

# Package ‘MatrixRider’

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**Type** Package

**Title** Obtain total affinity and occupancies for binding site matrices  
on a given sequence

**Version** 1.43.0

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**Description** Calculates a single number for a whole sequence that  
reflects the propensity of a DNA binding protein to interact  
with it. The DNA binding protein has to be described with a PFM  
matrix, for example gotten from Jaspar.

**biocViews** GeneRegulation, Genetics, MotifAnnotation

**License** GPL-3

**Depends** R (>= 3.1.2)

**Imports** methods, TFBSTools, IRanges, XVector, Biostrings

**Suggests** RUnit, BiocGenerics, BiocStyle, JASPAR2014

**LinkingTo** IRanges, XVector, Biostrings, S4Vectors

**NeedsCompilation** yes

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

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| MatrixRider-package | <i>Calculate total affinity and occupancies for binding site matrices on a given sequence</i> |
|---------------------|-----------------------------------------------------------------------------------------------|

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## Description

Calculates a single number for a whole sequence that reflects the propensity of a DNA binding protein to interact with it. The DNA binding protein has to be described with a PFM matrix, for example gotten from Jaspar.

## Author(s)

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## Examples

```
library(JASPAR2014)
library(TFBSTools)
library(Biostrings)
pfm <- getMatrixByID(JASPAR2014,"MA0004.1")
## The following sequence has a single perfect match
## thus it gives the same results with all cutoff values.
sequence <- DNAString("CACGTG")
getSeqOccupancy(sequence, pfm, 0.1)
getSeqOccupancy(sequence, pfm, 1)
```

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|                 |                                                                       |
|-----------------|-----------------------------------------------------------------------|
| getSeqOccupancy | <i>Computes the total affinity or the occupancy at a given cutoff</i> |
|-----------------|-----------------------------------------------------------------------|

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## Description

The affinity/occupancy is calculated on the given DNAString for the given PFMatrix (or all the ones in the PFMatrix list given).

## Usage

```
getSeqOccupancy(sequence, pfm, cutoff)
```

## Arguments

|          |                                                                                                                                                                                                                                                                                                                                                                             |
|----------|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| sequence | A <a href="#">DNAString</a> object with the sequence for which affinity will be computed.                                                                                                                                                                                                                                                                                   |
| pfm      | A <a href="#">PFMatrix</a> or a <a href="#">PFMatrixList</a> object with the matrixes whose affinity will be calculated. The background ( <a href="#">bg,XMatrix-method</a> ) of the given pfm is used to perform affinity calculations.                                                                                                                                    |
| cutoff   | numeric(1); between 0 and 1 (included): 0 corresponds to total affinity (i.e. summing all the affinities) while 1 to summing only values corresponding to the perfect match for a given <a href="#">PFMatrix</a> . See vignette for details on how scores are calculated. If <b>MatrixRider</b> is installed, open the vignette with <code>vignette("MatrixRider")</code> . |

**Value**

numeric; the resulting total affinity calculated on the given fasta. If a [PFMatrixList](#) has been passed then a named numeric vector with the affinities for all the PFMs. The vignette has all the details on the calculations (such as PFM to PWM conversion and pseudocounts).

**Examples**

```
library(JASPAR2014)
library(TFBSTools)
library(Biostrings)
pfm <- getMatrixByID(JASPAR2014,"MA0004.1")
## The following sequence has a single perfect match
## thus it gives the same results with all cutoff values.
sequence <- DNASTring("CACGTG")
getSeqOccupancy(sequence, pfm, 0.1)
getSeqOccupancy(sequence, pfm, 1)

pfm2 <- getMatrixByID(JASPAR2014,"MA0005.1")
pfms <- PFMatrixList(pfm, pfm2)
names(pfms) <- c(name(pfm), name(pfm2))
## This calculates total affinity for both the PFMatrixes.
getSeqOccupancy(sequence, pfms, 0)
```

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