Package 'rGADEM'

October 16, 2019

Type Package

Title de novo motif discovery

Version 2.32.0

Date 2014-04-01

Author Arnaud Droit, Raphael Gottardo, Gordon Robertson and Leiping Li

Maintainer Arnaud Droit <arnaud.droit@crchuq.ulaval.ca>

Depends R (>= 2.11.0), Biostrings, IRanges, BSgenome, methods, seqLogo

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.

License Artistic-2.0

biocViews Microarray, ChIPchip, Sequencing, ChIPSeq, MotifDiscovery

git_url https://git.bioconductor.org/packages/rGADEM

git_branch RELEASE_3_9

git_last_commit 180fece

git_last_commit_date 2019-05-02

Date/Publication 2019-10-15

R topics documented:

`align-class` *Class "align"*

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 cuttoff 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.

Author(s)

Arnaud Droit <arnaud.droit@crchuq.ulaval.ca>

See Also

`gadem` , `motif`, `parameters`

Examples

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

GADEM *Motif Analysis with rGADEM*

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 (numGeneration 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).

maxSpaceWidth	Maximal number of unspecified nucleotides in spaced dyads (default: 10). minSpaceWidth and maxSpaceWidth control the lengths of spaced dyads, and, with exTrim, control motif lengths. Longer motifs can be discovered by setting maxSpaceWidth to larger values (e.g. 50).
useChIPscore	Use top-scoring sequences for deriving PWMs. Sequence (quality) scores are stored in sequence header (see documentation). 0 - no (default, randomly select sequences), 1 - yes.
numEM	Number of EM steps (default: 40). One might want to set it to a larger value (e.g. 80) in a seeded run, because such runs are fast.
fEM	Fraction of sequences used in EM to obtain PWMs in an unseeded analysis (default: 0.5). For unseeded motif discovery in a large dataset (e.g. >10 million nt), one might want to set -fEM to a smaller value (e.g., 0.3 or 0.4) to reduce run time.
widthWt	For -posWt 1 or 3, width of central sequence region with large EM weights for PWM optimization (default: 50). This argument is ignored when weightType is 0 (uniform prior) or 2 (Gaussian prior).
fullScan	GADEM keeps two copies of the input sequences internally: one (D) for discovering PWMs and one (S) for scanning for binding sites using the PWMs Once a motif is identified, its instances in set D are always masked by Ns. However, masking motif instances in set S is optional, and scanning unmasked sequences allows sites of discovered motifs to overlap.
slideWinPWM	sliding window for comparing pwm similarity (default : 6).
stopCriterion	Number of generations without new motifs before stopping analysis.
numBackgSets	Number of sets of background sequences (default: 10). The background sequences are simulated using the [a,c,g,t] frequencies in the input sequences, with length matched between the two sets. The background sequences are used as the random sequences for assessing motif enrichment in the input data.
weightType	Weight profile for positions on the sequence. 0 - no weight (uniform spatial prior, default), 1 (gaussian prior) and 2 (triangle prior) - small or zero weights for the ends and large weights for the center (e.g. the center 50 bp). Consider using 1 or 2 if you expect strong central enrichment (as in ChIP-seq) and your sequences are long(e.g. >200 bp).
bFileName	Reading user-specified background models.
Spwm	File name for the seed PWM, when a seeded approach is used. can be used as the starting PWM for the EM algorithm. This will help find an expected motif and is much faster than unseeded de novo discovery.Also, when a seed PWM is specified, the run results are deterministic, so only a single run is needed (repeat runs with the same settings will give identical results). In contrast, unseeded runs are stochastic, and we recommend comparing results from several repeat runs.
minSites	Minimal number of sites required for a motif to be reported (default: numSeq/20)
maskR	Mask low-complexity sequences or repeats; 'aaaaaaaa', 'tttttttt', 'cacacaca', 'tgtgtgtg', 'tatatatat', 'ggaggaggagga','gaggaggaggag','agaagaagaaga','ctcctcctcctc','tcctcctcctcc','tc or 'cagcagcagcagcag' (default: 0-no masking,1-masking)
nmotifs	Number of motifs sought (default: 25)

Author(s)

Arnaud Droit <arnaud.droit@crchuq.ulaval.ca>

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 *Class "gadem"*

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.

Author(s)

Arnaud Droit <arnaud.droit@crchuq.ulaval.ca>

See Also

motif , align, parameters

Examples

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

---

motif-class *Class "motif"*

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)

Arnaud Droit <arnaud.droit@crchuq.ulaval.ca>

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.

Author(s)

Arnaud Droit <arnaud.droit@crchuq.ulaval.ca>

See Also

gadem , align, motif

Examples

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

---

readPWMfile *Read Transfac File*

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)

Arnaud Droit <<arnaud.droit@ircm.qc.ca>>

Examples

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

Index