

Package ‘rGADEM’

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Type Package

Title de novo motif discovery

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Imports Biostrings, IRanges, methods, graphics, seqLogo

Suggests BSgenome.Hsapiens.UCSC.hg19

Description rGADEM is an efficient de novo motif discovery tool for large-scale genomic sequence data. It is an open-source R package, which is based on the GADEM software.

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biocViews Microarray, ChIPchip, Sequencing, ChIPSeq, MotifDiscovery

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align-class	<i>Class "align"</i>
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Description

This object contains the individual motifs identified but also the location (seqID and position) of the sites in the original sequence data. It also included the spaced dyad from which the motifs is derived, PWM score p-value cutoff for the run.

Objects from the Class

Objects can be created by calls of the form `new("align", ...)`.

Slots

seq :Motif identified .
chr :Chromosome identified.
start :Sequence start.
end :Sequence end.
strand :Strand position.
seqID :Sequence identification.
pos :Position identification.
pval :p-Value for each identification.
fastaHeader :Fasta accession.

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See Also

[gadem](#), [motif](#), [parameters](#)

Examples

```
showClass("align")
```

Description

It is an R implementation of GADEM, a powerful computational tools for de novo motif discovery.

Usage

```
GADEM(Sequences, seed=1, genome=NULL, verbose=FALSE, numWordGroup=3, numTop3mer=20,
      numTop4mer=40, numTop5mer=60, numGeneration=5, populationSize=100,
      pValue=0.0002, eValue=0.0, extTrim=1, minSpaceWidth=0, maxSpaceWidth=10,
      useChIPscore=0, numEM=40, fEM=0.5, widthWt=80, fullScan=0, slideWinPWM=6,
      stopCriterion=1, numBackgSets=10, weightType=0,
      bFileName="NULL", Spwm="NULL", minSites =-1, maskR=0, nmotifs=25)
```

Arguments

Sequences	Sequences from BED or FASTA file are converted into XString object view
seed	When a seed is specified, the run results are deterministic
genome	Specify the genome
verbose	Print immediate results on screen [TRUE=yes (default), FALSE=no]. These results include the motif consensus sequence, number of sites (in sequences subjected to EM optimization, see -fEM, above), and ln(E-value).
numWordGroup	number of non-zero k-mer groups
numTop3mer	Number of top-ranked trimers for spaced dyads (default: 20).
numTop4mer	Number of top-ranked tetramers for spaced dyads (default: 40).
numTop5mer	Number of top-ranked pentamers for spaced dyads (default: 60).
numGeneration	Number of genetic algorithm (GA) generations (default: 5).
populationSize	GA population size (default: 100). Both default settings should work well for most datasets (ChIP-chip and ChIP-seq). The above two arguments are ignored in a seeded analysis, because spaced dyads and GA are no longer needed (num-Generation is set to 1 and populationSize is set to 10 internally, corresponding to the 10 maxp choices).
pValue	P-value cutoff for declaring BINDING SITES (default: 0.0002). Depending on data size and the motif, you might want to assess more than one value. For ChIP-seq data (e.g., 10 thousand +/-200-bp max-center peak cores), p=0.0002 often seems appropriate. However, short motifs may require a less stringent setting.
eValue	ln(E-value) cutoff for selecting MOTIFS (default: 0.0). If a seeded analysis fails to identify the expected motif, run GADEM with -verbose 1 to show motif ln(E-value)s on screen, then rerun with a larger ln(E-value) cutoff. This can help in identifying short and/or low abundance motifs, for which the default E-value threshold may be too low.
extTrim	Base extension and trimming (1 -yes, 0 -no) (default: 1).
minSpaceWidth	Minimal number of unspecified nucleotides in spaced dyads (default: 0).

Examples

```

library(BSgenome.Hsapiens.UCSC.hg19)
pwd<-"" #INPUT FILES- BedFiles, FASTA, etc.
path<- system.file("extdata", "Test_100.bed", package="rGADEM")
BedFile<-paste(pwd,path,sep="")
BED<-read.table(BedFile,header=FALSE,sep="\t")
BED<-data.frame(chr=as.factor(BED[,1]),start=as.numeric(BED[,2]),end=as.numeric(BED[,3]))
#Create RD files
rgBED<-IRanges(start=BED[,2],end=BED[,3])
Sequences<-RangedData(rgBED,space=BED[,1])

gadem<-GADEM(Sequences,verbose=1,genome=Hsapiens)

```

gadem-class	<i>Class "gadem"</i>
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Description

This object contains all gadem output information.

