Package ‘motifmatchr’

May 30, 2024

Type Package

Title Fast Motif Matching in R

Version 1.26.0

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.

License GPL-3 + file LICENSE

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_19
git_last_commit cd370a8
git_last_commit_date 2024-04-30

Repository Bioconductor 3.19

Date/Publication 2024-05-29

Author Alicia Schep [aut, cre], Stanford University [cph]
Contents

example_motifs ............................................. 2
matchMotifs .................................................. 2
motifCounts ................................................... 5
motifMatches .................................................. 6
motifmatchr .................................................... 7
motifmatchr Deprecated .................................... 7
motifScores .................................................... 8
pwmType ....................................................... 9

Index 10

Example

example_motifs  example_motifs

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")

matchMotifs  matchMotifs

Description

Find motif matches
matchMotifs

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 = 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 PFMatrix, PFMatrixList, PWMMatrix, PWMMatrixList
subject either GenomicRanges, DNAStringSet, DNAString, or character vector
matchMotifs

... additional arguments depending on inputs

- **genome**: BSgenome object, DNAStringSet, or FaFile, or short string signifying genome build recognized by getBSgenome. Only required if subject is GenomicRanges or RangedSummarizedExperiment 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 GenomicRanges or RangedSummarizedExperiment, these ranges can be used to specify what ranges the input sequences correspond to. These ranges will be incorporated into the SummarizedExperiment 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 = PWMatrixList, subject = DNAStringSet`: PWMatrixList/DNAStringSet
- `pwms = PWMatrixList, subject = character`: PWMatrixList/character
- `pwms = PWMatrixList, subject = DNAString`: PWMatrixList/DNAString
- `pwms = PWMatrixList, subject = GenomicRanges`: PWMatrixList/GenomicRanges
- `pwms = PWMatrixList, subject = RangedSummarizedExperiment`: PWMatrixList/RangedSummarizedExperiment
- `pwms = PWMatrixList, subject = BSgenomeViews`: PWMatrixList/BSGenomeViews
- `pwms = PFMatrixList, subject = ANY`: PFMatrixList/ANY
- `pwms = PWMMatrix, subject = ANY`: PWMMatrix/ANY
- `pwms = PFMatrix, subject = ANY`: PFMatrix/ANY
**Examples**

```r
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")
```

---

**Description**

get motif counts from SummarizedExperiment object

**Usage**

```r
motifCounts(object)
```

## S4 method for signature 'SummarizedExperiment'

```r
motifCounts(object)
```

**Arguments**

- `object` SummarizedExperiment object with counts assay

**Value**

matrix with counts

**Methods (by class)**

- SummarizedExperiment: method for SummarizedExperiment

**Examples**

```r
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")

motifCounts(motif_ix)

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)
motifmatchr

motifmatchr: Fast Motif Matching in R

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

motifmatchr deprecated

Deprecated functions in motifmatchr

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

Description

generate 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,
pwmType

data(example_motifs, package = "motifmatchr")
pwmType(TFBSTools::toPWM(example_motifs[[1]]))
pwmType(TFBSTools::toPWM(example_motifs[[1]], type = "prob"))
Index

* datasets
  example_motifs, 2

* internal
  pwmType, 9

DNAString, 3
DNAStringSet, 3, 4
example_motifs, 2
FaFile, 4
GenomicRanges, 3, 4
GenomicRangesList, 4
getBSgenome, 4
IRangesList, 4

match_motifs (motifmatchr_deprecated), 7
matchMotifs, 2, 7
matchMotifs, PFMATRIX, ANY-method
  (matchMotifs), 2
matchMotifs, PFMATRIX, ANY-method
  (matchMotifs), 2
matchMotifs, PWMatrix, ANY-method
  (matchMotifs), 2
matchMotifs, PWMatrix, ANY-method
  (matchMotifs), 2
matchMotifs, PWMatrixList, BSgenomeViews-method
  (matchMotifs), 2
matchMotifs, PWMatrixList, character-method
  (matchMotifs), 2
matchMotifs, PWMatrixList, DNAString-method
  (matchMotifs), 2
matchMotifs, PWMatrixList, DNAStringSet-method
  (matchMotifs), 2
matchMotifs, PWMatrixList, GenomicRanges-method
  (matchMotifs), 2
matchMotifs, PWMatrixList, RangedSummarizedExperiment-method
  (matchMotifs), 2
motif_counts (motifmatchr_deprecated), 7
motif_matches (motifmatchr_deprecated), 7
motif_scores (motifmatchr_deprecated), 7
motifCounts, 5, 7
motifCounts, SummarizedExperiment-method
  (motifCounts), 5
motifMatches, 6, 7
motifMatches, SummarizedExperiment-method
  (motifMatches), 6
motifmatchr, 7
motifmatchr-package (motifmatchr), 7
motifmatchr_deprecated, 7
motifScores, 7, 8
motifScores, SummarizedExperiment-method
  (motifScores), 8

PFMatrix, 3
PFMatrixList, 2, 3
PWMatrix, 3
PWMatrixList, 3
pwmType, 9

RangedSummarizedExperiment, 4