Package: ChIPanalyser (via r-universe)

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Type Package

Title ChIPanalyser: Predicting Transcription Factor Binding Sites

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Citation Zabet NR, Adryan B (2015) Estimating binding properties of transcription factors from genome-wide binding profiles. Nucleic Acids Res., 43, 84–94.

Description ChIPanalyser is a package to predict and understand TF binding by utilizing a statistical thermodynamic model. The model incorporates 4 main factors thought to drive TF binding: Chromatin State, Binding energy, Number of bound molecules and a scaling factor modulating TF binding affinity. Taken together, ChIPanalyser produces ChIP-like profiles that closely mimic the patterns seens in real ChIP-seq data.

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Collate 2AllS4Class_ProfileParameters.R 3AllGenerics.R 4AllMethods.R AllInitialize.R AllShowMethods.R computeChIPProfile.R computeOccupancy.R computeOptimal.R computePWMScore.R computeGenomeWide.R parallelInternalFunctionsDev.R GenomicProfileGenericFunctions.R plotOccupancy.R plotOptimalHeatMapDev.R DataPreprocessingDev.R DataPreprocessingGenericFunctionsDev.R profileAccuracyEstimateDev.R GAAnalysis.R GAGeneric.R

Depends R (>= 3.5.0),GenomicRanges, Biostrings, BSgenome, RcppRoll, parallel

Imports methods, IRanges, S4Vectors,grDevices,graphics,stats,utils,rtracklayer,ROCR, BiocManager,GenomeInfoDb,RColorBrewer

Suggests BSgenome.Dmelanogaster.UCSC.dm6,knitr, RUnit, BiocGenerics

Encoding UTF-8

LazyData true

biocViews Software, BiologicalQuestion, WorkflowStep, Transcription, Sequencing, ChipOnChip, Coverage, Alignment, ChIPSeq, SequenceMatching, DataImport ,PeakDetection

VignetteBuilder knitr

RoxygenNote 7.2.1

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`ChIPanalyser-package` *ChIPanalyser: Predicting Transcription Factor Binding Sites*

Description

ChIPanalyser is a package to predict and understand TF binding by utilizing a statistical thermodynamic model. The model incorporates 4 main factors thought to drive TF binding: Chromatin State, Binding energy, Number of bound molecules and a scaling factor modulating TF binding affinity. Taken together, ChIPanalyser produces ChIP-like profiles that closely mimic the patterns seens in real ChIP-seq data.

Details

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Index: This package was not yet installed at build time.

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References

Zabet NR, Adryan B (2015) Estimating binding properties of transcription factors from genome-wide binding profiles. Nucleic Acids Res., 43, 84–94.

Examples

```
#Data extraction
data(ChIPanalyserData)
# path to Position Frequency Matrix
PFM <- file.path(system.file("extdata",package="ChIPanalyser"),"BEAF-32.pfm")
#As an example of genome, this example will run on the Drosophila genome

if(!require("BSgenome.Dmelanogaster.UCSC.dm6", character.only = TRUE)){
    if (!requireNamespace("BiocManager", quietly=TRUE))
        install.packages("BiocManager")
    BiocManager::install("BSgenome.Dmelanogaster.UCSC.dm6")
}
library(BSgenome.Dmelanogaster.UCSC.dm6)
DNASequenceSet <- getSeq(BSgenome.Dmelanogaster.UCSC.dm6)
#Building data objects
GPP <- genomicProfiles(PFM=PFM,PFMFormat="JASPAR",BPFrequency=DNASequenceSet)

chip<-processingChIP(chip,top)
# Computing Genome Wide
GenomeWide <- computeGenomeWideScores(DNASequenceSet = DNASequenceSet,
    genomicsProfiles = GPP)

#Compute PWM Scores
PWMScores <- computePWMScore(genomicsProfiles = GenomeWide,
    DNASequenceSet = DNASequenceSet,
    loci = top, chromatinState = Access)
#Compute Occupnacy
Occupancy <- computeOccupancy(genomicsProfiles = PWMScores,
    parameterOptions = OPP)

#Compute ChIP profiles
chipProfile <- computeChIPProfile(genomicProfiles = Occupancy,
     loci = top,
    parameterOptions = OPP)
#Estimating accuracy estimate
AccuracyEstimate <- profileAccuracyEstimate(genomicProfiles = chipProfile,
     ChIPScore = chip,
     parameterOptions = OPP)
```

---

averageExpPWMScore *Accessor for* averageExpPWMScore *slot in a* genomicProfiles *object.*

Description

Extract or Access averageExpPWMScore slot in a genomicProfiles

Usage

```
averageExpPWMScore(object)
```

Arguments

object	object is a genomicProfiles

Details

As a general rule, averageExpPWMScore is computed and updated internally by computeGenomeWideScores. Idealy, this slot should not be updated by user. The averageExpPWMScore is the sum of the exponential of every PWM score for a given DNA sequence and divided by the length of the said DNA sequence (DNASequenceLength). This can either be the full length sequence or only the accessible sequence (see computeGenomeWideScores).

Value

Returns the averageExpPWMScore of a genomicProfiles when computed.

Author(s)

Patrick C.N. Martin <pcnmartin@gmail.com>

References

Zabet NR, Adryan B (2015) Estimating binding properties of transcription factors from genome-wide binding profiles. Nucleic Acids Res., 43, 84–94.

Examples

```
# Accessing Data
data(ChIPanalyserData)
# path to Position Frequency Matrix
PFM <- file.path(system.file("extdata",package="ChIPanalyser"),"BEAF-32.pfm")
# Building genomicProfiles object
GPP <- genomicProfiles(PFM=PFM,PFMFormat="JASPAR")
# Extracting AllSitesAboveThreshold slot
averageExpPWMScore(GPP)

## Note this slot is now empty as nothing has yet been computed
```

averageExpPWMScore-methods *~~ Methods for Function* averageExpPWMScore *~~*

Description

~~ Methods for function averageExpPWMScore ~~

Methods:

signature(object = "genomicProfilesInternal")

backgroundSignal *Accessor method for the* backgroundSignal *slot in a* parameterOptions *object.*

Description

Extract or access the backgroundSignal slot in a parameterOptions object.

Usage

```
backgroundSignal(object)
```

Arguments

object	object is an parameterOptions

Details

Default Value: 0

When computing computeOccupancy, a ChIP-seq background signal is used to scale Occupancy by considering both a backgroundSignal and a maxSignal. The backgroundSignal is also used to nomalise occupancies against maxOccupancy. The backgroundSignal usually comes from experimental data and is provided by user. As a general rule, if ChIP-seq data is available and will be used in computeChIPProfile , profileAccuracyEstimate or plotOccupancyProfile, it is advised to use the backgroundSignal from this data. We strongly encourage to set values when building a parameterOptions object.

Value

Returns a backgroundSignal of a parameterOptions object.

Author(s)

Patrick C.N. Martin <pcnmartin@gmail.com>

References

Zabet NR, Adryan B (2015) Estimating binding properties of transcription factors from genome-wide binding profiles. Nucleic Acids Res., 43, 84–94. Patrick C.N. Martin and Nicolae Radu Zabe (2020) Dissecting the binding mechanisms of transcription factors to DNA using a statistical thermodynamics framework. CSBJ, 18, 3590-3605.

