Package ‘TFBSTools’

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Title Software Package for Transcription Factor Binding Site (TFBS) Analysis
Description TFBSTools is a package for the analysis and manipulation of transcription factor binding sites. It includes matrices conversion between Position Frequency Matrix (PFM), Position Weight Matrix (PWM) and Information Content Matrix (ICM). It can also scan putative TFBS from sequence/alignment, query JASPAR database and provides a wrapper of de novo motif discovery software.
VignetteBuilder knitr
Imports Biobase(>= 2.28), Biostrings(>= 2.36.4), BiocGenerics(>= 0.14.0), BiocParallel(>= 1.2.21), BSgenome(>= 1.36.3), caTools(>= 1.17.1), CNEr(>= 1.4.0), DirichletMultinomial(>= 1.10.0), GenomeInfoDb(>= 1.6.1), GenomicRanges(>= 1.20.6), gtools(>= 3.5.0), grid, IRanges(>= 2.2.7), methods, RSQLite(>= 1.0.0), rtracklayer(>= 1.28.10), seqLogo(>= 1.34.0), S4Vectors(>= 0.9.25), TFMPvalue(>= 0.0.5), XML(>= 3.98-1.3), XVector(>= 0.8.0)
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Motif-methods.r  PFM-methods.r  Wrappers-methods.r  
DirichletMixture.r  TFFM.R  TFFMseqLogo.R  IO.R  Enrichment.R

**Author**  Ge Tan [aut, cre]  
**Maintainer**  Ge Tan <ge.tan09@imperial.ac.uk>

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**R topics documented:**

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TFBSTools-package

TFBSTools-package

TFBS software package.

Description

TFBS includes a set of tools for transcription factor binding site detection and analysis as well as database interface functions for JASPAR, etc.

Author(s)

Ge Tan

calConservation-methods
calConservation method

Description

Calculate the conservation score for a pairwise alignment given a smooth window size.

Usage

calConservation(aln1, aln2, windowSize=51L, which=“1”)  

Arguments

aln1 A DNAString object, a DNAStringSet or a character object, which contains the pairwise alignments. When the last two objects have a length of 2, the argument aln2 can be missing.

aln2 A DNAString, a character object or missing.

windowSize The size of the sliding window (in nucleotides) for calculating local conservation in the alignment. This should be an odd value.

which The conservation profile of Which sequence in the alignments is computed. It can be "1" or "2".

Value

A numeric vector with the same length of alignment is returned.

Author(s)

Ge Tan

See Also

searchAln
Description

The functions to initialize, store matrix or delete matrix in JASPAR database.

Usage

```r
## S4 method for signature 'character'
deleteMatrixHavingID(x, IDs)
## S4 method for signature 'SQLiteConnection'
deleteMatrixHavingID(x, IDs)
## S4 method for signature 'JASPAR2014'
deleteMatrixHavingID(x, IDs)
## S4 method for signature 'character,PFMatrixList'
storeMatrix(x, pfmList)
## S4 method for signature 'SQLiteConnection,PFMatrixList'
storeMatrix(x, pfmList)
## S4 method for signature 'JASPAR2014,PFMatrixList'
storeMatrix(x, pfmList)
## S4 method for signature 'character,PFMatrix'
storeMatrix(x, pfmList)
## S4 method for signature 'SQLiteConnection,PFMatrix'
storeMatrix(x, pfmList)
## S4 method for signature 'JASPAR2014,PFMatrix'
storeMatrix(x, pfmList)
## S4 method for signature 'SQLiteConnection'
initializeJASPARDB(x, version=c("2014", "2016"))
## S4 method for signature 'character'
initializeJASPARDB(x, version=c("2014", "2016"))
## S4 method for signature 'JASPAR2014'
initializeJASPARDB(x, version)
## S4 method for signature 'JASPAR2016'
initializeJASPARDB(x, version)
```

Arguments

- `x` A character vector of length 1 for the path of JASPAR SQLite file, or a `SQLiteConnection` object.
- `IDs` JASPAR stable IDs.
- `pfmList` The `PFMatrixList` object, or `pfm` object.
- `version` Which version of JASPAR to create. So far, it supports 2014 and 2016.

Value

If the operation works, a "success" will be returned.
Examples

initializeJASPARDB("jaspar.sqlite", version="2014")
data("MA0043")
storeMatrix("jaspar.sqlite", MA0043)
deleteMatrixHavingID("jaspar.sqlite","MA0043.1")
file.remove("jaspar.sqlite")

---

**Description**

This function trains the Dirichlet multinomial mixture models parameters for a set of profile matrices.

**Usage**

\texttt{dmmEM(x, K=6, alg=c("C", "R"))}

**Arguments**

- **x**: x can be a matrix, PFMatrixList or JASPAR2014 to be trained.
- **K**: The maximal number of components to test in the mixture model when \texttt{alg} is "C". Then an optimal number of components between 1 and K will be chosen based on the fitness of the model. The fixed number of components to use when \texttt{alg} is "R". The default is 6.
- **alg**: The algorithm to use. "C" uses the implementation from \texttt{DirichletMultinomial} package which has more advanced feature and performance. "R" uses our own implementation in R.

**Details**

When using the implementation from \texttt{DirichletMultinomial} package, the final number of components can be 1:K. An internal selection will be made based on the maximum likelihood. When using the implementation of R, the number of component is fixed to K.

**Value**

A list of trained alpha0, pmix and likelihood during the training.

**Methods**

\texttt{signature(x = "ANY")}
\texttt{signature(x = "matrix")}
\texttt{signature(x = "PFMatrixList")}

**Author(s)**

Ge Tan
getEmissionProb

See Also

rPWMdmm

Examples

data(MA0003.2)
data(MA0004.1)

pfmList <- PFMatrixList(pfml=MA0003.2, pfm2=MA0004.1, use.names=TRUE)
dmmParameters <- dmmEM(pfmList, K=6, alg="C")

gEmissionProb

Get the emission distribution parameters.

Description

This function accesses the emission distribution parameters of the TFFM.

Usage

gEmissionProb(tffm)

Arguments

tffm A TFFMFirst object or a TFFMDetail object.

Details

This function accesses the emission distribution parameters for each position of the TFFM. It returns the probability of emitting certain nucleotide based on the nucleotide on the previous site.

Value

A matrix of numeric with dimensions of 16 * ncol(tffm).

Author(s)

Ge Tan

See Also

getPosProb
getMatrixByID

Examples

```r
xmlFirst <- file.path(system.file("extdata", package="TFBSTools"),
  "tffm_first_order.xml")
tffmFirst <- readXMLTFFM(xmlFirst, type="First")
getEmissionProb(tffmFirst)

xmlDetail <- file.path(system.file("extdata", package="TFBSTools"),
  "tffm_detailed.xml")
tffmDetail <- readXMLTFFM(xmlDetail, type="Detail")
getEmissionProb(tffmDetail)
```

getMatrixByID

Basic JASPAR database search functions getMatrixByID, getMatrixByName

Description

This method fetches matrix data under the given ID or name from the database and returns a XMatrix object.

Usage

```r
## S4 method for signature 'character'
getMatrixByID(x, ID)
## S4 method for signature 'SQLiteConnection'
getMatrixByID(x, ID)
## S4 method for signature 'JASPAR2014'
getMatrixByID(x, ID)
## S4 method for signature 'character'
getMatrixByName(x, name)
## S4 method for signature 'SQLiteConnection'
getMatrixByName(x, name)
## S4 method for signature 'JASPAR2014'
getMatrixByName(x, name)
```

Arguments

- `x`: character() for the path of JASPAR SQLite file, a SQLiteConnection object, a JASPAR2014, or a JASPAR2016 object.
- `ID`: character() of JASPAR stable ID(s). See more details below.
- `name`: character() of JASPAR stable name(s).

Details

For getMatrixByID, ID is a string which refers to the stable JASPAR ID (usually something like "MA0001") with or without version numbers. "MA0001" will give the latest version on MA0001, while "MA0001.2" will give the second version, if existing.

For getMatrixByName, according to the current JASPAR data model, name is not necessarily a unique identifier. Also, names change over time. In the case where there are several matrices with the same name in the database, the function fetches the first one and prints a warning. You’ve been warned. Some matrices have multiple versions. The function will return the latest version. For specific versions, use getMatrixByID(ID.version)
Value

A PFMMatrix object is returned when input ID or name is length 1. Otherwise, PFMMatrixList is returned.

