

# Package ‘CSAR’

November 16, 2025

**Type** Package

**Title** Statistical tools for the analysis of ChIP-seq data

**Version** 1.63.0

**Date** 2025-07-24

**Author** Jose M Muino

**Description** Statistical tools for ChIP-seq data analysis. The package includes the statistical method described in Kaufmann et al. (2009) PLoS Biology: 7(4):e1000090. Briefly, Taking the average DNA fragment size subjected to sequencing into account, the software calculates genomic single-nucleotide read-enrichment values. After normalization, sample and control are compared using a test based on the Poisson distribution. Test statistic thresholds to control the false discovery rate are obtained through random permutation.

**Depends** R (>= 2.15.0), S4Vectors, IRanges, Seqinfo, GenomicRanges

**Maintainer** Jose M Muino <jose.muino@live.com>

**Suggests** ShortRead, Biostrings

**Imports** stats, utils

**License** Artistic-2.0

**LazyLoad** yes

**LazyData** yes

**biocViews** ChIPSeq, Transcription, Genetics

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|              |                                                            |
|--------------|------------------------------------------------------------|
| CSAR-package | <i>Statistical tools for the analysis of ChIP-seq data</i> |
|--------------|------------------------------------------------------------|

---

Description

Statistical tools for ChIP-seq data analysis.  
The package is oriented to plant organisms, and compatible with standard file formats in the plant research field.

Details

|           |              |
|-----------|--------------|
| Package:  | CSAR         |
| Type:     | Package      |
| Version:  | 1.0          |
| Date:     | 2009-11-09   |
| License:  | Artistic-2.0 |
| LazyLoad: | yes          |

Author(s)

Jose M Muino  
Maintainer: Jose M Muino <jose.muino@wur.nl>

References

Muino et al. (submitted). Plant ChIP-seq Analyzer: An R package for the statistcal detection of protein-bound genomic regions.  
Kaufmann et al.(2009).Target genes of the MADS transcription factor SEPALLATA3: integration of developmental and hormonal pathways in the Arabidopsis flower. PLoS Biology; 7(4):e1000090.

## Examples

```
##For this example we will use the a subset of the SEP3 ChIP-seq data (Kaufmann, 2009)
data("CSAR-dataset");
##We calculate the number of hits for each nucleotide posotion for the control and sample. We do that just for chromo
nhitsS<-mappedReads2Nhits(sampleSEP3_test,file="sampleSEP3_test",chr=c("CHR1v01212004"),chrL=c(10000))
nhitsC<-mappedReads2Nhits(controlSEP3_test,file="controlSEP3_test",chr=c("CHR1v01212004"),chrL=c(10000))

##We calculate a score for each nucleotide position
test<-ChIPseqScore(control=nhitsC,sample=nhitsS)

##We calculate the candidate read-enriched regions
win<-sigWin(test)

##We generate a wig file of the results to visualize teh in a genome browser
score2wig(test,file="test.wig")

##We calculate relative positions of read-enriched regions regarding gene position
d<-distance2Genes(win=win,gff=TAIR8_genes_test)

##We calculate table of genes with read-enriched regions, and their location
genes<-genesWithPeaks(d)

##We calculate two sets of read-enrichment scores through permutation
permutatedWinScores(nn=1,sample=sampleSEP3_test,control=controlSEP3_test,fileOutput="test",chr=c("CHR1v01212004"),chrL=c(10000))
permutatedWinScores(nn=2,sample=sampleSEP3_test,control=controlSEP3_test,fileOutput="test",chr=c("CHR1v01212004"),chrL=c(10000))

###Next function will get all permutated score values generated by permutatedWinScores function.
##This represent the score distribution under the null hypothesis and therefore it can be use to control the error of
nulldist<-getPermutatedWinScores(file="test",nn=1:2)

##From this distribution, several cut-off values can be calculated to control the error of our test.
##Several functions in R can be used for this purpose.
##In this package we had implemented a simple method for the control of the error based on FDR"
getThreshold(winscores=values(win)$score,permutatedScores=nulldist,FDR=.01)
```