Examples

```
# Building occupancyProfileParameters object
OPP <- parameterOptions()
#Viewing single value in object
backgroundSignal(OPP)
```

---

backgroundSignal-methods

~~ *Methods for Function* backgroundSignal ~~

Description

~~ Methods for function backgroundSignal ~~

Methods:

signature(object = "parameterOptions")

---

backgroundSignal<- *Setter method for* backgroundSignal *slot in a* parameterOptions

---

Description

Setter method for backgroundSignal slot in a parameterOptions

Usage

```
backgroundSignal(object)<-value
```

Arguments

object	object is an parameterOptions object.
value	value is the value to be assigned to the backgroundSignal slot in parameterOptions. backgroundSignal should be a positive value. Defualt value is 0.

Details

Defualt value: 0. When computing computeOccupancy, a ChIP-seq background signal is used to scale Occupancy by considering both a backgroundSignal and a maxSignal. The backgroundSignal is also used to nomalise occupancies to maxOccupancy. The backgroundSignal usually comes from experimental data and is provided by user. As a general rule, if ChIP-seq data is available and will be used in computeChIPProfile , profileAccuracyEstimate or plotOccupancyProfile, it is advised to use the backgroundSignal from this data. We strongly encourage to set values when building a parameterOptions object.

Value

Returns a parameterOptions object with a new value assigned to the backgroundSignal slot.

Author(s)

Patrick C.N. Martin <pcnmartin@gmail.com>

References

Zabet NR, Adryan B (2015) Estimating binding properties of transcription factors from genome-wide binding profiles. Nucleic Acids Res., 43, 84–94. Patrick C.N. Martin and Nicolae Radu Zabe (2020) Dissecting the binding mechanisms of transcription factors to DNA using a statistical thermodynamics framework. CSBJ, 18, 3590-3605.

Examples

```
# Building occupancyProfileParameters object
OPP <- parameterOptions()
# Setting new value for backgroundSignal
backgroundSignal(OPP) <- 0.2
# Viewing whole object with new updated value
OPP
#Viewing single value in object
backgroundSignal(OPP)
```

---

backgroundSignal<-methods

~~ *Methods for Function* backgroundSignal<- ~~

Description

~~ Methods for function backgroundSignal<- ~~

Methods:

backgroundSignal(object)<-value

boundMolecules *Accessor methods for* boundMolecules *slot in* parameterOptions *object.*

Description

Extract or Access boundMolecules slot in parameterOptions object.

Usage

```
boundMolecules(object)
```

Arguments

object	object is a parameterOptions object.

Details

Defaut value: 1000

When computing occupancy (computeOccupancy), a value for the number of bound Molecules to DNA is needed. This value can be updated and set in a parameterOptions object. If the number of molecules is unknown,it is possible to infer this value with computeOptimal. We strongly encourage to set values when building a parameterOptions object.

Value

Returns boundMolecules slot in parameterOptions object.

Author(s)

Patrick C.N. Martin <pcnmartin@gmail.com>

References

Zabet NR, Adryan B (2015) Estimating binding properties of transcription factors from genome-wide binding profiles. Nucleic Acids Res., 43, 84–94.

Examples

```
# Building parameterOptions object
OPP <- parameterOptions()
#Checking single value by slot accessor
boundMolecules(OPP)
```

---

boundMolecules-methods

~~ *Methods for Function* boundMolecules ~~

Description

~~ Methods for function boundMolecules ~~

Methods:

signature(object = "parameterOptions")

---

boundMolecules<- *Setter method for the* boundMolecules *slot in a* parameterOptions *object.*

Description

Setter method for the boundMolecules slot in a parameterOptions object.

Usage

```
boundMolecules(object)<-value
```

Arguments

object	object is a parameterOptions object.
value	value is a positive integer or vector of positive integers describing the number ofmolecules bound to DNA. Defaut value is 1000.

Details

Default value: 1000 When computing occupancy (computeOccupancy), a value for the number of bound Molecules to DNA is needed. This value can be updated and set in a parameterOptions object. If the number of molecules is unknown, it is possible to infer this value with computeOptimal. We strongly encourage to set values when building a parameterOptions object.

Value

Returns a parameterOptions object with an updated value for boundMolecules.

Author(s)

Patrick C.N. Martin <pcnmartin@gmail.com>

References

Zabet NR, Adryan B (2015) Estimating binding properties of transcription factors from genome-wide binding profiles. Nucleic Acids Res., 43, 84–94. Patrick C.N. Martin and Nicolae Radu Zabe (2020) Dissecting the binding mechanisms of transcription factors to DNA using a statistical thermodynamics framework. CSBJ, 18, 3590-3605.

Examples

```
# Building parameterOptions object
OPP <- parameterOptions()
# Setting new boundMolecules value in OPP
boundMolecules(OPP) <- 5000
#Checking value in whole object
OPP
#Checking single value by slot accessor
boundMolecules(OPP)
```

`boundMolecules<-methods` *~~ Methods for Function* `boundMolecules<-` *~~*

Description

~~ Methods for function `boundMolecules<-` ~~

Methods:

`signature(object = "parameterOptions", value = "vector")`

`BPFrequency` *Accessor method for* `BPFrequency` *slot in a* `genomicProfiles` *object.*

Description

Extract or Access `BPFrequency` slot in a `genomicProfiles` object.

Usage

```
BPFrequency(object)
```

Arguments

`object`	`object` is a `genomicProfiles`

Details

Default value is c(0.25,0.25,0.25,0.25) When generating a Postion Weight Matrix from a Position Frequency Matrix, the probability of occurrence of each base pair (Base Pair Frequency) is necessary (as originally described by Gary Stormo). It is possible to set custom values for BPFrequency with a vector of length 4 containing the probability of occurrence of each base pair (A,C,G,T) in order. If Base pair frequency is unknown, BPFrequency will compute base pair frequency from a DNA sequence. The nature of this sequence can be a BSgenome or a DNAStringSet. In order to decrease run time, it is advised to use DNAStringSet

Value

Returns BPFrequency slot in genomicProfiles object.

Author(s)

Patrick C.N. Martin <pcnmartin@gmail.com>

References

Zabet NR, Adryan B (2015) Estimating binding properties of transcription factors from genome-wide binding profiles. Nucleic Acids Res., 43, 84–94.

Examples

```
data(ChIPanalyserData)
# path to Position Frequency Matrix
PFM <- file.path(system.file("extdata",package="ChIPanalyser"),"BEAF-32.pfm")
# Building genomicProfiles object
GPP <- genomicProfiles(PFM=PFM,PFMFormat="JASPAR")
#Extracting BPFrequency slot
BPFrequency(GPP)
```

BPFrequency-methods *~~ Methods for Function* BPFrequency ~~

Description

~~ Methods for function BPFrequency ~~

Methods:

```
signature(object = "genomicProfilesInternal")
```

BPFrequency<- *Setter method for* BPFrequency *slot in a* genomicProfiles *object.*

Description

Setter method for BPFrequency slot in a genomicProfiles object. If base pair frequency is unknown, BPFrequency will compute base pair frequency from a DNA sequence.