Objects from the Class

Objects can be created by calls of the form `new("gadem", ...)`.

Slots

motifList List of input PWM.
parameters List of rGADEM parameters.

Methods

[signature(x = "gadem"): subset gadem object.
[[signature(x = "gadem"): subset gadem object.
nMotifs signature(x = "gadem"): Number of motifs identified
names signature(x = "gadem"): Assign motifs names.
dim signature(x = "gadem"): Number of sequences identified for each motifs.
consensus signature(x = "gadem"):Sequence of consensus motifs.
nOccurrences signature(x = "gadem"):View of PWMs.
plot, gadem-method signature(x = "gadem"):Plot.
startPos signature(x = "gadem"):Start position for each sequences.
endPos signature(x = "gadem"):End position for each sequences.
getPWM signature(x = "gadem"):End position for each sequences.

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See Also

[motif](#), [align](#), [parameters](#)

Examples

```
showClass("gadem")
```

motif-class	<i>Class "motif"</i>
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Description

This object contains contains PWM, motif consensus, motif length and all aligned sequences for a specific motif

Objects from the Class

Objects can be created by calls of the form `new("motif_gadem", ...)`.

Slots

pwm :PWM results.

consensus :Sequences consensus.

alignList :List of sequences alignment.

name :Name of sequences.

Author(s)

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See Also

[gadem](#), [align](#), [parameters](#)

Examples

```
showClass("gadem")
```

parameters-class *Class "parameters"*

Description

This object contains contains parameters of GADEM analysis

Objects from the Class

Objects can be created by calls of the form `new("motif_gadem", ...)`.

Slots

numWordGroup :Number of non-zero k-mer groups.
numTop3mer :Number of top-ranked trimers for spaced dyads (default: 20).
verbose :Print immediate results on screen [1=yes (default), 0=no].
numTop4mer :Number of top-ranked tetramers for spaced dyads (default: 40).
numTop5mer :Number of top-ranked pentamers for spaced dyads (default: 60).
numGeneration :Number of genetic algorithm (GA) generations (default: 5).
populationSize :GA population size (default: 100).
pValue :P-value cutoff for declaring BINDING SITES (default: 0.0002).
eValue :ln(E-value) cutoff for selecting MOTIFS (default: 0.0).
extTrim :Base extension and trimming (1 -yes, 0 -no) (default: 1).
minSpaceWidth :Minimal number of unspecified nucleotides in spaced dyads (default: 0).
maxSpaceWidth :Maximal number of unspecified nucleotides in spaced dyads (default: 10).
useChIPscore :Use top-scoring sequences for deriving PWMs.
numEM :Number of EM steps (default: 40).
fEM :Fraction of sequences used in EM to obtain PWMs in an unseeded analysis (default: 0.5).
widthWt :For -posWt 1 or 3, width of central sequence region with large EM weights for PWM optimization (default: 50).
fullScan :GADEM keeps two copies of the input sequences internally.
slideWinPWM :Sliding window for comparing pwm similarity (default : 6).
stopCriterion
numBackgSets :Number of sets of background sequences (default: 10).
weightType :Weight profile for positions on the sequence.
bFileName :Reading user-specified background models.
Spwm :File name for the seed PWM, when a seeded approach is used.
nSequences :Number of input sequences.
maskR :Mask low-complexity sequences or repeats.
nmotifs :Maximal number of motifs sought.

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See Also

[gadem](#), [align](#), [motif](#)

Examples

```
showClass("parameters")
```

readPWMfile	<i>Read Transfac File</i>
-------------	---------------------------

Description

This function is use to read standard Transfac type file.

Usage

```
readPWMfile(file)
```

Arguments

`file` Transfac file's name.

Details

This function is designed to read standard Transfac type file. For more information about the format, please refere to <http://mcast.sdsc.edu/doc/transfac-format.html>

Value

A list of matrix.

Author(s)

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Examples

```
#####Database and Scores#####  
path <- system.file("extdata","jaspar2009.txt",package="rGADEM")  
jaspar <- readPWMfile(path)
```

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