---

ChIPseqScore

---

*Calculate read-enrichment scores for each nucleotide position*


---

## Description

Calculate read-enrichment scores for each nucleotide position

## Usage

```
ChIPseqScore(control, sample, backg = -1, file = NA, norm = 3 * 10^9, test = "Ratio",times=1e6,digits=2)
```

**Arguments**

|         |                                                                                                                                                                         |
|---------|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| control | data.frame structure obtained by mappedReads2Nhits                                                                                                                      |
| sample  | data.frame structure obtained by mappedReads2Nhits                                                                                                                      |
| backg   | Due low coverage in the control, there could be regions with no hits. Any region with a hit value lower than backg in the control will be set to the value of backg     |
| file    | Name of the file where you wan to save the results (if desired)                                                                                                         |
| norm    | Integer value. Number of hits will be reported by number of hits per norm nucleotides                                                                                   |
| test    | Use a score based on the poisson distribution ("Poisson") or in the ratio ("Ratio")                                                                                     |
| times   | To be memory efficient, CSAR will only upload to the RAM memory fragments of length times. A bigger value means more RAM memory needed but whole process will be faster |
| digits  | Number of decimal digits used to report the score values                                                                                                                |

**Details**

Different sequencing efforts yield different number of sequenced reads, for this reason the "number of hits" at each nucleotide position is normalized by the total number of nucleotides sequenced. Subsequently, the number of hits for the sample is normalize to have the same mean and variance than the control, for each chromosome independently or for the whole set of chromosomes (depending of the value of normEachChrInd). Due low coverage, there could be regions with no hits. Any region with a hit value lower than backg in the control will be set to the value of backg For each nucleotide position, a read-enrichment score will be calculated with the Poisson test, or with the ratio.

**Value**

A list to be used for other functions of the CSAR package

|           |                                                                               |
|-----------|-------------------------------------------------------------------------------|
| chr       | Chromosome names                                                              |
| chrL      | Chromosome length (bp)                                                        |
| filenames | Name of the files where the score values are storaged                         |
| digits    | Score values storaged on the files need to be divided by $10^{\text{digits}}$ |

**Author(s)**

Jose M Muino, <jose.muino@wur.nl>

**References**

Muino et al. (submitted). Plant ChIP-seq Analyzer: An R package for the statistical detection of protein-bound genomic regions.  
 Kaufmann et al.(2009).Target genes of the MADS transcription factor SEPALLATA3: integration of developmental and hormonal pathways in the Arabidopsis flower. PLoS Biology; 7(4):e1000090.

See Also

CSAR-package

Examples

```
##For this example we will use the a subset of the SEP3 ChIP-seq data (Kaufmann, 2009)
data("CSAR-dataset");
##We calculate the number of hits for each nucleotide posotion for the control and sample. We do that just for chromo
nhitsS<-mappedReads2Nhits(sampleSEP3_test,file="sampleSEP3_test",chr=c("CHR1v01212004"),chrL=c(10000))
nhitsC<-mappedReads2Nhits(controlSEP3_test,file="controlSEP3_test",chr=c("CHR1v01212004"),chrL=c(10000))

##We calculate a score for each nucleotide position
test<-ChIPseqScore(control=nhitsC,sample=nhitsS)
```

---

|                |                                                                                      |
|----------------|--------------------------------------------------------------------------------------|
| distance2Genes | <i>Calculate relative positions of read-enriched regions regarding gene position</i> |
|----------------|--------------------------------------------------------------------------------------|

---

Description

Calculate relative positions of read-enrichment regions regarding gene position

Usage

```
distance2Genes(win, gff, t = 1, d1 = -3000, d2 = 1000)
```

Arguments

|     |                                                                                                |
|-----|------------------------------------------------------------------------------------------------|
| win | GRange structure obtained with the function sigWin                                             |
| gff | Data.frame structure obtained after loading a desired gff file                                 |
| t   | Integer. Only distances of read-enriched regions with a score bigger than t will be considered |
| d1  | Negative integer. Minimum relative position regarding the start of the gene to be considered   |
| d2  | Positive integer. Maximum relative position regarding the end of the gene to be considered     |

Value

data.frame structure where each row represents one relative position, and each column being:

|          |                                                   |
|----------|---------------------------------------------------|
| peakName | read-enriched region name                         |
| p1       | relative position regarding the start of the gene |
| p2       | relative position regarding the end of the gene   |
| gene     | name of the gene                                  |
| le       | length (bp) of the gene                           |

Author(s)

Jose M Muino, <jose.muino@wur.nl>

References

Muino et al. (submitted). Plant ChIP-seq Analyzer: An R package for the statistical detection of protein-bound genomic regions.  
Kaufmann et al.(2009).Target genes of the MADS transcription factor SEPALLATA3: integration of developmental and hormonal pathways in the Arabidopsis flower. PLoS Biology; 7(4):e1000090.