Usage

```
BPFrequency(object)<-value
```

Arguments

object	object is a genomicProfiles object.
value	value can three different objects: A vector of length 4 containing the probability of occurrence of each base pair (A,C,G,T) in order. Default value is c(0.25,0.25,0.25,0.25). A BSgenome of the organism of interest. The base pair frequency will automatically be computed and updated in genomicProfiles. A DNAStringSet of the organisme of interest. The base pair frequency will automatically be computed and updated in genomicProfiles (Prefered method).

Details

Default value is c(0.25,0.25,0.25,0.25) When generating a Postion Weight Matrix from a Position Frequency Matrix, the probability of occurrence of each base pair (Base Pair Frequency) is necessary (as originally described by Gary Stormo). It is possible to set custom values for BPFrequency with a vector of length 4 containing the probability of occurrence of each base pair (A,C,G,T) in order. If Base pair frequency is unknown, BPFrequency will compute base pair frequency from a DNA sequence when building a genomicProfiles object. The nature of this sequence can be aBSgenome object or a DNAStringSet. In order to decrease run time, it is advised to use DNAStringSet.

Value

Returns a genomicProfiles object with an updated value for BPFrequency.

Author(s)

Patrick C.N. Martin <pcnmartin@gmail.com>

References

Zabet NR, Adryan B (2015) Estimating binding properties of transcription factors from genome-wide binding profiles. Nucleic Acids Res., 43, 84–94. Patrick C.N. Martin and Nicolae Radu Zabe (2020) Dissecting the binding mechanisms of transcription factors to DNA using a statistical thermodynamics framework. CSBJ, 18, 3590-3605.

Examples

```
data(ChIPanalyserData)
# path to Position Frequency Matrix
PFM <- file.path(system.file("extdata",package="ChIPanalyser"),"BEAF-32.pfm")
#As an example of genome, this example will run on the Drosophila genome

if(!require("BSgenome.Dmelanogaster.UCSC.dm6", character.only = TRUE)){
    if (!requireNamespace("BiocManager", quietly=TRUE))
        install.packages("BiocManager")
    BiocManager::install("BSgenome.Dmelanogaster.UCSC.dm6")
    }
library(BSgenome.Dmelanogaster.UCSC.dm6)
DNASequenceSet <- getSeq(BSgenome.Dmelanogaster.UCSC.dm6)
# Building genomicProfiles object
GPP <- genomicProfiles(PFM=PFM,PFMFormat = "JASPAR", BPFrequency=DNASequenceSet)
# Updating BPFrequency
## !! Note!! BPFrequency is used to compute PWM from PFM
## IF updated after building GPP, then it will not influence PWM
## Advised to build with BPFrequency directly
BPFrequency(GPP) <- DNASequenceSet
BPFrequency(GPP) <- c(0.25,0.25,0.25,0.25)
```

`BPFrequency<-methods` *~~ Methods for Function* `BPFrequency<-` *~~*

Description

~~ Methods for function `BPFrequency<-` ~~

Methods:

`signature(object = "genomicProfilesInternal", value = "DNAStringSet")`

`signature(object = "genomicProfilesInternal", value = "vector")`

`ChIPanalyserData` *ChIPanalyserData*

Description

`ChIPanalyserData` is derived from real biological data. The source organism is *Drosophila melanogaster*. The data can be described as genomic data as it contains DNA sequences, loci, genetic information, DNA accessibility data and ChIP-seq data.

Usage

```
data(ChIPanalyserData)
```

Format

1. Accessis GRanges containing DNA Accesibility data for the sequences described above.
2. csis GRanges containing Chromatin State data for the sequences described above.
3. topis GRanges containing a locus of interest. In this case *eve strip Locus* on chromosome 2R in *Drosophila melanogaster*
4. chipis a GRanges containing ChIP score of the eve strip locus in *Drosophila melanogaster*.
5. geneRefis a GRanges containing UCSC gene reference information

Value

Returns a set of Rdata objects as described above.

Source

Transcription Factor PFM: Berkeley Drosophila Transcription Network Project (bdtnp.lbl.gov)

References

Zabet NR, Adryan B (2015) Estimating binding properties of transcription factors from genome-wide binding profiles. Nucleic Acids Res., 43, 84–94. Patrick C.N. Martin and Nicolae Radu Zabe (2020) Dissecting the binding mechanisms of transcription factors to DNA using a statistical thermodynamics framework. CSBJ, 18, 3590-3605.

Examples

```
data(ChIPanalyserData)
```

---

chipMean *Accessor method for* chipMean *slot in a* parameterOptions *object.*

Description

Accessor method for chipMean slot in a parameterOptions object.

Usage

```
chipMean(object)
```

Arguments

object	object is a parameterOptions

Details

Default vlaue : 150 When computing ChIP-seq like profiles (computeChIPProfile, the occupancy values given by computeOccupancy are transformed into ChIP-seq like profiles. The average size of a ChIP-seq peak was described by Kaplan (Kaplan et al. , 2011). It is advised to use the average width of ChIP peaks from actual ChIP-seq data. We strongly encourage to set values when building a parameterOptions object.

Value

Returns chipMean slot from a parameterOptions object.

Author(s)

Patrick C.N. Martin <pcnmartin@gmail.com>

References

Zabet NR, Adryan B (2015) Estimating binding properties of transcription factors from genome-wide binding profiles. Nucleic Acids Res., 43, 84–94.

Kaplan T.,Li X.-Y.,Sabo P.J.,Thomas S.,Stamatoyannopoulos J.A., Biggin M.D., EisenM.B. Quantitative models of the mechanisms that control genome-wide patterns of transcription factor binding during early Drosophila development, PLoS Genet.,2011, vol. 7 pg. e1001290

Examples

```
# Building parameterOptions object
OPP <- parameterOptions()
#Accessing chipMean slot in OPP
chipMean(OPP)
```

---

chipMean-methods *~~ Methods for Function* chipMean *~~*

Description

~~ Methods for function chipMean ~~

Methods:

chipMean(object)

chipMean<- *Access methods for* chipMean *slot in* parameterOptions *object.*

Description

Access methods for chipMean slot in parameterOptions object.

Usage

```
chipMean(object)<-value
```

Arguments

object	object is a parameterOptions object.
value	value is a positive numeric value that will be assigned to the chipMean slot. chipMean describes the average size of a ChIP-seq peak in base pairs.

Details

Default vlaue : 150 When computing ChIP-seq like profiles (computeChIPProfile, the occupancy values given by computeOccupancy are transformed into ChIP-seq like profiles. The average size of a ChIP-seq peak was described by Kaplan (Kaplan et al. , 2011). It is advised to use the average width of ChIP peaks from actual ChIP-seq data. We strongly encourage to set values when building a parameterOptions object.

Value

Returns a parameterOptions object with an updated value for chipMean slot.

Author(s)

Patrick C.N. Martin <pcnmartin@gmail.com>

References

Zabet NR, Adryan B (2015) Estimating binding properties of transcription factors from genome-wide binding profiles. Nucleic Acids Res., 43, 84–94.

