg.source**: textual description of where the background distribution is derived from
- **bg.fwd**: affinity scores (odds) for the forward strand. PWMs as columns
- **bg.rev**: affinity scores (odds) for the reverse strand. PWMs as columns
- **pwms**: the pwms for which the background has been compiled

**PWMGEVBackground**  
*Generalized Extreme Values (GEV) background for P-values*

**Description**

The three parameters of the GEV distribution are fitted by doing linear regression on log of sequence length.

**Slots**

- **bg.source**: textual description of where the background distribution is derived from
- **bg.loc**: linear regression model for estimating the location parameter based on log(L), list of lm objects of PWMs
- **bg.scale**: linear regression model for estimating the scale parameter based on log(L), list of lm objects of PWMs
- **bg.shape**: linear regression model for estimating the shape parameter based on log(L), list of lm objects of PWMs
- **pwms**: the pwms for which the background has been compiled
**PWMLognBackground**

*Lognormal background distribution for a set of PWMs*

**Description**

Lognormal background distribution for a set of PWMs

**Slots**

- `bg.source`: textual description of where the background distribution is derived from
- `bg.len`: the length to which the background is normalized to. This is a vector of values, can have a different value for each motif.
- `bg.mean`: the mean value of the lognormal distribution at `bg.len`
- `bg.sd`: the standard deviation of the lognormal distribution at `bg.len`
- `pwms`: the pwms for which the background has been compiled

---

**PWMUnscaled**

*Create a PWM from PFM*

**Description**

The PWM function from Biostrings without unit scaling

**Usage**

```r
PWMUnscaled(x, id = "", name = "", type = c("log2probratio", "prob"), prior.params = c(A = 0.25, C = 0.25, G = 0.25, T = 0.25), pseudo.count = prior.params, unit.scale = FALSE, seq.count = NULL)
```

**Arguments**

- `x`: the integer count matrix representing the motif, rows as nucleotides
- `id`: a systematic ID given to this PWM, could include the source, version, etc
- `name`: the name of the transcription factor (TF) to which the PWM corresponds to
- `type`: the type of PWM calculation, either as log2-odds, or posterior probability (frequency matrix)
- `prior.params`: the pseudocounts for each of the nucleotides
- `pseudo.count`: the pseudo-count values if different from priors
- `unit.scale`: if to unit.scale the pwm (default is no unit scaling)
- `seq.count`: if `x` is a normalised PFM (i.e. with probabilities instead of sequence counts), then this sequence count will be used to convert `x` into a count matrix
Details

By default the Biostrings package scales the log-odds score so it is within 0 and 1. In this function we take a more traditional approach with no unit scaling and offer unit scaling as an additional parameter.

See ?PWM from Biostrings for more information on input arguments.

Value

a new PWM object representing the PWM

Examples

```r
if(require("PWMEnrich.Dmelanogaster.background")){
  data(MotifDb.Dmel.PFM)
  ttk = MotifDb.Dmel.PFM["ttk"]

  PWMUnscaled(ttk, id="ttk-JASPAR", name="ttk") # make a PWM with uniform background
  PWMUnscaled(ttk, id="ttk-JASPAR", name="ttk", prior.params=c("A"=0.2, "C"=0.3, "G"=0.3, "T"=0.2)) # custom background

  prior = getBackgroundFrequencies("dm3", quick=TRUE) # get background for drosophila (quick mode on a reduced dataset)
  PWMUnscaled(ttk, id="ttk-JASPAR", name="ttk", prior.params=prior) # convert using genomic background
}
```

---

**readMotifs**  
Read in motifs in JASPAR or TRANSFAC format

Description

The format is autodetected based on file format. If the autodetection fail then the file cannot be read.

Usage

```
readMotifs(file, remove.acc = FALSE)
```

Arguments

- **file** the filename
- **remove.acc** if to remove accession numbers. If TRUE, the AC entry in TRANSFAC files is ignored, and the accession is stripped from JASPAR, e.g. motif with name "MA0211.1 bap" would become just "bap". If FALSE, both the AC and ID are used to generate the TRANSFAC name and the original motif names are preserved in JASPAR files.