See Also

genesWithPeaks, CSAR-package

Examples

```
##For this example we will use the a subset of the SEP3 ChIP-seq data (Kaufmann, 2009)
data("CSAR-dataset");
##We calculate the number of hits for each nucleotide posotion for the control and sample. We do that just for chromo
nhitsS<-mappedReads2Nhits(sampleSEP3_test,file="sampleSEP3_test",chr=c("CHR1v01212004"),chrL=c(10000))
nhitsC<-mappedReads2Nhits(controlSEP3_test,file="controlSEP3_test",chr=c("CHR1v01212004"),chrL=c(10000))

##We calculate a score for each nucleotide position
test<-ChIPseqScore(control=nhitsC,sample=nhitsS)

##We calculate the candidate read-enriched regions
win<-sigWin(test)

##We calculate relative positions of read-enriched regions regarding gene position
d<-distance2Genes(win=win,gff=TAIR8_genes_test)
```

---

|                |                                                                              |
|----------------|------------------------------------------------------------------------------|
| genesWithPeaks | <i>Provide table of genes with read-enriched regions, and their location</i> |
|----------------|------------------------------------------------------------------------------|

---

Description

Provide table of genes with read-enriched regions, and their location

Usage

genesWithPeaks(distances)

Arguments

distances            data.frame structure obtained by distances2Genes

**Details**

This function report for each gene, the maximum peak score in different regions near of the gene. The input of the function is the distances between genes and peaks calculated by distance2Genes

**Value**

data.frame structure with each coloumn being:

|           |                                                                     |
|-----------|---------------------------------------------------------------------|
| name      | name of the gene                                                    |
| max3kb1kb | maximum score value for the region 3Kb upstream to 1Kb downstream   |
| u3000     | maximum score value for the region 3Kb upstream to 2Kb upstream     |
| u2000     | maximum score value for the region 2Kb upstream to 1Kb upstream     |
| u1000     | maximum score value for the region 1Kb upstream to 0Kb upstream     |
| d0        | maximum score value for the region 0Kb upstream to 0Kb downstream   |
| d1000     | maximum score value for the region 0Kb downstream to 1Kb downstream |

**Author(s)**

Jose M Muino, <jose.muino@wur.nl>

**References**

Muino et al. (submitted). Plant ChIP-seq Analyzer: An R package for the statistcal detection of protein-bound genomic regions.  
 Kaufmann et al.(2009).Target genes of the MADS transcription factor SEPALLATA3: integration of developmental and hormonal pathways in the Arabidopsis flower. PLoS Biology; 7(4):e1000090.

**See Also**

distance2Genes,CSAR-package

**Examples**

```
##For this example we will use the a subset of the SEP3 ChIP-seq data (Kaufmann, 2009)
data("CSAR-dataset");
##We calculate the number of hits for each nucleotide posotion for the control and sample. We do that just for chromo
nhitsS<-mappedReads2Nhits(sampleSEP3_test,file="sampleSEP3_test",chr=c("CHR1v01212004"),chrL=c(10000))
nhitsC<-mappedReads2Nhits(controlSEP3_test,file="controlSEP3_test",chr=c("CHR1v01212004"),chrL=c(10000))

##We calculate a score for each nucleotide position
test<-ChIPseqScore(control=nhitsC,sample=nhitsS)

##We calculate the candidate read-enriched regions
win<-sigWin(test)

##We calculate relative positions of read-enriched regions regarding gene position
d<-distance2Genes(win=win,gff=TAIR8_genes_test)
```

```
##We calculate table of genes with read-enriched regions, and their location  
genes<-genesWithPeaks(d)
```