Author(s)

Ge Tan

See Also

getMatrixSet

Examples

library(JASPAR2014)
db <- file.path(system.file("extdata", package="JASPAR2014"), "JASPAR2014.sqlite")

## character and ID
pfm <- getMatrixByID(db, ID="MA0003")

## character and IDs
pfmList <- getMatrixByID(db, ID=c("MA0003", "MA0004"))

## character and name
pfm <- getMatrixByName(db, name="TFAP2A")

## character and name
pfmList <- getMatrixByName(db, name=c("TFAP2A", "Arnt"))

## JASPAR2014 and ID
pfm <- getMatrixByID(JASPAR2014, ID="MA0003")
getMatrixSet

Arguments

x  a character vector of length 1 for the path of JASPAR SQLite file, a SQLiteConnection object, or a JASPAR2014 object.

opts a search options options list. See more details below.

Details

The search options include three categories:

(1) Database basic criterias:

all=c(TRUE, FALSE)

ID: a unique identifier for each model. CORE matrices always have a "MAnnnnIDs.Version".

name: The name of the transcription factor. As far as possible, the name is based on the standardized Entrez gene symbols. In the case the model describes a transcription factor hetero-dimer, two names are concatenated, such as RXR-VDR. In a few cases, different splice forms of the same gene have different binding specificity: in this case the splice form information is added to the name, based on the relevant literature.

collection=c("CORE", "CNE", "PHYLOFACTS", "SPLICE", "POLII", "FAM", "PBM", "PBM_HOMEO", "PBM_HLH", all_versions=c(FALSE, TRUE): We constantly update the profiles in JASPAR. Some profiles may have multiple versions. By default, only the latest version will be returned.

species: The species source for the sequences, in Latin (Homo sapiens) or NCBI tax IDs (9606).

matrixtype=c("PFM", "PWM", "ICM")

(2) Tags based criterias:

class: Structural class of the transcription factor, based on the TFCaT system. Examples: "Zipper- Type", "Helix-Turn-Helix", etc.

type: Methodology used for matrix construction: "SELEX", "ChIP-seq", "PBM", etc.

tax_group: Group of species, currently consisting of "plants", "vertebrates", "insects", "urochordat", "nematodes", "fungi".

family: Structural sub-class of the transcription factor, based on the TFCA T system.

Acc: A representative protein accession number in Genbank for the transcription factor. Human takes precedence if several exists.

medline: relevant publication reporting the sites used in the mode building.

Pazar_tf_id: PAZAR database id.

(3) Further criterias:

min_ic (minimum total information content of the matrix)

length (minimum sites length)

sites (minimum average sites number per base)

When all is TRUE, it will get all the matrices and has higher priority over other options. Then ID has the second highest priority, and will ignore all the following options. The rest options are combined in search with AND, while multiple elements under one options have the logical operator OR.

Value

A PFMatrixList object.
getPosProb

Author(s)
Ge Tan

See Also
getMatrixByID, getMatrixByName

Examples

library(JASPAR2014)
db <- file.path(system.file("extdata", package="JASPAR2014"),
  "JASPAR2014.sqlite")
opts <- list()
opts["species"] <- 9606
opts["type"] <- "SELEX"
opts["all_versions"] <- FALSE
siteList <- getMatrixSet(db, opts)
siteList2 <- getMatrixSet(JASPAR2014, opts)

getPosProb

Get the emission probabilities of nucleotides

Description
Get the emission probabilities of ACGT at each position of TFFM.

Usage
getPosProb(tffm)

Arguments
tffm A TFFMFirst object or a TFFMDetail object.

Details
This function calculates the probabilities of emitting nucleotides ACGT at each position of TFFM.

Value
A matrix of numeric with dimensions of 4 * ncol(tffm).

Author(s)
Ge Tan

See Also
gEmissionProb
IUPAC2Matrix

Examples

xmlFirst <- file.path(system.file("extdata", package="TFBSTools"), "tffm_first_order.xml")
tffmFirst <- readXMLTFFM(xmlFirst, type="First")
getPosProb(tffmFirst)

xmlDetail <- file.path(system.file("extdata", package="TFBSTools"), "tffm_detailed.xml")
tffmDetail <- readXMLTFFM(xmlDetail, type="Detail")
getPosProb(tffmDetail)

IUPAC2Matrix

Description

Convert a IUPAC string into a Position Weight Matrix

Usage

IUPAC2Matrix(x)

Arguments

x

The IUPAC string.

Details

The mapping between IUPAC Extended Genetic Alphabet and the DNA bases letters are from IUPAC_CODE_MAP in Biostrings package.

Value

A matrix with position weight.

Author(s)

Ge Tan

Examples

x <- "RMGNV"
IUPAC2Matrix(x)
Some example PFM matrices.

Description

Some example PFM matrices from JASPAR 2014.

Usage

\begin{verbatim}
data(MA0004.1) data(MA0003.2) data(MA0048) data(MA0043)
\end{verbatim}

Format

The format is: PFMatrix object.

Details

Some examples PFM matrices from JASPAR 2014.

Value

The PFMatrix object.

Source

http://jaspar.genereg.net/

Examples

\begin{verbatim}
data(MA0004.1) data(MA0003.2) data(MA0048) data(MA0043)
\end{verbatim}

makeFlatFileDir

Generate "FlatFileDir" directory

Description

On JASPAR web service, "FlatFileDir" includes all the *.pfm and a matrix_list.txt file

Usage

makeFlatFileDir(JASPAR)

Arguments

JASPAR A JASPAR object. Now it can be JASPAR2014 or JASPAR2016.
Details

The matrix_list.txt file contains each pfm per line. Each line has the ID, total information content, name, class and tags of one pfm.

Value

The generated files are under "FlatFileDir" directory.

Author(s)

Ge Tan

Examples

library(JASPAR2014)
makeFlatFileDir(JASPAR2014)

MotifSet  Class "MotifSet"

Description

This MotifSet object is a container for storing the generated motifs from Motif identification softwares, such as MEME.

Usage

## Constructor
MotifSet(motifList=GRangesList(), motifEvalues=numeric(), subjectSeqs=DNASTringSet())

Arguments

motifList  A GRangesList. Each GRanges store the starts, ends, strand, seqnames and scores information of one motif sites sequences.

motifEvalues  A numeric vector of the E values generated from MEME for each motif.

subjectSeqs  A DNASTringSet object. It stores the original sequences which are scanned by the software.

Value

A MotifSet object is returned.
Methods

signature(x = "MotifSet"): Getter

`consensusMatrix` signature(x = "MotifSet") (x, as.prob = FALSE, shift = 0L, width = NULL, ...): Calculate the consensus matrix. Other arguments, please check the `consensusMatrix` in Biostrings package.

`length` signature(x = "MotifSet"): Returns the number of motifs.

`sitesSeq` signature(x = "MotifSet") (x, n=10L, type="none"): Gets the sites sequences.

n is the number of bases to include from flanking region.

Type controls "all", "left", "right" or "none" flanking sequences are included.

Author(s)

Ge Tan

See Also

`runMEME`

Examples

```r
## Not run:

motifSet <- runMEME(file.path(system.file("extdata", package="TFBSTools"),
  "crp0.s"),
  binary="/usr/local/Cellar/meme/4.10.1/bin/meme",
  arguments=list("-nmotifs"=3))

sitesSeq(motifSet, type="all")
sitesSeq(motifSet, type="none")

consensusMatrix(motifSet)

## End(Not run)
```

description

Parse the output file from "MEME".

Usage

`parseMEMEOutput(x)`

Arguments

x character(1): the filename of the "MEME" output.

Value

A list of motifs and evalues is returned.
permuteMatrix-methods

Author(s)
Ge Tan

See Also
runMEME

Examples
memeOutput <- file.path(system.file("extdata", package="TFBSTools"),
"meme.output")
parseMEMEOutput(memeOutput)

Description
This method simply shuffles the columns in matrices. This can either be done by just shuffling columns within each selected matrix, or by shuffling columns among all selected matrices.