Kaplan T.,Li X.-Y.,Sabo P.J.,Thomas S.,Stamatoyannopoulos J.A., Biggin M.D.,EisenM.B. Quantitative models of the mechanisms that control genome-wide patterns of transcription factor binding during early Drosophila development, PLoS Genet.,2011, vol. 7 pg. e1001290

Examples

```
# Building parameterOptions object
OPP <- parameterOptions()
# Setting new value for slot
chipMean(OPP) <- 250
```

`chipMean<-methods` ~~ *Methods for Function* `chipMean<-` ~~

Description

~~ Methods for function `chipMean<-` ~~

Methods:

`chipMean(object)<-value`

`ChIPScore-class` *Class* `"ChIPScore"`

Description

`ChIPScore` is the result of the `processingChIP` function. This object contains the extracted ChIP Score from ChIP data, the loci of interest and optional paramters associated to ChIPanalyser. The loci of interest will either be user provided or the top n regions as defined by the reduce argument im `processingChIP`. This object has the sole purpose of aiding the storage and parsing of data and parameters.

Objects from the Class

Object of this class are created internaly and will be parsed to other objects as is.

Slots

`scores`**:** Object of class `"list"` List of extracted ChIP scores

`loci`**:** Object of class `"loci"` GRanges containing loci of interest

`ploidy`**:** Object of class `"numeric"` Ploidy level of the organism

`boundMolecules`**:** Object of class `"vector"` Number of Bound molecules to the DNA

`backgroundSignal`**:** Object of class `"numeric"` ChIP background signal (average ChIP score)

`maxSignal`**:** Object of class `"numeric"` max ChIP signal

`lociWidth`**:** Object of class `"numeric"` Width of loci if reduce is used and no loci are provided

`chipMean`**:** Object of class `"numeric"` Average ChIP peak width

`chipSd`**:** Object of class `"numeric"` Standard Deviation of ChIP peak width

`chipSmooth`**:** Object of class `"vector"` Smoothing window width for ChIP score

`stepSize`**:** Object of class `"numeric"` Defining resolution size of ChIP like profiles (10bp = signal will be only considered every 10bp)

`removeBackground`**:** Object of class `"numeric"` Signal Threshold to be removed. Default removes all negative scores

`noiseFilter`: Object of class `"character"` Type of noise filter to be used on ChIP data.

`PWMThreshold`: Object of class `"numeric"` Threshold of PWM scores that will be selected

`strandRule`: Object of class `"character"` Rule to compute strand score (max, mean or sum)

`whichstrand`: Object of class `"character"` Which strand should be used to compute PWM scores.

`lambdaPWM`: Object of class `"vector"` Lambda value - Scaling factor to the PWM

`naturalLog`: Object of class `"logical"` PFM to PWM conversion log transform (natural log or log2)

`noOfSites`: Object of class `"nos"` Number of Sites in the PWM that should be used to compute PWM scores.

`PWMpseudocount`: Object of class `"numeric"` PWM pseudocount value for PFM to PWM conversion.

`paramTag`: Object of class `"character"` Internal Tag - Code progression

Extends

Class `"parameterOptions"`, directly.

Methods

.loci<- `signature(object = "ChIPScore", value = "loci")`: ...

.scores<- `signature(object = "ChIPScore", value = "list")`: ...

initialize `signature(.Object = "ChIPScore")`: ...

loci `signature(object = "ChIPScore")`: ...

scores `signature(object = "ChIPScore")`: ...

show `signature(object = "ChIPScore")`: ...

Author(s)

Patrick C.N. Martin

References

Zabet NR, Adryan B (2015) Estimating binding properties of transcription factors from genome-wide binding profiles. Nucleic Acids Res., 43, 84–94. Patrick C.N. Martin and Nicolae Radu Zabe (2020) Dissecting the binding mechanisms of transcription factors to DNA using a statistical thermodynamics framework. CSBJ, 18, 3590-3605.

See Also

`processingChIP`

Examples

```
showClass("ChIPScore")
```

chipSd *Accessor method for* chipSd *slot in a* parameterOptions *object.*

Description

Access or Extract chipSd slot in a parameterOptions object.

Usage

```
chipSd(object)
```

Arguments

object	object is a parameterOptions

Details

When computing ChIP-seq like profiles (computeChIPProfile, the occupancy values given by computeOccupancy are transformed into ChIP-seq like profiles. The average size of a ChIP-seq peak was described by Kaplan (Kaplan et al. , 2011). The average peak size is subject to variation. This variation is accounted for with chipSd. It is advised to use the standard deviation of ChIP peak width from actual ChIP-seq data. We strongly encourage to set values when building a parameterOptions object.

Value

Returns a parameterOptions object with an updated value for chipSd.

Author(s)

Patrick C.N. Martin <pcnmartin@gmail.com>

References

Zabet NR, Adryan B (2015) Estimating binding properties of transcription factors from genome-wide binding profiles. Nucleic Acids Res., 43, 84–94.

Kaplan T.,Li X.-Y.,Sabo P.J.,Thomas S.,Stamatoyannopoulos J.A., Biggin M.D., Eisen M.B. Quantitative models of the mechanisms that control genome-wide patterns of transcription factor binding during early Drosophila development, PLoS Genet.,2011, vol. 7 pg. e1001290

Examples

```
# Building parameterOptions object
OPP <- parameterOptions()
# Accessing chipSd slot
chipSd(OPP)
```

chipSd-methods ~~ *Methods for Function* chipSd ~~

Description

~~ Methods for function chipSd ~~

Methods:

chipSd(object)

chipSd<- *Setter methods for* chipSd *slot in a* parameterOptions *object.*

Description

Setter methods for chipSd slot in a parameterOptions object.

Usage

```
chipSd(object)<-value
```

Arguments

object	object is parameterOptions object.
value	value is a positive nurmeric value that will be assigned to chipSd slot. Default value is 150.

Details

When computing ChIP-seq like profiles (computeChIPProfile, the occupancy values given by computeOccupancy are transformed into ChIP-seq like profiles. The average size of a ChIP-seq peak was described by Kaplan (Kaplan et al. , 2011). The average peak size is subject to variation. This variation is accounted for with chipSd. It is advised to use the standard deviation of ChIP peak width from actual ChIP-seq data. We strongly encourage to set values when building a parameterOptions object.

Value

Returns a parameterOptions object with an updated value for chipSd.

Author(s)

Patrick C.N. Martin <pcnmartin@gmail.com>

References

Zabet NR, Adryan B (2015) Estimating binding properties of transcription factors from genome-wide binding profiles. Nucleic Acids Res., 43, 84–94.

Kaplan T.,Li X.-Y.,Sabo P.J.,Thomas S.,Stamatoyannopoulos J.A., Biggin M.D., Eisen M.B. Quantitative models of the mechanisms that control genome-wide patterns of transcription factor binding during early Drosophila development, PLoS Genet.,2011, vol. 7 pg. e1001290

Examples

```
# Building parameterOptions object
OPP <- parameterOptions()
# Setting new value for chipSd slot
chipSd(OPP) <-  250
```

`chipSd<-methods` ~~ *Methods for Function* `chipSd<-` ~~

Description

~~ Methods for function `chipSd<-` ~~

Methods:

`chipSd(object)<-value`

`chipSmooth` *Accessor methods for* `chipSmooth` *slot in a* `parameterOptions` *object.*

Description

Access or Extract `chipSmooth` slot in a `parameterOptions` object.

Usage

```
chipSmooth(object)
```

Arguments

`object`	`object` is a `parameterOptions` object.