---

```
getPermutatedWinScores
```

*Obtain the read-enrichment score distribution under the null hypothesis*

---

### Description

Obtain the read-enrichment score distribution under the null hypothesis

### Usage

```
getPermutatedWinScores(file, nn)
```

### Arguments

|      |                                                   |
|------|---------------------------------------------------|
| file | Name of the file generated by permutatedWinScores |
| nn   | ID for the multiple permutation process           |

### Value

Numeric vector of score values under permutation

### Author(s)

Jose M Muino, <jose.muino@wur.nl>

### References

Muino et al. (submitted). Plant ChIP-seq Analyzer: An R package for the statistical detection of protein-bound genomic regions.  
Kaufmann et al.(2009).Target genes of the MADS transcription factor SEPALLATA3: integration of developmental and hormonal pathways in the Arabidopsis flower. PLoS Biology; 7(4):e1000090.

### See Also

CSAR-package, permutatedWinScores



## Examples

```
##For this example we will use the a subset of the SEP3 ChIP-seq data (Kaufmann, 2009)
data("CSAR-dataset");
##We calculate the number of hits for each nucleotide posotion for the control and sample. We do that just for chromo
nhitsS<-mappedReads2Nhits(sampleSEP3_test,file="sampleSEP3_test",chr=c("CHR1v01212004"),chrL=c(10000))
nhitsC<-mappedReads2Nhits(controlSEP3_test,file="controlSEP3_test",chr=c("CHR1v01212004"),chrL=c(10000))

##We calculate two sets of read-enrichment scores through permutation
permutedWinScores(nn=1,sample=sampleSEP3_test,control=controlSEP3_test,fileOutput="test",chr=c("CHR1v01212004"),chrL=c(10000))
permutedWinScores(nn=2,sample=sampleSEP3_test,control=controlSEP3_test,fileOutput="test",chr=c("CHR1v01212004"),chrL=c(10000))

###Next function will get all permuted score values generated by permutedWinScores function.
##This represent the score distribution under the null hypotesis and therefore it can be use to control the error of
nulldist<-getPermutedWinScores(file="test",nn=1:2)
```

---

|              |                                                                                      |
|--------------|--------------------------------------------------------------------------------------|
| getThreshold | <i>Calculate the threshold value corresponding to control FDR at a desired level</i> |
|--------------|--------------------------------------------------------------------------------------|

---

## Description

Calculate the threshold value corresponding to control FDR at a desired level

## Usage

```
getThreshold(winscores, permutedScores, FDR)
```

## Arguments

|                |                                                                    |
|----------------|--------------------------------------------------------------------|
| winscores      | Numeric vector with score values obtained from the sigWin function |
| permutedScores | Numeric vector with the permuted read-enrichment score values      |
| FDR            | Numeric value with the desired FDR control                         |

## Details

This is a very simple function to obtain the threshold value of our test statistic controlling FDR at a desired level. Other functions implemented in R (eg: multtest) could be more sophisticated. Basically, for each possible threshold value, the proportion of error type I is calculated assuming that the permuted score distribution is a optimal estimation of the score distribution under the null hypothesis. This is, the proportion of permuted scores exceding the considered threshold value is used as an estimation of the error type I of our stastitic. FDR is obtained as the ratio of the proportion of error type I by the proportion of significant tests.

**Value**

A table with the columns being:

|           |                                                          |
|-----------|----------------------------------------------------------|
| threshold | The threshold value                                      |
| p-value   | The p-value obtained from the permuted score ditribution |
| FDR       | The FDR control obtained using threshold                 |

**Author(s)**

Jose M Muino, <jose.muino@wur.nl>

**References**

Muino et al. (submitted). Plant ChIP-seq Analyzer: An R package for the statistical detection of protein-bound genomic regions.

Kaufmann et al.(2009).Target genes of the MADS transcription factor SEPALLATA3: integration of developmental and hormonal pathways in the Arabidopsis flower. PLoS Biology; 7(4):e1000090.