Usage
permuteMatrix(x, type="intra")

Arguments
x
A matrix which meets the PFM standard, PFMatrix object, or PFMatrixList object.
type
The type of shuffling. It can be "intra" or "inter", which shuffle within each matrix, or between all the matrix.

Value
A object with shuffled matrix.

Author(s)
Ge Tan

Examples
data("MA0043")
pfmSubject <- MA0043
data("MA0048")
pfmQuery <- MA0048
#opts = list()
#opts[["class"]]= "Ig-fold"
#pfmList = getMatrixSet(JASPAR2014, opts)
pfmList <- PFMatrixList(pfmSubject, pfmQuery)
foo = permuteMatrix(pfmQuery)
foo1 = permuteMatrix(pfmList, type="intra")
foo2 = permuteMatrix(pfmList, type="inter")
PFMSimilarity-methods

Description

Given a PFMatrix or a normal matrix, align it with another set of PFMatrix to assess the similarity.

Usage

PFMSimilarity(pfmSubject, pfmQuery, openPenalty=3, extPenalty=0.01)

Arguments

- **pfmSubject**: A matrix, PFMatrix or PFMatrixList object, which is compared with query matrix.
- **pfmQuery**: A matrix, PFMatrix or IUPAC character object.
- **openPenalty**: The gap open penalty used in the modified Needleman-Wunsch algorithm. By default, it is 3.
- **extPenalty**: The gap extension penalty used in the modified Needleman-Wunsch algorithm. By default, it is 0.01.

Value

For each pfmSubject, an absolute score and a relative percentage score is returned. The maximum absolute score is 2 times the width of the smaller matrix in the comparison pair.

Author(s)

Ge Tan

References


Examples

```R
library(Biostrings)
library(JASPAR2016)
## Example matrix from JASPAR database
profileMatrix <- matrix(as.integer(
  c(13, 13, 3, 1, 54, 1, 1, 0, 3, 2, 5,
    13, 39, 5, 53, 0, 1, 50, 1, 0, 37, 0, 17,
    17, 2, 37, 0, 0, 52, 3, 0, 53, 8, 37, 12,
    11, 0, 9, 0, 0, 0, 0, 52, 1, 6, 15, 20)),
  nrow=4, byrow=TRUE, dimnames=list(DNA_BASES))
pfmQuery <- PFMatrix(profileMatrix=profileMatrix)
 pfmSubjects <- getMatrixSet(JASPAR2016,
     opts=list(ID=c("MA0500", "MA0499", "MA0521",
       "MA0697", "MA0048", "MA0751",
       "MA0832")))

PFMSimilarity(pfmSubjects, pfmQuery)
```
**Description**

This function measures the similarity of two PWM matrix in three measurements: "normalised Euclidean distance", "Pearson correlation" and "Kullback Leibler divergence".

**Usage**

```r
PWMSimilarity(pwmSubject, pwmQuery, method=c("Euclidean", "Pearson", "KL"))
```

**Arguments**

- `pwmSubject` A matrix or `PWMatrix` or `PWMatrixList` object.
- `pwmQuery` A matrix or `PWMatrix` object.
- `method` The method can be "Euclidean", "Pearson", "KL".

**Details**

When `pwmSubject` and `pwmQuery` have different number of columns, the smaller PWM will be shifted from the start position of larger PWM and compare all the possible alignments. Only the smallest distance, divergence or largest correlation will be reported.

**Value**

A numeric value is returned.

**Methods**

- `signature(pwmSubject = "matrix", pwmQuery = "matrix")`
- `signature(pwmSubject = "matrix", pwmQuery = "PWMatrix")`
- `signature(pwmSubject = "PWMatrix", pwmQuery = "matrix")`
- `signature(pwmSubject = "PWMatrix", pwmQuery = "PWMatrix")`
- `signature(pwmSubject = "PWMatrixList", pwmQuery = "matrix")`
- `signature(pwmSubject = "PWMatrixList", pwmQuery = "PWMatrix")`
- `signature(pwmSubject = "PWMatrixList", pwmQuery = "PWMatrixList")`

**References**


**See Also**

`PFMSimilarity`
Examples

```r
data(MA0003.2)
data(MA0004.1)
pwm1 = toPWM(MA0003.2, type="prob")
pwm2 = toPWM(MA0004.1, type="prob")
PWMSimilarity(pwm1, pwm2, method="Euclidean")
```

---

**readJASPARMatrix**  
*Read JASPAR format matrix*

Description

Read a JASPAR format matrix file with ‘individual’ matrix or ‘all’ matrices in one file.

Usage

```r
readJASPARMatrix(fn, type = c("individual", "all"))
```

Arguments

- `type` character(1): It can be ‘individual’ or ‘all’.

Details

An example of ‘individual’ format matrix file is available at [http://jaspar.genereg.net/html/DOWNLOAD/JASPAR_CORE/pfm/individual/MA0001.1.pfm](http://jaspar.genereg.net/html/DOWNLOAD/JASPAR_CORE/pfm/individual/MA0001.1.pfm)

An example of ‘all’ format matrix file is available at [http://jaspar.genereg.net/html/DOWNLOAD/JASPAR_CORE/pfm/nonredundant/pfm_all.txt](http://jaspar.genereg.net/html/DOWNLOAD/JASPAR_CORE/pfm/nonredundant/pfm_all.txt)

Value

When ‘individual’, a `PFMatrix` object is returned. When ‘all’, a `PFMatrixList` object is returned.

Author(s)

Ge Tan

See Also

`makeFlatFileDir`

Examples

```r
fn <- file.path(system.file("extdata", package="TFBSTools"),
                "MA0001.1.pfm")
readJASPARMatrix(fn, type="individual")
fn <- file.path(system.file("extdata", package="TFBSTools"),
                "pfm_all_example.txt")
readJASPARMatrix(fn, type="all")
```
Description
Read the output xml files from the Python module “TFFM” into R.

Usage

```r
readXMLTFFM(fn, type=c("First", "Detail"))
```

Arguments

- **fn**: The path of xml file.
- **type**: The type of xml file. It can be one of the two types of xml files, "First" or "Detail".

Value
A `TFFMFirst` object or a `TFFMDetail` object is returned.

Author(s)
Ge Tan

See Also
- `TFFM`

Examples

```r
xmlFirst <- file.path(system.file("extdata", package="TFBSTools"),
                      "tffm_first_order.xml")
tffmFirst <- readXMLTFFM(xmlFirst, type="First")
```

Description
This function samples matrices from trained Dirichlet mixture model based on selected matrices.

Usage

```r
rPWMDmm(x, alpha0, pmix, N=1, W=6)
```
Arguments

- **x**: x can be a matrix, PFMatrixList. The count matrix on which the sampling is based.
- **alpha0**: The trained Dirichlet mixture parameters.
- **pmix**: The trained mixing proportions of the components.
- **N**: The number of matrices to sample.
- **W**: The desired width of matrix from the sampling.

Details

This feature enables the users to generate random Position Frequency Matrices (PFMs) from selected profiles.

We assume that each column in the profile is independent and described by a mixture of Dirichlet multinomials in which the letters are drawn from a multinomial and the multinomial parameters are drawn from a mixture of Dirichlets. Within this model each column has its own set of multinomial parameters but the higher level parameters – those of the mixture prior is assumed to be common to all Jaspar matrices. We can therefore use a maximum likelihood approach to learn these from the observed column counts of all Jaspar matrices. The maximum likelihood approach automatically ensures that matrices receive a weight relative to the number of counts it contains.

Drawing samples from the prior distribution will generate PWMs with the same statistical properties as the Jaspar matrices as a whole. PWMs with statistical properties like those of the selected profiles can be obtained by drawing from a posterior distribution which is proportional to the prior times a multinomial likelihood term with counts taken from one of the columns of the selected profiles.

Each 4-dimensional column is sampled by the following three-step procedure: 1. draw the mixture component according to the distribution of mixing proportions, 2. draw an input column randomly from the concatenated selected profiles and 3. draw the probability vector over nucleotides from a 4-dimensional Dirichlet distribution. The parameter vector alpha of the Dirichlet is equal to the sum of the count (of the drawn input) and the parameters of the Dirichlet prior (of the drawn component).

