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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Author Elena Grassi
Maintainer Elena Grassi <grassi.e@gmail.com>
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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License GPL-3
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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)

Elena Grassi <elena.grassi@unito.it>

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").
**getSeqOccupancy**

**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**

```r
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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