**See Also**

CSAR-package, getPermutatedWinScores, sigWin

**Examples**

```
##For this example we will use the a subset of the SEP3 ChIP-seq data (Kaufmann, 2009)
data("CSAR-dataset");
##We calculate the number of hits for each nucleotide posotion for the control and sample. We do that just for chromo
nhitsS<-mappedReads2Nhits(sampleSEP3_test,file="sampleSEP3_test",chr=c("CHR1v01212004"),chrL=c(10000))
nhitsC<-mappedReads2Nhits(controlSEP3_test,file="controlSEP3_test",chr=c("CHR1v01212004"),chrL=c(10000))

##We calculate a score for each nucleotide position
test<-ChIPseqScore(control=nhitsC,sample=nhitsS)

##We calculate the candidate read-enriched regions
win<-sigWin(test)

##We calculate two sets of read-enrichment scores through permutation
permutatedWinScores(nn=1,sample=sampleSEP3_test,control=controlSEP3_test,fileOutput="test",chr=c("CHR1v01212004"),chrL=c(10000))
permutatedWinScores(nn=2,sample=sampleSEP3_test,control=controlSEP3_test,fileOutput="test",chr=c("CHR1v01212004"),chrL=c(10000))

###Next function will get all permutated score values generated by permutatedWinScores function.
##This represent the score distribution under the null hypotesis and therefore it can be use to control the error of
nullldist<-getPermutatedWinScores(file="test",nn=1:2)

##From this distribution, several cut-off values can be calculated to control the error of our test.
##Several functions in R can be used for this purpose.
##In this package we had implemented a simple method for the control of the error based on FDR"
getThreshold(winscores=values(win)$score,permutatedScores=nullldist,FDR=.01)
```

---

|                 |                          |
|-----------------|--------------------------|
| loadMappedReads | <i>Load mapped reads</i> |
|-----------------|--------------------------|

---

**Description**

This function load the output file of a read mapping software (eg:SOAP)

**Usage**

```
loadMappedReads(file, format = "SOAP", header = FALSE)
```

**Arguments**

|        |                                                                                                                                                                                                                                                                 |
|--------|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| file   | File name to load                                                                                                                                                                                                                                               |
| format | Format of the file. "SOAP" for the output of the soap software and "MAQ" for the maq software. Other user formats can be provided as a character vector for the file column names. Columns named: "Nhits", "lengthRead", "strand", "chr", and "pos" are needed. |
| header | Logical value indicating if the first line of the file should be skipped (TRUE) or not (FALSE)                                                                                                                                                                  |

**Value**

data.frame structure that can be used by mappedReads2Nhits

**Author(s)**

Jose M Muino, <jose.muino@wur.nl>

**References**

Muino et al. (submitted). Plant ChIP-seq Analyzer: An R package for the statistical detection of protein-bound genomic regions.  
Kaufmann et al.(2009).Target genes of the MADS transcription factor SEPALLATA3: integration of developmental and hormonal pathways in the Arabidopsis flower. PLoS Biology; 7(4):e1000090.

**See Also**

CSAR-package

**Examples**

```
##We load the mapped reads:  
#sample<-loadMappedReads(file=file,format="SOAP",w=300,header=F)  
##where file is the name and path of the output file of the mapping process.
```

---

|                   |                                                                              |
|-------------------|------------------------------------------------------------------------------|
| mappedReads2Nhits | <i>Calculate number of overlapped extended reads per nucleotide position</i> |
|-------------------|------------------------------------------------------------------------------|

---

### Description

Calculate number of overlapped extended reads per nucleotide position

### Usage

```
mappedReads2Nhits(input, file, chr = c("chr1", "chr2", "chr3", "chr4", "chr5"), chrL = "TAIR9", w = 300)
```