Details

When computing ChIP-seq like (`computeChIPProfile`) profile from occupancy data (see `computeOccupancy`), the profiles are smoothed using a window of a given size. The default value is set at 250 base pairs. If `chipSmooth` is set to 0 then the profile will not be smoothed. We strongly encourage to set values when building a `parameterOptions` object.

Value

Returns the chipSmooth slot in an parameterOptions object.

Author(s)

Patrick C.N. Martin <pcnmartin@gmail.com>

References

Zabet NR, Adryan B (2015) Estimating binding properties of transcription factors from genome-wide binding profiles. Nucleic Acids Res., 43, 84–94. Patrick C.N. Martin and Nicolae Radu Zabe (2020) Dissecting the binding mechanisms of transcription factors to DNA using a statistical thermodynamics framework. CSBJ, 18, 3590-3605.

Examples

```
# Building parameterOptions object
OPP <- parameterOptions()
# Accessing chipSd slot
chipSmooth(OPP)
```

---

chipSmooth-methods *~~ Methods for Function* chipSmooth *~~*

Description

~~ Methods for function chipSmooth ~~

Methods:

signature(object = "parameterOptions")

---

chipSmooth<- *Setter method for* chipSmooth *slot in* parameterOptions *object.*

Description

Setter method for chipSmooth slot in parameterOptions object.

Usage

```
chipSmooth(object) <- value
```

Arguments

object	object is a parameterOptions object.
value	value is the positive numeric value to be assigned to the chipSmooth slot in parameterOptions Default value is 250 base pairs.

Details

When computing ChIP-seq like (computeChIPProfile) profile from occupancy data (see computeOccupancy), the profiles are smoothed using a window of a given size. The default value is set at 250 base pairs.If chipSmooth is set to 0 then the profile will not be smoothed. We strongly encourage to set values when building a parameterOptions object.

Value

Returns a parameterOptions object with an updated value for chipSmooth slot.

Author(s)

Patrick C.N Martin <pm16057@essex.ac.uk>

References

Zabet NR, Adryan B (2015) Estimating binding properties of transcription factors from genome-wide binding profiles. Nucleic Acids Res., 43, 84–94.

Examples

```
# Building parameterOptions object
OPP <- parameterOptions()
# Setting new value for chipSd slot
chipSmooth(OPP) <-  250
```

---

chipSmooth<-methods ~~ *Methods for Function* chipSmooth<- ~~

Description

~~ Methods for function chipSmooth<- ~~

Methods:

signature(object = "parameterOptions", value = "vector")

computeChIPProfile *Computing ChIP-seq like profiles from Occupancy data.*

Description

computeChIPProfile compute ChIP-seq like profile from occupancy data. Occupancy data is computed using computeOccupancy.

Usage

```
computeChIPProfile(genomicProfiles, loci, parameterOptions = NULL,
    norm = TRUE, method = c("moving_kernel","truncated_kernel","exact"),
    peakSignificantThreshold= NULL,cores=1, verbose = TRUE)
```

Arguments

genomicProfiles
: genomicProfiles is the result of computeOccupancy. This object should be a genomicProfiles object.

loci
: loci is either a GRanges or ChIPScore object. ChIPScore-class will be the result of processingChIP. This object represents the set of Loci you are interested in analysing. If you have followed the full ChIPanalyser pipe line, you would have used the processingChIP function that would return a ChIPScore-class object containing your loci of interest. GRanges are also supported if you are only using part of the pipeline.

parameterOptions
: parameterOptions is a parameterOptions object. This object is used to store the numerous paramters offered by ChIPanalyser. This argument is optional as all arguments are also parse in both ChIPScore-class and genomicProfiles objects. If you wanted to make some last minute changes, parameterOptions is the way to go. We recomend that you set your desired options before hand.

norm
: norm is a logical value. If TRUE, the ChIP-seq like profile will be normalised towards maximum Occupancy. If FALSE, the profile will be left as is.

method
: method is a character string of one of the following: c("moving_kernel","truncated_kernel","exact"). If set to moving_kernel, the peaks will be approximated using Rcpp (Default). If set to truncated_kernel, the peaks will be approximated however this method does not require Rcpp. If set to exact, the peaks will not be approximated.

peakSignificantThreshold
: peakSignificantThreshold is a threshold at which peaks will be selected. IMPORTANT: if you select "moving_kernel" as described in method then this threshold is a numeric value describing the peak tail hight cutoff value (Default = 0.001). In the case of "truncated_kernel" and "exact", the threhsold represents a distance in base pair from the peak summit at which the peak should be cut (Default = 1250). The default is set to NULL in this function. This just means that either the value is provided bu user with the appropriate method. If not, the default will be selected depending on the method selected.

cores	cores is the number of cores that will be used to compute ChIP profiles.
verbose	verbose is a logical value. If TRUE, progress messages will be displayed in console. If FALSE, no progress messages will be dispalyed in console.

Details

computeChIPProfile converts Transcription Factor occuapncy to a profile resembling the one of a ChIP-seq profile. Internally a few paramters are required to build a ChIP like profile. These parameters are either defined and stored in a ChIPScore object (Paramters are updated based on your ChIP data), a genomicProfiles (user defined at the start of the analysis) or a parameterOptions (if you want to update values as you go along)

Value

Returns a genomicProfiles objec containing all ChIP-seq like profile for every combination of lambdaPWM and boundMolecules provided by the user.

Author(s)

Patrick C.N. Martin <pcnmartin@gmail.com>

References

Zabet NR, Adryan B (2015) Estimating binding properties of transcription factors from genome-wide binding profiles. Nucleic Acids Res., 43, 84–94. Patrick C.N. Martin and Nicolae Radu Zabe (2020) Dissecting the binding mechanisms of transcription factors to DNA using a statistical thermodynamics framework. CSBJ, 18, 3590-3605.

Examples

```
#Extracting Data
data(ChIPanalyserData)
# path to Position Frequency Matrix
PFM <- file.path(system.file("extdata",package="ChIPanalyser"),"BEAF-32.pfm")
#As an example of genome, this example will run on the Drosophila genome

if(!require("BSgenome.Dmelanogaster.UCSC.dm6", character.only = TRUE)){
    if (!requireNamespace("BiocManager", quietly=TRUE))
        install.packages("BiocManager")
    BiocManager::install("BSgenome.Dmelanogaster.UCSC.dm6")
    }
library(BSgenome.Dmelanogaster.UCSC.dm6)
DNASequenceSet <- getSeq(BSgenome.Dmelanogaster.UCSC.dm6)
# Building genomicProfiles object
GPP <- genomicProfiles(PFM=PFM, PFMFormat="JASPAR",BPFrequency=DNASequenceSet)


# Computing Genome Wide
GenomeWide <- computeGenomeWideScores(genomicProfiles = GPP,
    DNASequenceSet = DNASequenceSet)
```

```
#Compute PWM Scores
PWMScores <- computePWMScore(genomicProfiles = GenomeWide,
     DNASequenceSet = DNASequenceSet, loci = top, chromatinState = Access)
#Compute Occupnacy
Occupancy <- computeOccupancy(genomicProfiles = PWMScores)

#Compute ChIP profiles
chipProfile <- computeChIPProfile(genomicProfiles=Occupancy,loci=top)
chipProfile
```

---

computeGenomeWideScores

Computing Genome Wide scores

Description

computeGenomeWideScores compute the max and min PWM score over the entire genome.

