

# Package ‘motifmatchr’

April 15, 2020

**Type** Package

**Title** Fast Motif Matching in R

**Version** 1.8.0

**Date** 2017-03-08

**Maintainer** Alicia Schep <aschep@gmail.com>

**Description** Quickly find motif matches for many motifs and many sequences. Wraps C++ code from the MOODS motif calling library, which was developed by Pasi Rastas, Janne Korhonen, and Petri Martinmäki.

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**Imports** Matrix, Rcpp, methods, TFBSTools, Biostrings, BSgenome, S4Vectors, SummarizedExperiment, GenomicRanges, IRanges, Rsamtools, GenomeInfoDb

**Depends** R (>= 3.3)

**Suggests** testthat, knitr, rmarkdown, BSgenome.Hsapiens.UCSC.hg19

**biocViews** MotifAnnotation

**LinkingTo** Rcpp, RcppArmadillo

**SystemRequirements** C++11

**RoxygenNote** 6.0.1

**VignetteBuilder** knitr

**Encoding** UTF-8

**git\_url** <https://git.bioconductor.org/packages/motifmatchr>

**git\_branch** RELEASE\_3\_10

**git\_last\_commit** a576d99

**git\_last\_commit\_date** 2019-10-29

**Date/Publication** 2020-04-14

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example_motifs	<i>example_motifs</i>
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### Description

A few example motifs from JASPAR 2016 for trying out motifmatchr

### Usage

```
data(example_motifs)
```

### Value

[PFMatrixList](#) of length 3

### Examples

```
data(example_motifs, package = "motifmatchr")
```

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matchMotifs	<i>matchMotifs</i>
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### Description

Find motif matches

### Usage

```
matchMotifs(pwms, subject, ...)
```

```
## S4 method for signature 'PFMatrixList,DNAStringSet'
matchMotifs(pwms, subject,
  genome = NULL, bg = c("subject", "genome", "even"), out = c("matches",
  "scores", "positions"), p.cutoff = 5e-05, w = 7, ranges = NULL)
```

```
## S4 method for signature 'PFMatrixList,character'
matchMotifs(pwms, subject, genome = NULL,
```

```

bg = c("subject", "genome", "even"), out = c("matches", "scores",
"positions"), p.cutoff = 5e-05, w = 7, ranges = NULL)

## S4 method for signature 'PWMMatrixList,DNAString'
matchMotifs(pwms, subject, genome = NULL,
  bg = c("subject", "genome", "even"), out = c("matches", "scores",
"positions"), p.cutoff = 5e-05, w = 7, ranges = NULL)

## S4 method for signature 'PWMMatrixList,GenomicRanges'
matchMotifs(pwms, subject,
  genome = GenomeInfoDb::genome(subject), bg = c("subject", "genome",
"even"), out = c("matches", "scores", "positions"), p.cutoff = 5e-05,
w = 7)

## S4 method for signature 'PWMMatrixList,RangedSummarizedExperiment'
matchMotifs(pwms, subject,
  genome = GenomeInfoDb::genome(subject), bg = c("subject", "genome",
"even"), out = c("matches", "scores", "positions"), p.cutoff = 5e-05,
w = 7)

## S4 method for signature 'PWMMatrixList,BSgenomeViews'
matchMotifs(pwms, subject,
  bg = c("subject", "genome", "even"), out = c("matches", "scores",
"positions"), p.cutoff = 5e-05, w = 7)

## S4 method for signature 'PFMatrixList,ANY'
matchMotifs(pwms, subject, ...)

## S4 method for signature 'PWMMatrix,ANY'
matchMotifs(pwms, subject, ...)

## S4 method for signature 'PFMatrix,ANY'
matchMotifs(pwms, subject, ...)

```

## Arguments

pwms	either <a href="#">PFMatrix</a> , <a href="#">PFMatrixList</a> , <a href="#">PWMMatrix</a> , <a href="#">PWMMatrixList</a>
subject	either <a href="#">GenomicRanges</a> , <a href="#">DNAStringSet</a> , <a href="#">DNAString</a> , or character vector
...	additional arguments depending on inputs
genome	BSgenome object, <a href="#">DNAStringSet</a> , or <a href="#">FaFile</a> , or short string signifying genome build recognized by <a href="#">getBSgenome</a> . Only required if subject is <a href="#">GenomicRanges</a> or <a href="#">RangedSummarizedExperiment</a> or if bg is set to "genome"
bg	background nucleotide frequencies. Default is to compute based on subject, i.e. the specific set of sequences being evaluated. See <a href="#">Details</a> .
out	what to return? see <a href="#">return</a> section
p.cutoff	p-value cutoff for returning motifs
w	parameter controlling size of window for filtration; default is 7
ranges	if subject is not <a href="#">GenomicRanges</a> or <a href="#">RangedSummarizedExperiment</a> , these ranges can be used to specify what ranges the input sequences correspond to. These ranges will be incorporated into the <a href="#">SummarizedExperiment</a> output if out is

"matches" or "scores" or will be used to give absolute positions of motifs if out is "positions"

## Details

Background nucleotide frequencies can be set to "subject" to use the subject sequences or ranges for computing the nucleotide frequencies, "genome" for using the genome frequencies (in which case a genome must be specified), "even" for using 0.25 for each base, or a numeric vector with A, C, G, and T frequencies.