Value

a list of 4xL matrices representing motifs (four nucleotides as rows)
Examples

# read in example TRANSFAC motifs without accession codes (just IDs)
readMotifs(system.file(package="PWMEnrich", dir="extdata", file="example.transfac"), remove.acc=TRUE)

# read in the JASPAR insects motifs provided as example
readMotifs(system.file(package="PWMEnrich", dir="extdata", file="jaspar-insecta.jaspar"), remove.acc=TRUE)

```
# read in example TRANSFAC motifs without accession codes (just IDs)
readMotifs(system.file(package="PWMEnrich", dir="extdata", file="example.transfac"), remove.acc=TRUE)

# read in the JASPAR insects motifs provided as example
readMotifs(system.file(package="PWMEnrich", dir="extdata", file="jaspar-insecta.jaspar"), remove.acc=TRUE)
```

reverseComplement      Reverse complement for the PWM object

Description

Finds the reverse complement of the PWM

Arguments

- `x`: an object of type PWM

Examples

```r
## Not run:
registerCoresPWMEnrich(4) # use 4 CPU cores in PWMEnrich
registerCoresPWMEnrich() # use maximal number of CPUs
registerCoresPWMEnrich(NULL) # do not use parallel execution

## End(Not run)
```

```
## Not run:
registerCoresPWMEnrich(4) # use 4 CPU cores in PWMEnrich
registerCoresPWMEnrich() # use maximal number of CPUs
registerCoresPWMEnrich(NULL) # do not use parallel execution

## End(Not run)
```
scanWithPWM

Scan the whole sequence on both strands

Description

The whole sequence is scanned with a PWM and scores returned beginning at each position. Partial motif matches are not done, thus the last #length of motif]-1 scores are NA.

Usage

scanWithPWM(pwm, dna, pwm.rev = NULL, odds.score = FALSE,
both.strands = FALSE, strand.fun = "mean")

Arguments

pwm: PWM object
dna: a DNAString or other sequence from Biostrings
pwm.rev: the reverse complement for a pwm (if it is already pre-computed)
ods.score: if to return raw scores in odds (not logodds) space
both.strands: if to return results on both strands
strand.fun: which function to use to summarise values over two strands (default is "mean")

Details

The function returns either an odds average (*not* log-odds average), maximal score on each strand, or scores on both strands.

The function by default returns the score in log2 following the package Biostrings.

Value

a vector representing scores starting at each position, or a matrix with score in the two strands

Examples

if(require("PWMEnrich.Dmelanogaster.background")){
data(MotifDb.Dmel.PFM)

reverseComplement(MotifDb.Dmel.PFM["ttk"])) # reverse complement of the ttk PWM
}

ttk = MotifDb.Dmel["ttk"]

scanWithPWM(ttk, DNAString("CGTAGGATAAAGTAACT")) # odds average over the two strands expressed as log2-odds
scanWithPWM(ttk, DNAString("CGTAGGATAAAGTAACT"), both.strands=TRUE) # log2-odds scores on both strands
}
**seqLogoGrid**

*Draw a motif logo on an existing viewport*

**Description**

This function comes from the `seqLogo` package. It has been modified to remove some unnecessary code as suggested by W Huber (https://stat.ethz.ch/pipermail/bioconductor/2010-September/035267.html).

**Usage**

```r
seqLogoGrid(pwm, ic.scale = TRUE, xaxis = TRUE, 
yaxis = TRUE, xfontsize = 10, yfontsize = 10, 
xmargin.scale = 1, ymargin.scale = 1, title = "", 
titlefontsize = 15)
```

**Arguments**

- `pwm`: numeric The 4xW position weight matrix.
- `ic.scale`: logical If TRUE, the height of each column is proportional to its information content. Otherwise, all columns have the same height.
- `xaxis`: logical If TRUE, an X-axis will be plotted.
- `yaxis`: logical If TRUE, a Y-axis will be plotted.
- `xfontsize`: numeric Font size to be used for the X-axis.
- `yfontsize`: numeric Font size to be used for the Y-axis.
- `xmargin.scale`: the scaling parameter for the X-axis margin. Useful when plotting more than one logo on a page
- `ymargin.scale`: the scaling parameter for the Y-axis margin. Useful when plotting more than one logo on a page
- `title`: to be shown on the top
- `titlefontsize`: the font size of the title

**Details**

Use this function for more advanced plotting where the viewports are directly set up and maintained (see package `grid`).