Usage

```
computeGenomeWideScores(genomicProfiles, DNASequenceSet, chromatinState = NULL, parameterOptions = NUL
```

Arguments

genomicProfiles	genomicProfiles is a genomicProfiles object containing the PFM, PWM of interest.
DNASequenceSet	DNASequenceSet is a BSgenome or DNAStringSet containing the sequence of the organism of interest.
chromatinState	chromatinState is a GRanges object containing the chromatin States. This can either represent regions of accessible DNA or Chromatin state affinities.
parameterOptions	parameterOptions is a parameterOptions object containing parameters that you wish to change. The genomicProfiles object will be updated using the values assigned to parameterOptions
cores	cores is the number or cores that will be used (Numeric value - Default = 1)
verbose	verbose is a logical value that will determine if internal progress message will be printed.

Details

computeGenomeWideScores function computes PWM scores over the entire genome (or accessible Genome if chromatin State are provided). Genome wide scores are used to determine the maximum and minimum PWM score as well as the average exponential score. These scores will in turn be used to determine which score are above the PWM theshold. The average exponential score is an integrale part of the equation used to compute Occupancy. Using defualt settings, ChIPanalyser will only compute occupancy on the top 70% of PWM scores. This threshold can be changed. See PWMThreshold

Value

Returns a genomicsProfiles object with updated values for max score, min score and averageExpPWMScore.

Author(s)

Patrick C.N Martin <pm16057@essex.ac.uk>

References

Zabet NR, Adryan B (2015) Estimating binding properties of transcription factors from genome-wide binding profiles. Nucleic Acids Res., 43, 84–94. Patrick C.N. Martin and Nicolae Radu Zabe (2020) Dissecting the binding mechanisms of transcription factors to DNA using a statistical thermodynamics framework. CSBJ, 18, 3590-3605.

Examples

```
if(!require("BSgenome.Dmelanogaster.UCSC.dm6", character.only = TRUE)){
    if (!requireNamespace("BiocManager", quietly=TRUE))
        install.packages("BiocManager")
    BiocManager::install("BSgenome.Dmelanogaster.UCSC.dm6")
    }
library(BSgenome.Dmelanogaster.UCSC.dm6)
DNASequenceSet <- getSeq(BSgenome.Dmelanogaster.UCSC.dm6)
# Building genomicProfiles object
GPP <- genomicProfiles(PFM=PFM,PFMFormat="JASPAR", BPFrequency=DNASequenceSet)


# Computing Genome Wide
GenomeWide <- computeGenomeWideScores(genomicProfiles = GPP,
    DNASequenceSet = DNASequenceSet)
```

---

computeOccupancy *Compute Occupancy values from PWM Scores based on model.*

Description

computeOccupancy will compute the Occupancy from PWM Scores. As described in detail in the vignette, ChIPanalyser uses PWM Scores, DNA Accessibility data, the number of bound molecules and a sclaing factor of Transcription Factor specificty. This function will compute occupancy using the values assigned to each variable.

Usage

```
computeOccupancy(genomicProfiles,parameterOptions = NULL,
    norm = TRUE, verbose = TRUE)
```

Arguments

genomicProfiles	genomicProfiles is a a genomicProfiles object resulting from computePWMScore. IT is important to use this resulting object as the occuapancy will only be computed for sites above a threshold.
parameterOptions	parameterOptions is a parameterOptions object containing the adequate values assigned to each Parameter. If not Supplied (parameterOptions = NULL), a new object will be created internally using default values.
norm	norm a logical value which determines if the occupancy should be normalised or not.
verbose	verbose a logical value which determines if progress messages are printed or not.

Details

computeOccupancy will compute the Occupancy from PWM Scores. As described in detail in the vignette, ChIPanalyser uses PWM Scores, DNA Accessibility data, the number of bound molecules and a sclaing factor of Transcription Factor specificty. This function will compute occupancy using the values assigned to each variable. It should also be noted that the parameterOptions object contains a set of parameters used to compute Occupancy (not only restricted to this). These parameters are often dependant on real ChIP-Seq data and will influence the goodness of fit between the predicted model an real ChIP-seq data. We strongly advise that the values assigned to each parameter should be customiszed in order to increase the model ageement with real world biological data.

Value

computeOccupancy will return a genomicProfiles. The main difference will reside in the profiles slot. This slot is generally a list or GRangesList. Within these list type structures are enclosed GRanges containing the positions of site above threshold, PWMScores and Occupancy for each site. The series of GRanges will depend on the number of loci that are tested and the number of element in the list will depend on the various combinations of lambdaPWM and boundMolecules.

Author(s)

Patrick C.N. Martin <pcnmartin@gmail.com>

References

Zabet NR, Adryan B (2015) Estimating binding properties of transcription factors from genome-wide binding profiles. Nucleic Acids Res., 43, 84–94.

Examples

```
#Data extraction
data(ChIPanalyserData)
# path to Position Frequency Matrix
PFM <- file.path(system.file("extdata",package="ChIPanalyser"),"BEAF-32.pfm")
```

```
#As an example of genome, this example will run on the Drosophila genome

if(!require("BSgenome.Dmelanogaster.UCSC.dm6", character.only = TRUE)){
    if (!requireNamespace("BiocManager", quietly=TRUE))
        install.packages("BiocManager")
    BiocManager::install("BSgenome.Dmelanogaster.UCSC.dm6")
    }
library(BSgenome.Dmelanogaster.UCSC.dm6)
DNASequenceSet <- getSeq(BSgenome.Dmelanogaster.UCSC.dm6)

#Building data objects
GPP <- genomicProfiles(PFM=PFM,PFMFormat="JASPAR",BPFrequency=DNASequenceSet)
OPP <- parameterOptions()
# Computing Genome Wide
GenomeWide <- computeGenomeWideScores(genomicProfiles = GPP,
    DNASequenceSet = DNASequenceSet)

#Compute PWM Scores
PWMScores <- computePWMScore(genomicProfiles = GenomeWide,
    DNASequenceSet = DNASequenceSet,
    loci = top,
    chromatinState = Access)
#Compute Occupnacy
Occupancy <- computeOccupancy(genomicProfiles = PWMScores,
    parameterOptions = OPP)
Occupancy
```

`computeOptimal` *compute Optimal Parameters*

Description

`ChIPanalyser` contains a set of functions some of which require two parameters known as `lambdaPWM` and as `boundMolecules`. These two paramters are not always known. `computeOptimal` will compute these values by maximising the correlation and minimising the Mean Squared Error between a predicted ChIP-seq-like profile and a real ChIP-seq profile for a given loci.

Usage

```
computeOptimal(genomicProfiles,DNASequenceSet, ChIPScore,chromatinState = NULL,
    parameterOptions = NULL, optimalMethod = "all",rank=FALSE,returnAll=TRUE,
    peakMethod="moving_kernel",cores=1)
```

Arguments

`genomicProfiles`

`genomicProfiles` is a `genomicProfiles` object containing at least a Postion Frequency Matrix or a Position Weight Matrix. It is strongly advised to cus-

tomize this object to increase goodness of fit of the model when compared to real ChIP-seq data.