Draws from a Dirichlet can be obtained in the following way from Gamma distributed samples: \((X_1, X_2, X_3, X_4) = (Y_1/V, Y_2/V, Y_3/V, Y_4/V) ~ \text{Dir}(a_1, a_2, a_3, a_4)\) where \(V = \text{sum}(Y_i) \sim \text{Gamma}(\text{shape} = \text{sum}(a_i), \text{scale} = 1)\).

Value

A list of matrices from the sampling.

Methods

signature(x = "PFMatrix")
signature(x = "matrix")
signature(x = "PFMatrixList")

Note

This code is based on the Matlab code original written by Ole Winther, binf.ku.dk, June 2006.

Author(s)

Ge Tan
References


See Also
dmmEM

Examples

data(MA0003.2)
data(MA0004.1)
pfmList <- PFMatrixList(pfm1=MA0003.2, pfm2=MA0004.1, use.names=TRUE)
dmmParameters <- dmmEM(pfmlist, 6)
rPWMdmm(MA0003.2, dmmParameters$alpha0, dmmParameters$pmix, N=1, W=6)

runMEME

Wrapper function for MEME

Description

This function builds position frequency matrices using an external program MEME written by Bailey and Elkan.

Usage

## S4 method for signature 'character'
runMEME(x, binary="meme", seqtype="DNA",
         arguments=list(), tmpdir=tempdir())

## S4 method for signature 'DNAStringSet'
runMEME(x, binary="meme", seqtype="DNA",
         arguments=list(), tmpdir=tempdir())

Arguments

x A character(1) vector of the path of fasta file or a XStringSet.
binary character(1): the path of MEME binary. By default, we assume the meme is in the PATH.
seqtype The sequence type. "AA" and "DNA" are allowed.
arguments A list: the addtional arguments for meme. This list takes the parameter of MEME as names of the elements, and the values of the parameters as the elements. For examples, arguments=list("-nmotifs"=3).
tmpdir A character(1) vector to change the defult R’s temp directory.

Value

A MotifSet object is returned.
Note

This wrapper is tested on “MEME” 4.10.1.

Author(s)

Ge Tan

References

http://meme-suite.org/

See Also

MotifSet

Examples

```r
## Not run:
motifSet <- runMEME(file.path(system.file("extdata", package="TFBSTools"),
"crp0.s"),
binary="/usr/local/Cellar/meme/4.10.1/bin/meme",
arguments=list("-nmotifs"=3))
## Get the site sequences
sitesSeq(motifSet, type="all")
sitesSeq(motifSet, type="none")

## Get the consensus matrix, then it can be used as a PFMatrix
consensusMatrix(motifSet)

## End(Not run)
```

Description

Sample ranges with same widths of input ranges from a set of subject ranges.

Usage

```r
sampleRanges(inputGRanges, subjectGRanges, ignore.strand=TRUE)
```

Arguments

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>inputGRanges</td>
<td>The input GRanges.</td>
</tr>
<tr>
<td>subjectGRanges</td>
<td>The subject GRanges.</td>
</tr>
<tr>
<td>ignore.strand</td>
<td>When set to TRUE, the strand information is ignored during the sampling. Otherwise, the input ranges on positive strand will only sample from subject ranges on positive strand.</td>
</tr>
</tbody>
</table>
Value

A GRanges object with the same length and widths of inputGRanges.

Author(s)

Ge Tan

Examples

```r
library(GenomicRanges)
inputGRanges <- GRanges(seqnames=c("chr1", "chr2"),
                         range=IRanges(start=c(2L, 10L), end=c(6L, 15L)),
                         strand=c("+", "-"))
subjectGRanges <- GRanges(
                         seqnames=c("chr1", "chr1", "chr1", "chr1",
                                    "chr2", "chr2"),
                         ranges=IRanges(start=c(20L, 20L, 30L, 30L, 7L, 25L),
                                        end=c(50L, 50L, 32L, 32L, 9L, 55L)),
                         strand=c("+", "-", "+", "-", "+", "-"))
set.seed(16)
sampleRanges(inputGRanges, subjectGRanges, ignore.strand=TRUE)
sampleRanges(inputGRanges, subjectGRanges, ignore.strand=FALSE)
```

---

**searchAln**

**searchAln method**

**Description**

Scans a pairwise alignment of nucleotide sequences with the pattern represented by the PWMatrix. It reports only those hits that are overlapped in the alignment of the two sequences and exceed a specified threshold score in both, AND are found in regions of the alignment above the specified conservation cutoff value.

**Usage**

```r
searchAln(pwm, aln1, aln2, seqname1="Unknown1", seqname2="Unknown2",
         min.score="80\%", windowSize=51L,
         cutoff=0.7, strand="*", type="any", conservation=NULL,
         mc.cores=1L)
```

**Arguments**

- **pwm**: A PWMatrix object or a PWMatrixList object.
- **aln1**: A DNAString, character, DNAStringSet or Axt object can be used to represent the pairwise alignment. When the last two objects are used and have a length of 2, the argument aln2 can be missing.
- **aln2**: A DNAString, character. It can be missing when aln1 is DNAStringSet or Axt object.
searchAln

seqname1,seqname2
A character object for the name of sequence. "Unknown1" and "Unknown2" are used by default. These two arguments are ignored when aln1 is Axt, or the seqnames are available from aln1.

min.score
The minimum score for the hit. Can be given an character string in the format of "80%" or as a single absolute value. When it is percentage value, it means the percentage of the maximal possible from the PWM.

windowSize
The size of the sliding window (in nucleotides) for calculating local conservation in the alignment. This should be an odd value.

cutoff
The conservation cutoff can be from 0 (0% identity) to 1 (100% identity). The regions which have lower conservation than the cutoff will be discarded from the results of the pattern searching. The conservation is calculated by comparing the alignments within the windowSize: 1 for match and 0 for mismatch and gap.

strand
When searching the alignment, we can search the positive strand or negative strand. While strand is ",*", it will search both strands and return the results based on the positive strand coordinate.

type
This argument can be "any" or "all". When it is "any", one motif will be kept if the maximal conservation value of the motif is larger than the cutoff. When it is "all", one motif will be kept if the minimal conservation value of the motif is larger than the cutoff.

conservation
A vector of conservation profile. If not supplied, the conservation profile will be computed internally on the fly.

mc.cores
The number of cpu threads to use when searching Axt. 1L is assigned by default.

Details
In brief, given a pairwise alignment of two sequences, first of all, we remove the gaps ("-", "-", "."). Then we scan both ungapped sequences with the pwm and return the hits that above min. score. Since we only want to keep the conserved hits, we choose the pair of motifs that overlap most in the alignment. Finally, the pair of motifs have to be conserved above the threshold cutoff.

In the returned SitePairSet, the coordinates of start, end are based on the ungapped sequences, instead of the original alignment. This is due to we are more concerned about the actual location of motif in the genome rather than in the alignment.

Value
A SitePairSet object is returned when pwm is a PWMatrix, while a SitePairSetList is returned when pwm is a PWMatrixList.

Author(s)
Ge Tan

See Also
searchSeq
Examples

data(MA0003.2)
data(MA0004.1)
pwm1 <- toPWM(MA0003.2)
pwm2 <- toPWM(MA0004.1)
pwmList <- PWMMatrixList(pwm1=pwm1, pwm2=pwm2)
# Two character objects
aln1 <- "ACACATGGCTCAGGCGAGTAAGTTTGATC---AAAGG----AAACGCAAAGTTTTCAAG"
aln2 <- "GTTTCATAGATGTACCTCAAGGCGAGTAATATATATATATAATATAATATATTTTCACT"
aln <- c(aln1=aln1, aln2=aln2)
library(Biostrings)
alnDNAStringSet <- DNAStringSet(c(aln1=aln1, aln2=aln2))

# PWMatrix, character, character
## Only scan the positive strand of the alignments
sitePairSet <- searchAln(pwm1, aln1, aln2, seqname1="aln1", seqname2="aln2",
                         min.score="70\%", cutoff=0.5,
                         strand="+", type="any")
## Only scan the negative strand of the alignments
sitePairSet <- searchAln(pwm1, aln1, aln2, seqname1="aln1", seqname2="aln2",
                         min.score="70\%", cutoff=0.5,
                         strand="-", type="any")
## Scan the both strands of the alignments
sitePairSet <- searchAln(pwm1, aln1, aln2, seqname1="aln1", seqname2="aln2",
                         min.score="70\%", cutoff=0.5,
                         strand="*", type="any")
## Convert the SitePairSet object into other R objects
as(sitePairSet, "data.frame")
as.data.frame(sitePairSet)
as(sitePairSet, "DataFrame")
as(sitePairSet, "GRanges")
writeGFF3(sitePairSet)
writeGFF2(sitePairSet)