### Arguments

|                |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |
|----------------|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| input          | data loaded with loadMappedReads or an AlignedRead object from the Short-Read package                                                                                                                                                                                                                                                                                                                                                                                           |
| file           | Name of the file where the results will be saved. If NA the results will not be saved in a file.                                                                                                                                                                                                                                                                                                                                                                                |
| chr            | Character vector containing the chromosome names as identified on input.                                                                                                                                                                                                                                                                                                                                                                                                        |
| chrL           | Numeric vector containing the length (bp) of the chromosomes. It should be in the same order than chr                                                                                                                                                                                                                                                                                                                                                                           |
| w              | Integer corresponding to the desired length of the extended reads. An advised value will be the average fragment length of the DNA submitted to sequence (usually 300 bp).                                                                                                                                                                                                                                                                                                      |
| considerStrand | Character value.<br>"Minimum"=>Default value. Report the minimum number of hits at each nucleotide position for both strands.<br>"Foward"=> Report the number of hits at each nucleotide position for the "foward" strands (the one denoted as "+" in q).<br>"Reverse"=>Report the number of hits at each nucleotide position for the "reverse" strands (the one denoted as "-" in q).<br>"Sum"=>Report the sum of number of hits at each nucleotide position for both strands. |
| uniquelyMapped | Logic value, If TRUE, only consider uniquely mapped reads.                                                                                                                                                                                                                                                                                                                                                                                                                      |
| uniquePosition | Logic value. If TRUE, only consider reads mapped in different positions.                                                                                                                                                                                                                                                                                                                                                                                                        |

### Value

A list to be used for other functions of the CSAR package

|        |                                                                |
|--------|----------------------------------------------------------------|
| chr    | Chromosome names                                               |
| chrL   | Chromosome length (bp)                                         |
| chrL_0 | Number of nucleotide positions with at least one extended read |
| chrL_0 | Number of nucleotide positions with at least one extended read |

|           |                                                        |
|-----------|--------------------------------------------------------|
| filenames | Name of the files where the Nhits values are stored    |
| c1        | Sum of all the Nhits values for each chromosome        |
| c2        | Sum of all the Nhits square values for each chromosome |

**Author(s)**

Jose M Muino, <jose.muino@wur.nl>

**References**

Muino et al. (submitted). Plant ChIP-seq Analyzer: An R package for the statistical detection of protein-bound genomic regions.

Kaufmann et al.(2009).Target genes of the MADS transcription factor SEPALLATA3: integration of developmental and hormonal pathways in the Arabidopsis flower. PLoS Biology; 7(4):e1000090.

**See Also**

CSAR-package

**Examples**

```
#For this example we will use the a subset of the SEP3 ChIP-seq data (Kaufmann, 2009)
data("CSAR-dataset");
#We calculate the number of hits for each nucleotide posotion for the sample. We do that just for chromosome chr1, an
nhitsS<-mappedReads2Nhits(sampleSEP3_test,file="sampleSEP3_test",chr=c("CHR1v01212004"),chrL=c(10000))
```

---

|                     |                                                              |
|---------------------|--------------------------------------------------------------|
| permutatedWinScores | <i>Calculate scores for permutated read-enriched regions</i> |
|---------------------|--------------------------------------------------------------|

---

**Description**

Calculate scores for permutated read-enriched regions

**Usage**

```
permutatedWinScores(nn = 1, control, sample, fileOutput, chr = c("chr1", "chr2", "chr3", "chr4", "chr5"))
```

**Arguments**

|            |                                                                                               |
|------------|-----------------------------------------------------------------------------------------------|
| nn         | ID to identify each permutation                                                               |
| control    | data.frame structure obtained by loading the mapped reads with the function LoadMappedReads() |
| sample     | data.frame structure obtained by loading the mapped reads with the function LoadMappedReads() |
| fileOutput | Name of the file were the results will be written                                             |