`DNASequenceSet` `DNASequenceSet` is a `DNAStringSet` or a `BSgenome` of the full sequence of the organism of interest.

`ChIPScore` `ChIPScore` is a named list containing ChIP-seq enrichements for each Loci of interest. This Profile should be normalised to a base pair level. In other words, there should be an enrichement score for each base pair of a given Locus.

`chromatinState` `chromatinState` is a `GRanges` object containing either accesible sites or DNA affinity scores.

`parameterOptions`
`parameterOptions` is a `parameterOptions` object. If this object is not provided (parameterOptions = NULL), a new object will be created internally. However, it is strongly advised to tailor this object to maximise the goodness of fit of the model when compared to ChIP-seq data.

`optimalMethod` `optimalMethod` is a character string which determines which method for optimal parameter selection should be selected. optimalMethod can be one of the following: pearson, spearman, kendall, ks, fscore, geometric,MSE, or all. Default is set to all.

`rank` `rank` is a logical value indicating if optimal parameters should be based on rank (parameter combination occuring the most over all regions) or avaerage score (best perfomring combination of paramters on average over all regions selected). DEFAULT = FALSE

`returnAll` `returnAll` is a logical value indicating if all internal objects should be returned. DEFAULT = TRUE. Internal objects are the following: Occupancy Scores, ChIP like profiles, goodness of fit metrics and optimal paramters. If set to FALSE, `computeOptimal` will only return the optimal parameters.

`peakMethod` `peakMethod` is a character string of one of the following: c("moving_kernel","truncated_kernel","exact"). If set to moving_kernel, the peaks will be approximated using Rcpp (Default). If set to truncated_kernel, the peaks will be approximated however this method does not require Rcpp. If set to exact, the peaks will not be approximated.

`cores` `cores` is the number cores that will be used to compute optimal set of parameters.

Details

In order to backward infer the values of `lambdaPWM` and `boundMolecules`, it is possible to use the `computeOptimal` to find these parameters. It should be noted that this functions requires a ChIP-seq data input. `ChIPScore` (ChIP-seq data). This should be the output of the `processingChIP` function.

Value

`computeOptimal` returns a list respectivly described as the optimal set of Parameters (lambda - `lambdaPWM` and `boundMolecules`), the optimal matrix (a matrix containing accuracy estimates dependant on the parameter chosen), and finally the chosen parameter. If the parameter that was chosen was "all", then each element of this list will contain the optimal set of parameters, optimal matricies for all of the aforementioned paramters (see `optimalMethod`).

Author(s)

Patrick C. N. Martin <pm16057@essex.ac.uk>

References

Zabet NR, Adryan B (2015) Estimating binding properties of transcription factors from genome-wide binding profiles. Nucleic Acids Res., 43, 84–94.

Examples

```
#Data extraction
data(ChIPanalyserData)
# path to Position Frequency Matrix
PFM <- file.path(system.file("extdata",package="ChIPanalyser"),"BEAF-32.pfm")
#As an example of genome, this example will run on the Drosophila genome

if(!require("BSgenome.Dmelanogaster.UCSC.dm6", character.only = TRUE)){
    if (!requireNamespace("BiocManager", quietly=TRUE))
        install.packages("BiocManager")
    BiocManager::install("BSgenome.Dmelanogaster.UCSC.dm6")
    }
library(BSgenome.Dmelanogaster.UCSC.dm6)
DNASequenceSet <- getSeq(BSgenome.Dmelanogaster.UCSC.dm6)
chip<-processingChIP(chip,top)
#Building data objects
GPP <- genomicProfiles(PFM=PFM,PFMFormat="JASPAR",BPFrequency=DNASequenceSet)
OPP <- parameterOptions()
#Computing Optimal set of Parameters
optimalParam <- computeOptimal(genomicProfiles = GPP,
    DNASequenceSet = DNASequenceSet,
    ChIPScore = chip,
    chromatinState = Access,
    parameterOptions = OPP,
    parameter = "all",
    peakMethod="moving_kernel")
```

`computePWMScore` *Compute PWM Scores of sites above threshold.*

Description

`computePWMScore` will compute and extract all sites that exhibit a PWM Score higher than a threshold. This threshold (see `PWMThreshold`) will determine the percentage of total sites that should NOT be considered.

Usage

```
computePWMScore(genomicProfiles,DNASequenceSet,
   loci = NULL, chromatinState = NULL,parameterOptions=NULL,cores=1, verbose = TRUE)
```

Arguments

DNASequenceSet	DNASequenceSet is a DNAStringSet or a BSgenome containing the full sequence of the organism of interest.
genomicProfiles	genomicProfiles is a genomicProfiles object resulting from the computeGenomeWideScores function.
loci	loci is a GRanges object containing the Loci of interest or a ChIPScore object result of processingChIP function.
parameterOptions	parameterOptions is a parameterOptions object containing parameters that you wish to parse/change when computing PWMScores.
chromatinState	chromatinState is a GRanges object sites of accessible DNA or DNA affinity scores.
cores	cores is the number of cores used to compute PWM Scores.
verbose	verbose is a logical value indicating if progress messages should be printed or not.

Details

After determining genome wide scores, it is possible to only compute and extract high affinity sites (in the sense that they have a high PWM Score). If a PWMThreshold is not set by user, the default value is set at 0.7. This means that 70 % of sites will NOT be selected. Only the top 30 % will be computed and extracted. If one is interested in all PWM Scores at a genome wide scale (or accessible DNA), this is possible by setting PWMThreshold to zero.

Value

computePWMScore will return a genomicProfiles object. The profiles slot will have been updated. This slot will now contain a GRangesList with each element being a GRanges. This GRanges will contain postion of each sites (start, end and strand) and the PWMScore associated to that site.

Author(s)

Patrick C.N. Martin <pcnmartin@gmail.com>

References

Zabet NR, Adryan B (2015) Estimating binding properties of transcription factors from genome-wide binding profiles. Nucleic Acids Res., 43, 84–94.

Examples

```
#Data extraction
data(ChIPanalyserData)
# path to Position Frequency Matrix
PFM <- file.path(system.file("extdata",package="ChIPanalyser"),"BEAF-32.pfm")
#As an example of genome, this example will run on the Drosophila genome
```

```
if(!require("BSgenome.Dmelanogaster.UCSC.dm6", character.only = TRUE)){
    if (!requireNamespace("BiocManager", quietly=TRUE))
        install.packages("BiocManager")
    BiocManager::install("BSgenome.Dmelanogaster.UCSC.dm6")
    }
library(BSgenome.Dmelanogaster.UCSC.dm6)
DNASequenceSet <- getSeq(BSgenome.Dmelanogaster.UCSC.dm6)
chip<-processingChIP(chip,top)
#Building data objects
GPP <- genomicProfiles(PFM=PFM,PFMFormat="JASPAR",BPFrequency=DNASequenceSet)


# Computing Genome Wide
GenomeWide <- computeGenomeWideScores(DNASequenceSet = DNASequenceSet,
    genomicProfiles = GPP)

#Compute PWM Scores
PWMScores <- computePWMScore(DNASequenceSet = DNASequenceSet,
    genomicProfiles = GenomeWide,
    loci  = chip, chromatinState = Access)
PWMScores
```

DNASequenceLength *Accessor method for* DNASequenceLength *slot in a* genomicProfiles

---

Description

Accessor method for DNASequenceLength slot in a genomicProfiles

Usage

```
DNASequenceLength(object)
```

Arguments

object	object is a genomicProfiles

Details

The model on which is based ChIPanalyser requires the length of the DNA sequence used to compute scores. In this circustance, this DNA Length is the total length of the DNA of the organism of interest or the the Accessible DNA at a genome wide scale.

