

# CSAR

April 12, 2012

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CSAR-package

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

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## 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

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## 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.

## 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
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 them 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"))
permutatedWinScores(nn=2,sample=sampleSEP3_test,control=controlSEP3_test,fileOutput="test",chr=c("CHR1v01212004"))

###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 used to control the test.
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)

```

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ChIPseqScore

*Calculate read-enrichment scores for each nucleotide position*


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## 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,
```

## 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 want 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 normalized to have the same mean and variance than the control, for each chromosome independently or for the whole set of chromosomes (depending on the value of normEachChrInd). Due to 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 stored
digits	Score values stored 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 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
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)
```

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

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genesWithPeaks

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

---

**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 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**

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 position for the control and sample. We do that just
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)
```

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```
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**

<code>file</code>	Name of the file generated by <code>permutatedWinScores</code>
<code>nn</code>	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
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("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
nullldist<-getPermutatedWinScores(file="test",nn=1:2)
```

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

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

### Usage

```
getThreshold(winscores, permutatedScores, FDR)
```

### Arguments

winscores	Numeric vector with score values obtained from the sigWin function
permutatedScores	Numeric vector with the permutated 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: multttest) could be more sophisticated. Basically, for each possible threshold value, the proportion of error type I is calculated assuming that the permutated score distribution is a optimal estimation of the score distribution under the null hypothesis. This is, the proportion of permutated scores exceding the considered threshold value is used as an estimation of the error type I of our statistic. 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 permutated 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 position for the control and sample. We do that just
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
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)

```

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

**Description**

Calculate number of overlapped extended reads per nucleotide position

**Usage**

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

**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. "Minimum"=>Default value. Report the minimum number of hits at each nucleotide position for both strands. "Foward"=> Report the number of hits at each nucleotide position for the "foward" strands (the one denoted as "+" in q).

"Reverse"=>Report the number of hits at each nucleotide position for the "reverse" strands (the one denoted as "-" in q).

"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_1	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 position for the sample. We do that just for chromosome 1
nhitsS<-mappedReads2Nhits(sampleSEP3_test,file="sampleSEP3_test",chr=c("CHR1v01212004"),chrL=c(10000))
```

---

permutatedWinScores     *Calculate scores for permutated read-enriched regions*

---

### Description

Calculate scores for permutated read-enriched regions

### Usage

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

### 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. "Minimum"=>Default value. Report the minimum number of hits at each nucleotide position for both strands. "Foward"=> Report the number of hits at each nucleotide position for the "foward" strands (the one denoted as "+" in q). "Reverse"=>Report the number of hits at each nucleotide position for the "reverse" strands (the one denoted as "-" in q). "Sum"=>Report the sum of number of hits at each nucleotide position for both strands.
uniquelyMapped	Logic value, If TRUE, only consider unquely 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 position for the control and sample. We do that just
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("CHR1v01212004"),chrL=c(10000))
permutatedWinScores(nn=2,sample=sampleSEP3_test,control=controlSEP3_test,fileOutput="test",chr=c("CHR1v01212004"),chrL=c(10000))
```

---

sampleSEP3\_test

*Partial dataset of a ChIP-seq experiment*

---

**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
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	<i>Calculate regions of read-enrichment</i>
--------	---

---

## 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 position for the control and sample. We do that just
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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