|                |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |
|----------------|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| chr            | Character vector containing the chromosome names as identified on q.                                                                                                                                                                                                                                                                                                                                                                                                            |
| chrL           | Numeric vector containing the length (bp) of the chromosomes. It should be in the same order than chr                                                                                                                                                                                                                                                                                                                                                                           |
| w              | Integer corresponding to the desired length of the extended reads.                                                                                                                                                                                                                                                                                                                                                                                                              |
| considerStrand | Character value.<br>"Minimum"=>Default value. Report the minimum number of hits at each nucleotide position for both strands.<br>"Foward"=> Report the number of hits at each nucleotide position for the "foward" strands (the one denoted as "+" in q).<br>"Reverse"=>Report the number of hits at each nucleotide position for the "reverse" strands (the one denoted as "-" in q).<br>"Sum"=>Report the sum of number of hits at each nucleotide position for both strands. |
| uniquelyMapped | Logic value, If TRUE, only consider uniquely mapped reads.                                                                                                                                                                                                                                                                                                                                                                                                                      |
| uniquePosition | Logic value. If TRUE, only consider reads mapped in different positions.                                                                                                                                                                                                                                                                                                                                                                                                        |
| norm           | Integer value. Number of hits will be reported by number of hits per norm nucleotides                                                                                                                                                                                                                                                                                                                                                                                           |
| backg          | Any region with a hit value lower than backg in the control will be set to the value of backg                                                                                                                                                                                                                                                                                                                                                                                   |
| t              | Numeric value. Read-enriched regions are calculated as genomic regions with score values bigger than t                                                                                                                                                                                                                                                                                                                                                                          |
| g              | Integer value. The maximum gap allowed between regions. Regions that are less than g bps away will be merged.                                                                                                                                                                                                                                                                                                                                                                   |
| times          | To be memory efficient, CSAR will only upload to the RAM memory fragments of length times. A bigger value means more RAM memory needed but whole process will be faster                                                                                                                                                                                                                                                                                                         |
| digits         | Number of decimal digits used to report the score values                                                                                                                                                                                                                                                                                                                                                                                                                        |
| test           | Use a score based on the poisson distribution ("Poisson") or in the ratio ("Ratio")                                                                                                                                                                                                                                                                                                                                                                                             |

### Details

The parameter values should be the same than the one used in sigWin, ChIPseqScore, and mappedReads2Nhits. The label "control" and "sample" is assigned to each read to identify from which group they came. Labels are randomly permuted, and read-enriched regions for this new permuted dataset are calculated.

### Value

The file filePutput is created with its values being the permuted score values.

### Author(s)

Jose M Muino, <jose.muino@wur.nl>

References

Muino et al. (submitted). Plant ChIP-seq Analyzer: An R package for the statistical detection of protein-bound genomic regions.  
Kaufmann et al.(2009).Target genes of the MADS transcription factor SEPALLATA3: integration of developmental and hormonal pathways in the Arabidopsis flower. PLoS Biology; 7(4):e1000090.

See Also

CSAR-package,getPermutatedWinScores

Examples

```
##For this example we will use the a subset of the SEP3 ChIP-seq data (Kaufmann, 2009)
data("CSAR-dataset");
##We calculate the number of hits for each nucleotide posotion for the control and sample. We do that just for chromo
nhitsS<-mappedReads2Nhits(sampleSEP3_test,file="sampleSEP3_test",chr=c("CHR1v01212004"),chrL=c(10000))
nhitsC<-mappedReads2Nhits(controlSEP3_test,file="controlSEP3_test",chr=c("CHR1v01212004"),chrL=c(10000))

##We calculate two sets of read-enrichment scores through permutation
permutatedWinScores(nn=1,sample=sampleSEP3_test,control=controlSEP3_test,fileOutput="test",chr=c("CHR1v0121200
permutatedWinScores(nn=2,sample=sampleSEP3_test,control=controlSEP3_test,fileOutput="test",chr=c("CHR1v0121200
```

---

|                 |                                                 |
|-----------------|-------------------------------------------------|
| sampleSEP3_test | <i>Partial dataset of a ChIP-seq experiment</i> |
|-----------------|-------------------------------------------------|

---

Description

Partial dataset of a Solexa DNA library obtained from a ChIP-seq experiment in Arabidopsis

Source

Kaufmann et al. (2009) Target Genes of the MADS Transcription Factor SEPALLATA3: Integration of Developmental and Hormonal Pathways in the \$Arabidopsis\$ Flower. PLoS Biol 7:e1000090

Examples

```
data(CSAR-dataset)
```

---

|           |                                                                                          |
|-----------|------------------------------------------------------------------------------------------|
| score2wig | <i>Save the read-enrichment scores at each nucleotide position in a .wig file format</i> |
|-----------|------------------------------------------------------------------------------------------|

---

## Description

Save the read-enrichment scores at each nucleotide position in a .wig file format that can be visualize by a genome browser (eg: Integrated Genome Browser)

