

# Package: motifmatchr (via r-universe)

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**Type** Package

**Title** Fast Motif Matching in R

**Version** 1.34.0

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**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.

**License** GPL-3 + file LICENSE

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

**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

**Config/pak/sysreqs**

make libgsl0-dev libbz2-dev liblzma-dev libxml2-dev libssl-dev xz-utils zlib1g-dev

**Repository** <https://bioc-release.r-universe.dev>

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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 'PWMMatrixList,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 'PWMMatrixList,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 = Seqinfo::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 = Seqinfo::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 Details.
out	what to return? see return 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 genomic 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



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

motifCounts(motif_ix)
```

---

motifMatches

*motifMatches*

---

### 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/PFMs 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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