Package 'MatrixRider'

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Type Package

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

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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.

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Depends R (>= 3.1.2)

Imports methods, TFBSTools, IRanges, XVector, Biostrings

Suggests RUnit, BiocGenerics, BiocStyle, JASPAR2014

LinkingTo IRanges, XVector, Biostrings, S4Vectors

NeedsCompilation yes

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MatrixRider-package *Calculate total affinity and occupancies for binding site matrices on a given sequence*

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)
```

getSeqOccupancy *Computes the total affinity or the occupancy at a given cutoff*

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 DNAString object with the sequence for which affinity will be computed.
pfm	A PFMatrix or a PFMatrixList object with the matrixes whose affinity will be calculated. The background (bg,XMatrix-method) 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 PFMatrix. See vignette for details on how scores are calculated. If **MatrixRider** is installed, open the vignette with `vignette("MatrixRider")`.

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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