## Value

Either returns a SummarizedExperiment with a sparse matrix with values set to TRUE for a match (if out == 'matches'), a SummarizedExperiment with a matches matrix as well as matrices with the maximum motif score and total motif counts (if out == 'scores'), or a [GenomicRangesList](#) or a list of [IRangesList](#) with all the positions of matches (if out == 'positions')

## Methods (by class)

- pwms = PWMMatrixList, subject = DNASTringSet: PWMMatrixList/DNASTringSet
- pwms = PWMMatrixList, subject = character: PWMMatrixList/character
- pwms = PWMMatrixList, subject = DNASTring: PWMMatrixList/DNASTring
- pwms = PWMMatrixList, subject = GenomicRanges: PWMMatrixList/GenomicRanges
- pwms = PWMMatrixList, subject = RangedSummarizedExperiment: PWMMatrixList/RangedSummarizedExperiment
- pwms = PWMMatrixList, subject = BSgenomeViews: PWMMatrixList/BSGenomeViews
- pwms = PFMatrixList, subject = ANY: PFMatrixList/ANY
- pwms = PWMMatrix, subject = ANY: PWMMatrix/ANY
- pwms = PFMatrix, subject = ANY: PFMatrix/ANY

## Examples

```
data(example_motifs, package = "motifmatchr")

# Make a set of peaks
peaks <- GenomicRanges::GRanges(seqnames = c("chr1", "chr2", "chr2"),
                                ranges = IRanges::IRanges(start = c(76585873, 42772928,
                                                                    100183786),
                                                            width = 500))

# Get motif matches for example motifs
motif_ix <- matchMotifs(example_motifs, peaks, genome = "BSgenome.Hsapiens.UCSC.hg19")
```



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motifMatches	<i>motifMatches</i>
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## Description

get motif matches from SummarizedExperiment object

## Usage

```
motifMatches(object)
```

```
## S4 method for signature 'SummarizedExperiment'  
motifMatches(object)
```

## Arguments

object            SummarizedExperiment object with matches assay

## Value

matrix with scores

## Methods (by class)

- SummarizedExperiment: method for SummarizedExperiment

## Examples

```
data(example_motifs, package = "motifmatchr")  
  
# Make a set of peaks  
peaks <- GenomicRanges::GRanges(seqnames = c("chr1", "chr2", "chr2"),  
                                  ranges = IRanges::IRanges(start = c(76585873, 42772928,  
                                                                  100183786),  
                                                                  width = 500))  
  
# Get motif matches for example motifs  
motif_ix <- matchMotifs(example_motifs, peaks,  
                          genome = "BSgenome.Hsapiens.UCSC.hg19")  
  
motifMatches(motif_ix)
```

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`motifmatchr`*motifmatchr: Fast Motif Matching in R*

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## Description

The motifmatchr package is designed for analyzing many sequences and many motifs to find which sequences contain which motifs.

## Details

motifmatchr uses the MOODS C++ library (developed by Pasi Rastas, Janne Korhonen, and Petri Martinmaki) internally for motif matching.

The primary method of motifmatchr is `matchMotifs`, which takes in motif PWMs/PFM and genomic ranges or sequences and returns either which ranges/sequences match which motifs or the positions of the matches.

Compared with alternative motif matching functions available in Bioconductor (e.g. `matchPWM` in Biostrings or `searchSeq` in TFBSTools), motifmatchr is designed specifically for the use case of determining whether many different sequences/ranges contain many different motifs.

## Author(s)

Alicia Schep

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`motifmatchr_deprecated`*Deprecated functions in motifmatchr*

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## Description

motifmatchr has moved functions and methods to camelCase from snake\_case. The following functions have been deprecated and replaced with a different name:

- `motif_matches` is now `motifMatches`
- `motif_counts` is now `motifCounts`
- `motif_scores` is now `motifScores`
- `match_motifs` is now `matchMotifs`

## Usage

```
motif_matches(...)
```

```
motif_counts(...)
```

```
motif_scores(...)
```

```
match_motifs(...)
```

**Arguments**

... arguments passed to new function

**Value**

calls the replacement function

**Author(s)**

Alicia Schep

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motifScores

*motifScores*

---

**Description**

get motif scores from SummarizedExperiment object

**Usage**

```
motifScores(object)
```

```
## S4 method for signature 'SummarizedExperiment'
motifScores(object)
```

**Arguments**

object SummarizedExperiment object with scores assay

**Value**

matrix with scores

**Methods (by class)**

- SummarizedExperiment: method for SummarizedExperiment

**Examples**

```
data(example_motifs, package = "motifmatchr")

# Make a set of peaks
peaks <- GenomicRanges::GRanges(seqnames = c("chr1", "chr2", "chr2"),
                                ranges = IRanges::IRanges(start = c(76585873, 42772928,
                                                                    100183786),
                                                            width = 500))

# Get motif matches for example motifs
motif_ix <- matchMotifs(example_motifs, peaks,
                        genome = "BSgenome.Hsapiens.UCSC.hg19",
                        out = "scores")

motifScores(motif_ix)
```



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