# PWMatrix, character, missing
sitePairSet <- searchAln(pwm1, aln, 
                         min.score="70\%", cutoff=0.5,
                         strand="*", type="any")

# PWMatrix, DNAString, DNAString
sitePairSet <- searchAln(pwm1, DNAString(aln1), DNAString(aln2),
                         seqname1="aln1", seqname2="aln2",
                         min.score="70\%", cutoff=0.5,
                         strand="*", type="any")

# PWMatrix, DNAStringSet, missing
sitePairSet <- searchAln(pwm1, alnDNAStringSet, 
                         min.score="70\%", cutoff=0.5,
                         strand="*", type="any")

# PWMMatrixList, character, character
sitePairSetList <- searchAln(pwmList, aln1, aln2, 
                          seqname1="aln1", seqname2="aln2",
                          min.score="70\%", cutoff=0.5,
                          strand="*", type="any")
## elementLenths of each pwm hits
## output
writeGFF2(sitePairSetList)
writeGFF3(sitePairSetList)
as(sitePairSetList, "DataFrame")
as.data.frame(sitePairSetList)
as(sitePairSetList, "data.frame")
as.data.frame(sitePairSetList)
as(sitePairSetList, "GRanges")

# PWMatrix, Axt, missing
library(CNEr)
axtFilesHg19DanRer7 <- file.path(system.file("extdata", package="TFBSTools"),
"hg19.danRer7.net.axt")
axtHg19DanRer7 <- readAxt(axtFilesHg19DanRer7)
sitePairSetList <- searchAln(pwm1, axtHg19DanRer7, min.score="80%",
windowSize=51L, cutoff=0.7, strand="*",
type="any", conservation=NULL, mc.cores=1)

## We may want to coordinates of motif in the genome
GRangesTFBS <- toGRangesList(sitePairSetList, axtHg19DanRer7)

searchPairBSgenome-methods

searchPairBSgenome method

Description

Given a chain file for liftover from one genome to another, it searches two BSgenome with a PWMatrix, and only reports the hits that are presents in two genomes with equivalent positions.

Usage

searchPairBSgenome(pwm, BSgenome1, BSgenome2, chr1, chr2,
min.score="80%", strand="*", chain)

Arguments

pwm A PWMatrix object or a PWMatrixList object.
BSgenome1, BSgenome2 A BSgenome class.
chr1, chr2 A character object, specifying the chromosomes you want to search.
min.score The minimum score for the hit. Can be given an character string in th format of "80%" or as a single absolute value.
strand When searching the alignment, we can search the positive "+" strand or negative "-" strand. While strand is "*", it will search both strands and return the results based on the positive strand coordinate.
chain A Chain object. It can be generated by import.chain from package rtracklayer. Please provide the chain from BSgenome1 to BSgenome2.

Value

A SitePairSet object is returned when pwm is a PWMatrix, while a SitePairSetList is returned when pwm is a PWMatrixList.
**searchSeq**

**Author(s)**
Ge Tan

**See Also**
searchAln

**Examples**

```r
## Not run:
library(rtracklayer)
library(JASPAR2014)
library(BSgenome.Hsapiens.UCSC.hg19)
library(BSgenome.Musculus.UCSC.mm10)
data("MA0004.1")
pfm <- MA0004.1
pwm <- toPWM(pfm)
chain <- import.chain(" Downloads/hg19ToMm10.over.chain")
sitepairset <- searchPairBSgenome(pwm, BSgenome.Hsapiens.UCSC.hg19,
                                  BSgenome.Musculus.UCSC.mm10,
                                  chr1="chr1", chr2="chr1",
                                  min.score="90%", strand="+",
                                  chain=chain)

## End(Not run)
```

**Description**

It scans a nucleotide sequence with the pattern represented by a PWM object and identifies putative transcription factor binding sites.

**Usage**

```r
searchSeq(x, subject, seqname="Unknown", strand="*", min.score="80%")
```

**Arguments**

- **x**: x can be a PWMMatrix object or a PWMMatrixList object.
- **subject**: A DNAStringSet, DNAString, XStringViews or MaskedDNAString object that will be scanned.
- **seqname**: This is sequence name of the target sequence. If subject is a DNAStringSet, the names of the DNAStringSet object will be used.
- **strand**: When searching the sequence, we can search the positive strand or negative strand. While strand is "*", it will search both strands and return the results based on the positive strand coordinate.
- **min.score**: The minimum score for the hit. Can be given an character string in the format of "80%" or as a single absolute value between 0 and 1. When it is percentage value, it represents the quantile between the minimal and the maximal possible value from the PWM.
Value

A Site object is returned when x is a PWMatrix object. A SiteList object is returned when x is a PWMatrixList or subject is a DNAStringSet.

Author(s)

Ge Tan

References


See Also

searchAln, matchPWM

Examples

data(MA0003.2)
data(MA0004.1)
pwm1 <- toPWM(MA0003.2)
pwm2 <- toPWM(MA0004.1)
pwmList <- PWMatrixList(pwm1=pwm1, pwm2=pwm2)
seq1 <- "GAATTCTCTTGGTGTAGCATTGCCTCAGGGCACACGTGCAAAATG"
seq2 <- "GTTTCACCATTGCCTCAGGGCATAAATATATAAAAAATATAATTTTCATC"

# PWMatrix, character
siteset <- searchSeq(pwm1, seq1, seqname="seq1", strand="+", min.score="80%")
siteset <- searchSeq(pwm1, seq1, seqname="seq1", strand="+", min.score=0.8)
## Only scan the negative strand of the input sequence
siteset <- searchSeq(pwm1, seq1, seqname="seq1", strand="-", min.score="80%")
## Scan both strands of the input sequences
siteset <- searchSeq(pwm1, seq1, seqname="seq1", strand="*", min.score="80%")
## Convert the SiteSet object into other R objects
as(siteset, "data.frame")
as(siteset, "DataFrame")
as(siteset, "GRanges")
writeGFF3(siteset)
writeGFF2(siteset)

# PWMatrixList, character
sitesetList <- searchSeq(pwmList, seq1, seqname="seq1", strand="*", min.score="80%")
## Convert the SiteSteList object into other R objects
as(sitesetList, "data.frame")
as(sitesetList, "DataFrame")
as(sitesetList, "GRanges")
writeGFF3(sitesetList)
writeGFF2(sitesetList)

# PWMatrix, DNAStringSet
library(Biostrings)
seqs <- DNAStringSet(c(seq1=seq1, seq2=seq2))
sitesetList <- searchSeq(pwm1, seqs, min.score="80%")
seqLogo

```
# PWMList, DNAStringSet
sitesetlist <- searchSeq(pwmList, seqs, min.score="80%")
```

---

**seqLogo**

*Plot a sequence logo*

**Description**

This function takes a ICMatrix or TFFM object and plot the sequence logo.

**Usage**

```r
seqLogo(x, ic.scale = TRUE, xaxis = TRUE, yaxis = TRUE, xfontsize = 15, yfontsize = 15)
```

**Arguments**

- `x`: x is a valid ICMatrix object or TFFM object.
- `ic.scale`: A logical value. If TRUE, the total height of one column is proportional to the information content at that position. Otherwise, all the columns will have the same height. Ignored for TFFM object.
- `xaxis`: A logical value. If TRUE, the x-axis will be plotted. Ignored for TFFM object.
- `yaxis`: A logical value. If TRUE, the y-axis will be plotted. Ignored for TFFM object.
- `xfontsize`: A numeric value. The font size for x-axis.
- `yfontsize`: A numeric value. The font size for y-axis.

**Details**

A sequence logo is a graphical representation of the matrix model, based on the information content of each position. The information content ranges from 0 (no base preference) to 2 (only 1 base used). If `ic.scale` is TRUE, the height of the logo at certain site is proportional to the information content value. And each stacked base (A, C, G, T)'s height is also proportional to the information content of each base at that position, and sorted based on the character size.

