

# Package ‘rGADEM’

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**Type** Package

**Title** de novo motif discovery

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**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

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## R topics documented:

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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.

### Author(s)

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

### 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 (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).   |



## 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)
```

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|             |                      |
|-------------|----------------------|
| 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.

## Author(s)

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

**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)**

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")
```

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

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**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)
```



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