---

**sequenceReport, MotifEnrichmentResults-method**

*Generate a motif enrichment report for a single sequence*

**Description**

Generate a motif enrichment report for a single sequence
toPWM

Convert motifs into PWMs

Description

Convert motifs into PWMs

Arguments

obj  a MotifEnrichmentResults object
seq.id  the sequence index or name
bg  if to use background corrected P-values to do the ranking (if available)
...

Value

a MotifEnrichmentReport object containing a table with the following columns:

• 'rank' - The rank of the PWM’s enrichment in the sequence
• 'target' - The name of the PWM’s target gene, transcript or protein complex.
• 'id' - The unique identifier of the PWM (if set during PWM creation).
• 'raw.score' - The raw score before P-value calculation
• 'p.value' - The P-value of motif enrichment (if available)

Examples

if(require("PWMEnrich.Dmelanogaster.background")){

  ###
  # load the pre-compiled lognormal background
  data(PWMLogn.dm3.MotifDb.Dmel)

  # scan two sequences for motif enrichment
  sequences = list(DNAString("GAAGTATCAAGTACCAGTAAGTCCCAGATGA"), DNAString("AGGTAGATAGAACAGTAGGCAATGAAGCCTAGTGA"))
  res = motifEnrichment(sequences, PWMLogn.dm3.MotifDb.Dmel)

  # reports for the two sequences
  r1 = sequenceReport(res, 1)
  r2 = sequenceReport(res, 2)

  # view the results
  r1
  r2

  # plot the top 10 most enriched motifs in the first, and then second sequence
  plot(r1[1:10])
  plot(r2[1:10])
}

}
useBigMemoryPWMEnrich

Usage

toPWM(motifs, ids = names(motifs), targets = names(motifs),
seq.count = 50, prior = c(A = 0.25, C = 0.25, G = 0.25, T = 0.25), ...)

Arguments

motifs a list of motifs either as position probability matrices (PPM) or frequency matrices (PFMs)
ids the set of IDs for the motifs (defaults to names of the ’motifs’ list)
targets the set of target TF names for the motifs (defaults to names of the ’motifs’ list)
seq.count provides a vector of sequence counts for probability matrices (PPMs)
prior frequencies of the four letters in the genome. Default is uniform background
... other parameters to PWMUnscaled

Examples

if(require("PWMEnrich.Dmelanogaster.background")){
data(MotifDb.Dmel.PFM)
toPWM(MotifDb.Dmel.PFM) # convert to PWM with uniform background
prior = getBackgroundFrequencies("dm3", quick=TRUE) # get background for drosophila (quick mode on a reduced dataset)
toPWM(MotifDb.Dmel.PFM, prior=prior) # convert with genomic background
}

useBigMemoryPWMEnrich

If to use a faster implementation of motif scanning that requires about 5 to 10 times more memory

Description

If to use a faster implementation of motif scanning that requires about 5 to 10 times more memory

Usage

useBigMemoryPWMEnrich(useBigMemory = FALSE)

Arguments

useBigMemory a boolean value denoting if to use big memory implementation

Examples

## Not run:
useBigMemoryPWMEnrich(TRUE) # switch to big memory implementation globally
useBigMemoryPWMEnrich(FALSE) # switch back to default implementation

## End(Not run)
[,PWMcutoffBackground-method

Get the background for a subset of PWMs

Description
Get the background for a subset of PWMs

Arguments
- x: the PWMCutoffBackground object
- i: the indicies of PWMs
- j: unused
- ... unused
- drop: unused

[,PWMEmpiricalBackground-method

Get the background for a subset of PWMs

Description
Get the background for a subset of PWMs

Arguments
- x: the PWMEmpiricalBackground object
- i: the indicies of PWMs
- j: unused
- ... unused
- drop: unused

[,PWMGEVBackground-method

Get the background for a subset of PWMs

Description
Get the background for a subset of PWMs

Arguments
- x: the PWMGEVBackground object
- i: the indicies of PWMs
- j: unused
- ... unused
- drop: unused
Get the background for a subset of PWMs

**Description**

Get the background for a subset of PWMs

**Arguments**

- x: the PWMLognBackground object
- i: the indices of PWMs
- j: unused
- ...: unused
- drop: unused
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