For a TFFM object, a novel graphical representation is used for capturing the dinucleotide dependencies on the TFFM. For the upper part of the sequence logo, we represent the nucleotide probabilities at position p for each possible nucleotide at position p-1. Hence, each column represents a position within a TFBS and each row the nucleotide probabilities found at that position. Each row assumes a specific nucleotide has been emitted by the previous hidden state. The intersection between a column corresponding to position p and row corresponding to nucleotide n gives the probabilities of getting each nucleotide at position p if n has been seen at position p-1. The opacity to represent the sequence logo is proportional to the probability of possible row to be used by the TFFM.

**Value**

No return value.
This function is based on the function seqLogo from the Bioconductor package seqLogo, especially for the plotting code of TFFM.

Author(s)

Ge Tan

References


See Also

toICM, ICMatrix,

Examples

```r
## ICMatrix
data(MA0003.2)
icm = toICM(MA0003.2)
seqLogo(icm, ic.scale = TRUE)

## TFFM
xmlFirst <- file.path(system.file("extdata", package="TFBSTools"),
    "tffm_first_order.xml")
tffmFirst <- readXMLTFFM(xmlFirst, type="First")
seqLogo(tffmFirst)
```

shannon.entropy (Calculate the Shannon entropy)

Description

This function calculates the Shannon entropy for a discrete random variable with finite n values sample.

Usage

shannon.entropy(p)

Arguments

p 
A numeric object with non-negative values.

Details

The entropy is calculated by $H(x) = -\sum_{i} p(x_i) \log_b(p(x_i))$. 

Value

A numeric value of entropy is returned.

Author(s)

Ge Tan

Examples

```r
x <- c(1, 1, 1, 1)
shannon.entropy(x)
```
```r
x <- c(1, 0, 0, 0)
shannon.entropy(x)
```

---

SitePairSet Class "SitePairSet"

Description

The SitePairSet object is a container for storing two SiteSet objects. Usually it is used to hold the results returned by searchAln.

Usage

```r
## Constructor
SitePairSet(siteset1, siteset2)
```

Arguments

- `siteset1`, `siteset2`
  Each SiteSet object is from one sequence in the pairwise alignment.

Value

A SitePairSet object.

Methods

- `siteset1` signature(x = "SitePairSet"): Gets the first SiteSet object.
- `siteset2` signature(x = "SitePairSet"): Gets the second SiteSet object.

Author(s)

Ge Tan

See Also

SitePairSet, searchAln
SitePairSetList-class

Class "SitePairSetList"

Description

The SitePairSetList class is a container for storing a collection of SitePairSet objects. Basically it is a SimpleList and is designed for manipulating the set of SitePairSet objects as a whole.

Usage

## Constructors:
SitePairSetList(..., use.names=TRUE)

Arguments

... The SitePairSet objects are supplied in .... A list of SitePairSet objects is also acceptable.
use.names A logical value. When TRUE, the names of the SitePairSet will be kept.

Value

A SitePairSetList object.

Author(s)

Ge Tan

See Also

SitePairSet,

SiteSet

Class "SiteSet"

Description

The SiteSet object is a container for storing a set of putative transcription factor binding sites on a nucleotide sequence (start, end, strand, score, pattern as a PWMatrix, etc.)

Usage

## Constructors:
SiteSet(views, score, strand="*", seqname="Unknown", sitesource="TFBS", primary="TF binding site", pattern)
Arguments

views  Object of class "XStringViews": It holds the start, end and the nucleotide sequence information of the transcription factor binding sites.

score  Object of class "numeric": A vector of PWM score for each putative binding site based on the PWM matrix.

strand  Object of class "character": The binding site is from the positive (+), negative (-) or unknown(*) strand.

seqname  Object of class "character": The sequence name of the sequence which contains these binding sites.

sitesource  Object of class "character": Currently it is set to "TFBS"

primary  Object of class "character": Currently it is set to "TF binding site"

pattern  Object of class "PWMatrix": The PWMatrix object which is used to search the binding sites.

Details

The score returned in SiteSet is the absolute score of each putative TFBS scanned by the corresponding PWM. The way of calculating the score is shown on the reference, Page 281.

Methods

[ signature(x = "SiteSet")]: Getter function.

length signature(x = "SiteSet"): The number of binding sites in this SiteSet.

pattern signature(x = "SiteSet"): Returns the PWMatrix used.

relScore signature(x = "SiteSet"): Gets relative score (between 0.0 to 1.0) with respect of the score range of the associated pattern (PWMatrix).

score signature(x = "SiteSet"): Returns the score of each site.

seqname signature(x = "SiteSet"): Returns the sequence name of the sequence which contains these sites.

strand signature(x = "SiteSet"): Returns the strand information.

views signature(x = "SiteSet"): Returns the views object.

start signature(x = "SiteSet"): Returns the start coordinates.

end signature(x = "SiteSet"): Returns the end coordinates.

pvalues signature(x = "SiteSet") (x, type=c("TFMPvalue", "sampling")): Calculates the empirical p-values for the scores with two methods: the exact method from TFMPaluve package or implementation of sampling in this package. The background probability for sampling is based on the PWM matrix in the SiteSet object.

Author(s)

Ge Tan

References

### SiteSetList

**See Also**

`searchSeq, searchAln, PWMMatrix, SiteSetList, SitePairSet`

**Examples**

```r
data(MA0003.2)
pwm <- toPWM(MA0003.2)
siteset <- searchSeq(pwm, "GAATTCTCTTTGTTGTAGTCTCTTGACAAAATG",
                   min.score="60%")
writeGFF3(siteset, scoreType="absolute")
as(siteset, "data.frame")
as(siteset, "DataFrame")
as(siteset, "GRanges")

relScore(siteset)
pvalues(siteset, type="TFMPvalue")
pvalues(siteset, type="sampling")
```

---

### SiteSetList

**Class** "SiteSetList"

**Description**

The `SiteSetList` class is a container for storing a collection of `SiteSet` objects. Basically it is a `SimpleList` and is designed for manipulating the set of `SiteSet` objects as a whole.

**Usage**

```r
## Constructors:
SiteSetList(..., use.names=TRUE)
```

**Arguments**

- ... The `SiteSet` objects are supplied in .... A list of `SiteSet` objects is also acceptable.
- use.names A logical value. When TRUE, the names of the `SiteSet` will be kept.

**Value**

A `SiteSetList` object.

**Methods**

- `pvalues` `signature(x = "SiteSetList")` (x, type=c("TFMPvalue", "sampling")): Calculates the empirical p-values for the scores.

**Author(s)**

Ge Tan

**See Also**

`SiteSet, searchSeq, searchAln`
Examples

```r
data(MA0003.2)
data(MA0004.1)
pwmList <- PWMMatrixList(MA0003.2=toPWM(MA0003.2), MA0004.1=toPWM(MA0004.1))
sitesetList <- searchSeq(pwmList, "GAATTCTCTGTTGTAGTCTCTTGACAAAATG", min.score="50%")

## elementNROWS of each pwm hits
library(S4Vectors)
elementNROWS(sitesetList)

## Output of SiteSetList
writeGFF3(sitesetList, scoreType="absolute")
as(sitesetList, "DataFrame")
as.data.frame(sitesetList)
as(sitesetList, "GRanges")

## Calculate the p-values
pvalues(sitesetList, type="TFMPvalue")
pvalues(sitesetList, type="sampling")
```

TFFM

The TFFM class

Description

The TFFM is a virtual class. Two classes are derived from this class: TFFMFirst and TFFMDetail. TFFMFirst class stands for the first-order TFFMs and TFFMDetail stands for the more detailed and descriptive TFFMs.

Usage

```r
## constructors:
TFFMFirst(ID="Unknown", name="Unknown", matrixClass="Unknown", strand="+", bg=c(A=0.25, C=0.25, G=0.25, T=0.25), tags=list(), profileMatrix=matrix(), type=character(), emission=list(), transition=matrix())
TFFMDetail(ID="Unknown", name="Unknown", matrixClass="Unknown", strand="+", bg=c(A=0.25, C=0.25, G=0.25, T=0.25), tags=list(), profileMatrix=matrix(), type=character(), emission=list(), transition=matrix())
```

Arguments

- `ID`, `name`, `matrixClass`, `strand`, `bg`, `tags`, `profileMatrix`: See `XMatrix`
- `type`: The type of TFFM.
- `emission`: The emission distribution parameters.
- `transition`: The transition probability matrix.
Value

A TFFM object.