## Usage

```
score2wig(experiment, file, t = 2, times = 1e6,description="", name="")
```

## Arguments

|             |                                                                                                                                                                         |
|-------------|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| experiment  | Output of the function ChIPseqScore                                                                                                                                     |
| file        | Name of the output .wig file                                                                                                                                            |
| t           | Only nucleotide positions with a read-enrichment score bigger than t will be reported                                                                                   |
| times       | To be memory efficient, CSAR will only upload to the RAM memory fragments of length times. A bigger value means more RAM memory needed but whole process will be faster |
| description | Character. It adds a description to the wig file. The description will be shown by the genome browser used to visualize the wig file.                                   |
| name        | Character. It adds a wig to the wig file. The name will be shown by the genome browser used to visualize the wig file.                                                  |

## Value

None. Results are printed in a file

## Author(s)

Jose M Muino, <jose.muino@wur.nl>

## References

Muino et al. (submitted). Plant ChIP-seq Analyzer: An R package for the statistical detection of protein-bound genomic regions.  
Kaufmann et al.(2009).Target genes of the MADS transcription factor SEPALLATA3: integration of developmental and hormonal pathways in the Arabidopsis flower. PLoS Biology; 7(4):e1000090.

## See Also

CSAR-package



## Examples

```
##For this example we will use the a subset of the SEP3 ChIP-seq data (Kaufmann, 2009)
data("CSAR-dataset");
##We calculate the number of hits for each nucleotide position for the control and sample. We do that just for chromosome 1
nhitsS<-mappedReads2Nhits(sampleSEP3_test,file="sampleSEP3_test",chr=c("CHR1v01212004"),chrL=c(10000))
nhitsC<-mappedReads2Nhits(controlSEP3_test,file="controlSEP3_test",chr=c("CHR1v01212004"),chrL=c(10000))

##Since we will not need the raw data anymore, we could delete it from the RAM memory
rm(sampleSEP3_test,controlSEP3_test);gc(verbose=FALSE)
##We calculate a score for each nucleotide position
test<-ChIPseqScore(control=nhitsC,sample=nhitsS)

##We generate a wig file of the results to visualize them in a genome browser
score2wig(test,file="test.wig")
```

sigWin

*Calculate regions of read-enrichment*

## Description

Calculate regions of read-enrichment

## Usage

```
sigWin(experiment, t = 1, g = 100)
```

## Arguments

|            |                                                                                                               |
|------------|---------------------------------------------------------------------------------------------------------------|
| experiment | Output of the function ChIPseqScore                                                                           |
| t          | Numeric value. Read-enriched regions are calculated as genomic regions with score values bigger than t        |
| g          | Integer value. The maximum gap allowed between regions. Regions that are less than g bps away will be merged. |

## Value

An object of type 'GRange' with its values being:

|          |                                                                        |
|----------|------------------------------------------------------------------------|
| seqnames | Chromosome name                                                        |
| ranges   | An IRanges object indicating start and end of the read-enriched region |
| posPeak  | Position of the maximum score value on the read-enriched region        |
| score    | Maximum score value on the read-enriched region                        |

## Author(s)

Jose M Muino, <jose.muino@wur.nl>

## References

Muino et al. (submitted). Plant ChIP-seq Analyzer: An R package for the statistical detection of protein-bound genomic regions.

Kaufmann et al.(2009).Target genes of the MADS transcription factor SEPALLATA3: integration of developmental and hormonal pathways in the Arabidopsis flower. PLoS Biology; 7(4):e1000090.

## See Also

CSAR-package

## Examples

```
##For this example we will use the a subset of the SEP3 ChIP-seq data (Kaufmann, 2009)
data("CSAR-dataset");
##We calculate the number of hits for each nucleotide posotion for the control and sample. We do that just for chromo
nhitsS<-mappedReads2Nhits(sampleSEP3_test,file="sampleSEP3_test",chr=c("CHR1v01212004"),chrL=c(10000))
nhitsC<-mappedReads2Nhits(controlSEP3_test,file="controlSEP3_test",chr=c("CHR1v01212004"),chrL=c(10000))

##We calculate a score for each nucleotide position
test<-ChIPseqScore(control=nhitsC,sample=nhitsS)

##We calculate the candidate read-enriched regions
win<-sigWin(test)
```

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