Methods

**ncol** signature(x = "TFFMFirst"): Get the length of First-order TFFM.

**ncol** signature(x = "TFFMDetail"): Get the length of detail TFFM.

**totalIC** signature(x = "TFFM"): Get the information content at each position.

Author(s)

Ge Tan

References


http://cisreg.cmmt.ubc.ca/TFFM/doc/#

Examples

```r
xmlFirst <- file.path(system.file("extdata", package="TFBSTools"),
                      "tffm_first_order.xml")
tffmFirst <- readXMLTFFM(xmlFirst, type="First")
tffm <- getPosProb(tffmFirst)
```

---

**toGRangesList-methods**

toGRangesList function

Description

Get the genomic coordinates from SitePairSetList.

Value

A list of two GRanges objects are returned, one for the target sequences and another for query sequences.

In the GRanges, strand is taken from the Axt object. In the meta-data columns, PWM matrix ID, the strand of matrix and match score are also returned.

Methods

signature(x = "SitePairSetList", axt = "Axt") Convert the relative coordinates to absolute coordinates.

Author(s)

Ge Tan
Examples

```r
data(MA0003.2)
pwm <- toPWM(MA0003.2)
library(CNEr)
axtFilesHg19DanRer7 <- file.path(system.file("extdata", package="TFBSTools"),
  "hg19.danRer7.net.axt")
axtHg19DanRer7 <- readAxt(axtFilesHg19DanRer7)
sitePairSet <- searchAln(pwm, axtHg19DanRer7, min.score="80%",
  windowSize=51L, cutoff=0.7, strand="*",
  type="any", conservation=NULL, mc.cores=1)
toGRangesList(sitePairSet, axtHg19DanRer7)
```

### toICM method

#### Description

Converts a raw frequency matrix (PFMatrix) to a information content matrix (ICMatrix). It takes the bases background frequencies, pseudocounts and schneider as parameters.

#### Usage

```r
toICM(x, pseudocounts=0.8, schneider=FALSE,
  bg=c(A=0.25, C=0.25, G=0.25, T=0.25))
```

#### Arguments

- `x`: For `toPWM`, a PFMatrix, rectangular DNAStringSet object ("rectangular" means that all elements have the same number of characters) with no IUPAC ambiguity letters, a rectangular character vector or a matrix with rownames containing at least A, C, G and T, or a PFMatrixList object.
- `pseudocounts`: A default value 0.8 is used.
- `schneider`: This logical parameter controls whether a Schneider correction will be done. See more details below.
- `bg`: bg is a vector of background frequencies of four bases with names containing A, C, G, T. When toPWM is applied to a PFMatrix, if bg is not specified, it will use the bg information contained in PFMatrix.

#### Details

The information content matrix has a column sum between 0 (no base preference) and 2 (only 1 base used). Usually this information is used to plot sequence log.

The information content at each position is computed

\[
D = \log_2(nrow(pfm)) + \text{colSums}(postProbs \times \log_2(postProbs))
\]

\[
\text{icm} = \text{posProbs} \times D
\]

where D is the total information content for each position. For detailed procedure of computation, please refer to the vignette.

If a Schneider correction will be done if requested. Please see the reference below for more comprehensive explanation.
Value

A ICMatrix object which contains the background frequency, pseudocounts and Schneider correction used.

Author(s)

Ge Tan

References


See Also

toPWM, XMatrix, seqLogo

Examples

```r
## Constructor a PFMatrix
pfm <- PFMatrix(ID="MA0004.1", name="Arnt", matrixClass="Zipper-Type", strand="+",
bg=c(A=0.25, C=0.25, G=0.25, T=0.25),
tags=list(family="Helix-Loop-Helix",
  species="10090",
tax_group="vertebrates",
medline="7592839", type="SELEX", ACC="P53762",
pazar_tf_id="TF0000003",
TFBSshape_ID="11", TFencyclopedia_ID="580"),
profileMatrix=matrix(c(4L, 19L, 0L, 0L, 0L, 0L,
  16L, 0L, 20L, 0L, 0L, 0L,
  0L, 1L, 0L, 20L, 0L, 20L,
  0L, 0L, 0L, 0L, 20L),
byrow=TRUE, nrow=4,
dimnames=list(c("A", "C", "G", "T")))
)

## Convert it into a PWMatrix
icm <- toICM(pfm, pseudocounts=0.8, schneider=TRUE)

## Conversion on PWMatrixList
data(MA0003.2)
data(MA0004.1)
PFMatrixList(pfm1=MA0003.2, pfm2=MA0004.1, use.names=TRUE)

icmList <- toICM(icmList, pseudocounts=0.8, schneider=TRUE)
```

**Description**

Converts a raw frequency matrix (PFMatrix) to a position weight matrix (PWMatrix). It takes the type, bases background frequencies, pseudocounts as parameters.
toPWM

Usage

toPWM(x, type=c("log2probratio", "prob"), pseudocounts=0.8, 
bg=c(A=0.25, C=0.25, G=0.25, T=0.25))

Arguments

x For toPWM, a PFMatrix, rectangular DNAStringSet object ("rectangular" means that all elements have the same number of characters) with no IUPAC ambiguity letters, a rectangular character vector or a matrix with rownames containing at least A, C, G and T, or a PFMatrixList object.

type The type of PWM generated, should be one of "log2probratio" or "prob". "log2probratio" will generate the PWM matrix in log-scale, while "prob" will give the PWM matrix in probability scale of 0 to 1.

pseudocounts pseudocounts is a numeric non-negative vector, which means you can specify different pseudocounts for each site. The values will be recycled if shorter than the length of sites. 0.8 is recommended. See the reference below for more details. In the TFBS perl module, the squared root of the column sum of the matrix, i.e., the number of motifs used to construct the PFM, is used.

bg bg is a vector of background frequencies of four bases with names containing A, C, G, T. When toPWM is applied to a PFMatrix, if bg is not specified, it will use the bg information contained in PFMatrix.

Details

The raw position frequency matrix (PFM) is usually converted into a position weight matrix (PWM), also known as position specific scoring matrix (PSSM). The PWM provides the probability of each base at certain position and used for scanning the genomic sequences. The implementation here is slightly different from PWM in Biostrings package by choosing the pseudocounts. Pseudocounts is necessary for correcting the small number of counts or eliminating the zero values before log transformation.

\[
postProbs = \frac{PFM + bg \ast pseudocounts}{ncol(PFM) + sum(bg) \ast pseudocounts}
\]

\[
priorProbs = bg/sum(bg)
\]

\[
PWM_{log2probratio} = \log_2 \frac{postProbs}{priorProbs}
\]

\[
PWM_{prob} = postProbs
\]

Value

A PWMatrix object that contains the background frequency and pseudocounts used.

Author(s)

Ge Tan

References


See Also
toICM, XMatrix, PWM

Examples

```r
## Construct a PFMatrix
pfm <- PFMatrix(ID="MA0004.1", name="Arnt", matrixClass="Zipper-Type", strand="+", bg=c(A=0.25, C=0.25, G=0.25, T=0.25),
profileMatrix=matrix(c(4L, 19L, 0L, 0L, 0L, 0L, 16L, 0L, 20L, 0L, 0L, 0L, 0L, 1L, 0L, 20L, 0L, 20L, 0L, 0L, 0L, 0L, 0L, 0L, 0L), byrow=TRUE, nrow=4),
dimnames=list(c("A", "C", "G", "T")))

## Convert it into a PWMMatrix
pwm <- toPWM(pfm, type="log2probratio", pseudocounts=0.8)

## Conversion on PWMMatrixList
data(MA0003.2)
data(MA0004.1)

## Construct a PWMMatrix
pfmList <- PFMatrixList(pfm1=MA0003.2, pfm2=MA0004.1, use.names=TRUE)

## Convert it into a PWMMatrix
pwmList <- toPWM(pfmList, pseudocounts=0.8)
```

Description

write the SiteSet, SitePairSet, SiteSetList, SitePairSetList into the GFF3 or GFF2 format.

Usage

```r
writeGFF3(x, scoreType=c("absolute", "relative"))
writeGFF2(x, scoreType=c("absolute", "relative"))
```

Arguments

- `x`: A SiteSet, SitePairSet, SiteSetList, or SitePairSetList object.
- `scoreType`: The score column can have absolute value or relative value.

Value

It returns nothing.

Author(s)

Ge Tan
XMatrix

"XMatrix" objects

Description

XMatrix is a virtual class. No objects can be created from it directly. Three classes are derived from this class: PFMatrix, PWMatrix and ICMatrix.

PFMatrix is a class whose instances are objects representing raw position frequency matrices (PFMs).

PWMatrix is a class whose instances are objects representing position weight matrices (PWMs). Compared with PFMatrix, it has extra slot pseudocounts.

ICMatrix is a class whose instances are objects representing information content matrices (ICMs). Compared with PWMatrix, it has extra slot schneider.

Usage

## Constructors:

PFMatrix(ID="Unknown", name="Unknown", matrixClass="Unknown", strand="+", bg=c(A=0.25, C=0.25, G=0.25, T=0.25), tags=list(), profileMatrix=matrix())

PWMatrix(ID="Unknown", name="Unknown", matrixClass="Unknown", strand="+", bg=c(A=0.25, C=0.25, G=0.25, T=0.25), tags=list(), profileMatrix=matrix(), pseudocounts=numeric())

ICMatrix(ID="Unknown", name="Unknown", matrixClass="Unknown", strand="+", bg=c(A=0.25, C=0.25, G=0.25, T=0.25), tags=list(), profileMatrix=matrix(), pseudocounts=numeric(), schneider=logical())

## Accessor-like methods:

## S4 method for signature 'XMatrix'

ID(x)

## S4 method for signature 'XMatrix'

bg(x)

## ... and more (see Methods)

Arguments

ID Object of class "character": A unique identifier for each matrix.

name Object of class "character": The name of the transcription factor. In JASPAR, as far as possible, the name is based on the standardized Entrez gene symbols. In the case the model describes a transcription factor hetero-dimer, two names are concatenated, such as RXR-VDR. In a few cases, different splice forms of the same gene have different binding specificity: in this case the splice form information is added to the name, based on the relevant literature.

matrixClass Object of class "character": Structural class of the transcription factor, based on the TFCaT system.

strand Object of class "character": Which strand is the binding sites sequences from.

bg Object of class "numeric": Background frequencies of the four bases. By default, it is equally 0.25.
tags Object of class "list": Some tags information about this model. Tags include:
(1) "family": Structural sub-class of the transcription factor, based on the TFCaT system.
(2) "species": The species source for the sequences, in NCBI tax IDs.
(3) "tax_group": Group of species, currently consisting of 4 larger groups: vertebrate, insect, plant, chordate.
(4) "medline": a ID to the relevant publication reporting the sites used in the model building.
(5) "type": Methodology used for matrix construction.
(6) "ACC": A representative protein accession number in Genbank for the transcription factor. Human takes precedence if several exists.
(7) "pazar_tf_id": a ID to PAZAR database.
(8) "TFBSshape_ID": a ID to TFBSshape database.
(9) "TFencyclopedia_ID": a ID to the Transcription Factor Encyclopedia.
(10) "comment": For some matrices, a curator comment is added.

profileMatrix Object of class "matrix": This is the matrix information.
pseudocounts Object of class "numeric": This is the pseudocounts used when computing ICM or PWM from PFM. By default, a threshold of 0.8 is used based on the previous research (doi:10.1093/nar/gkn1019).
schneider Object of class "logical": this logical value indicates whether the schneider correction is used during the conversion from PFM to ICM.
x Object of class XMatrix.

Value
A XMatrix object.

Methods

bg signature(x = "XMatrix"): Gets the background base frequencies.
bg<- signature(x = "XMatrix"): Sets the background base frequencies.
ID signature(x = "XMatrix"): Gets the ID information.
ID<- signature(x = "XMatrix"): Sets the ID information.
length signature(x = "XMatrix"): Gets the pattern length in nucleotides (i.e. number of columns in the matrix).
reverseComplement signature(x = "PWMatrix"): Generates the reverse complement matrix object. Note than the strand is XMatrix will also be changed to the opposite strand.
as.matrix signature(x = "XMatrix"): Returns the matrix in the XMatrix class.
totalIC signature(x = "ICMatrix"): Returns the information content vector.
Matrix signature(x = "XMatrix"): Gets the matrix stored in XMatrix object.
Matrix<- signature(x = "XMatrix"): Sets the matrix stored in XMatrix object.
matrixClass signature(x = "XMatrix"): Gets the matrix type of a XMatrix object.
matrixClass<- signature(x = "XMatrix"): Sets the matrix type of a XMatrix object.
name signature(x = "XMatrix"): Gets the name information.
name<- signature(x = "XMatrix"): Sets the name information.
strand signature(x = "XMatrix"): Gets the strand information of a XMatrix object.
tags signature(x = "XMatrix"): Gets a list object of tags information.
Author(s)
Ge Tan

See Also
toPWM, toICM

Examples

```
## Constructor pf PFMatrix
## Note that there is no XMatrix() constructor,
## but an XMatrix family of constructors: PFMatrix(), PWMatrix(), ICMatrix()
pfm <- PFMatrix(ID="MA0004.1", name="Arnt", matrixClass="Zipper-Type",
strand="+", bg=c(A=0.25, C=0.25, G=0.25, T=0.25),
tags=list(family="Helix-Loop-Helix", species="10090",
tax_group="vertebrates", medline="7592839", type="SELEX",
ACC="P53762", pazar_tf_id="TF0000003",
TFBSshape_ID="11", TFencyclopedia_ID="580"),
profileMatrix=matrix(c(4, 19, 0, 0, 0, 0,
16, 0, 20, 0, 0, 0,
0, 1, 0, 20, 0, 20,
0, 0, 0, 0, 20, 0),
byrow=TRUE, nrow=4,
dimnames=list(c("A", "C", "G", "T")))

## Construction from a set of binding sites sequences
sitesSeqs <- c("Human Gli1"= "GACCACCCA", "hIGFBP-6"= "GACCCCCCA",
"HNF-3beta"="GAACACCCA", "hPlakoglobin"= "GACCACCAA",
"rIGFBP-6"= "GTCCACCCA", "Sox-9"= "GGCCACCCA")
countMatrix <- consensusMatrix(sitesSeqs)
pfm <- PFMatrix(ID="Gli-1", name="Gli-1", profileMatrix=countMatrix)

## Coersion
as.matrix(pfm)
as(pfm, "matrix")

## Methods
pwm <- toPWM(pfm)
reverseComplement(pwm)
length(pfm)
```

XMatrixList

### Class "XMatrixList"

#### Description

The XMatrixList virtual class is a container for storing a collection of XMatrix objects. No object can be constructed directly from this virtual and it has three subclasses: PFMatrixList, PWMatrixList and ICMatrixList. Basically it is a SimpleList and is designed for manipulating the set of XMatrix objects as a whole.
Usage

## Constructors:
PFMatrixList(..., use.names=TRUE)
PWMatrixList(..., use.names=TRUE)
ICMatrixList(..., use.names=TRUE)

## Accessor-like methods:
## S4 method for signature 'XMatrixList'
ID(x)
## S4 method for signature 'XMatrixList'
name(x)
## S4 method for signature 'XMatrixList'
bg(x)
## S4 method for signature 'XMatrixList'
tags(x)
## S4 method for signature 'XMatrixList'
name(x)
## S4 method for signature 'XMatrixList'
strand(x)

Arguments

... The XMatrix objects are supplied in ....
use.names A logical value. When TRUE, the names of the XMatrix will be kept.
x A XMatrixList object.

Value

A XMatrixList object.

Author(s)
Ge Tan

See Also

XMatrix.

Examples

data(MA0003.2)
data(MA0004.1)

## Construction of PFMatrixList
pfmList <- PFMatrixList(pfm1=MA0003.2, pfm2=MA0004.1, use.names=TRUE)

## Construction of PFMatrixList from list of PFMatrix
pfmList <- do.call(PFMatrixList, list(pfm1=MA0003.2, pfm2=MA0004.1))
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