Value

Returns DNASequenceLength slot in a genomicProfiles object.

Author(s)

Patrick C. N. Martin <p.martin@essex.ac.uk>

References

Zabet NR, Adryan B (2015) Estimating binding properties of transcription factors from genome-wide binding profiles. Nucleic Acids Res., 43, 84–94.

Examples

```
#Data extraction
data(ChIPanalyserData)
# path to Position Frequency Matrix
PFM <- file.path(system.file("extdata",package="ChIPanalyser"),"BEAF-32.pfm")
#As an example of genome, this example will run on the Drosophila genome

if(!require("BSgenome.Dmelanogaster.UCSC.dm6", character.only = TRUE)){
    if (!requireNamespace("BiocManager", quietly=TRUE))
        install.packages("BiocManager")
    BiocManager::install("BSgenome.Dmelanogaster.UCSC.dm6")
}
library(BSgenome.Dmelanogaster.UCSC.dm6)
DNASequenceSet <- getSeq(BSgenome.Dmelanogaster.UCSC.dm6)

#Building genomicProfiles object
GPP <- genomicProfiles(PFM=PFM,PFMFormat="JASPAR",BPFrequency=DNASequenceSet)
# Computing Genome Wide
GenomceWide <- computeGenomeWideScores(DNASequenceSet = DNASequenceSet,
    genomicProfiles = GPP)

DNASequenceLength(GenomceWide)
```

DNASequenceLength-methods

~~ *Methods for Function* DNASequenceLength ~~

Description

~~ Methods for function DNASequenceLength ~~

Methods:

signature(object = "genomicProfilesInternal")

drop *Accessor Method for the* drop *slot in a* genomicProfiles *object.*

Description

Accessor Method for the drop slot in a genomicProfiles object.

Usage

```
drop(object)
```

Arguments

object	object is a genomicProfiles object.

Details

During certain computations, it is possible that the Loci of interest do no show any overlap with accesible DNA. If this were to be the case, a warning message will appear in the console but these inaccessible Loci will be stored in this slot. It is also for these reasons that it is imperative for Loci of interest to be named (in this case, a named GRanges).

Value

Returns a character string with loci containing no accesible DNA.

Author(s)

Patrick C.N. Martin <p.martin@essex.ac.uk>

References

Zabet NR, Adryan B (2015) Estimating binding properties of transcription factors from genome-wide binding profiles. Nucleic Acids Res., 43, 84–94.

Examples

```
# Loading data
data(ChIPanalyserData)
#Loading PFM files
PFM <- file.path(system.file("extdata",package="ChIPanalyser"),"BEAF-32.pfm")
#Building data objects
GPP <- genomicProfiles(PFM=PFM,PFMFormat="JASPAR")

# Loci with no acces - a warning message will be issued
#if loci do no contain accesible DNA
# Otherwise this slot will remain empty

drop(GPP)
```

drop-methods *~~ Methods for Function* drop *~~*

Description

~~ Methods for function drop ~~

Methods:

signature(object = "genomicProfilesInternal")

---

evolve *Running the ChIPanalyser implementation of a Genetic algorithm.*

Description

evolve pushes a starting population to evolve in a genetic algorithm.

Usage

```
evolve(population,DNASequenceSet,ChIPScore,
       genomicProfiles,parameters=NULL,generations=100,mutationProbability=0.3,
       offsprings=5,chromatinState=NULL,
       method="geometric", lambda=TRUE,
       checkpoint=TRUE,
       filename=NULL, cores=1)
```

Arguments

population	numeric value describing the number of individuals in the starting population. Alternatively - a starting population list as returned by generateStartingPopulation. NOTE: if numeric - the parameter argument is also required.
DNASequenceSet	DNAStringSet object containing DNA sequences of interest (Extracted from BSgenome)
ChIPScore	ChIPScore object as returned by the processingChIPfunction
genomicProfiles	genomicProfiles object containing minimal information (such as the PWM)
parameters	vector or list containing each parameter that should be added to the chromosome. See generateStartingPopulation
generations	numeric describing the number of generation before the Genetic algorithm should halt.
mutationProbability	numeric descrbining the rate of mutations for each surviving individual
offsprings	numeric descrbining the number of individuals surviving to the next generation

chromatinState	GRanges object containing chromatin state information. Each state should be labled in a meta data column named "name". It is advised to use numeric values for each state name.
method	character string describing the scoring metric that should be used. ChIPanalyser offers twelve different metrics: correlation coefficients (Pearson, Spearman and Kendall), Mean Squared Error (MSE), Kolmogorov–Smirnov Distance, precision, recall, accuracy, F-score, Matthew's correlation coefficient (MCC) and Area Under Curve Receiver Operator Characteristic (AUC ROC or just AUC)
lambda	logical describing if lambda value should be pre-computed. Setting to TRUE increases the speed of the algorithm.
checkpoint	logical describing if population parameters at each generations should be saved.
filename	character string that will serve as a prefix to the saved intermediate files.
cores	numeric describing the number of cores used to run the GA.

Details

ChIPanalyser offers a way of finding optimal solution by using a genetic algorithm. Instead of running the stadard analysis, TF binding affinities to chromatin states can be extracted via this more complex method. It should be noted that this method is better suited for the analysis of chromatin states. While the algorithm still works with simple DNA Accessibility, it would potentially take more time for accuracy minor gains.

Value

Returns a named list with three elements.

- database saves the data frame containing all scores for each individual since generation 1
- population saves the last population with chromosome values
- fitestsaves the fittest individual for a given generation

Author(s)

Patrick C.N. Martin <pcnmartin@gmail.com

Examples

```
library(ChIPanalyser)
data(ChIPanalyserData)
# See GA vignette for usage
```

generateStartingPopulation *Generate Starting population for ChIPanalyser Genetic algortihm*

Description

generateStartingPopulation generates a starting population with random traits for each individual

Usage

```
generateStartingPopulation(population,parameters,names=NULL)
```

Arguments

population	numeric value describing the number of individuals in the starting population.
parameters	vector or list containing each parameter that should be added to the chromosome.
names	character describing names that should be added to each individual.

Details

generateStartingPopulation generates a starting poppulation to be used in the genetic algortihm implemented in ChIPanalyser. There are two main ways a starting population can be generated:

1. by name Using names of each parameter that should be parse to each "chromosome". The possible paramters are N, lambda, PWMThreshold, CS (DNAAffinity or DNAAccessibility also works). CS values should also contain a numeric value associated to each chromatin state you wish to parse. e.g CS1 ... CS14 This will generate a value by sampling from a set of predefined value for each paramters.
2. by value range Using a named list (names for each parameters). Each element of the list should contain three numeric values : length of range, min value, max value. (Internally - values are parse to runif)

Value

Returns a list of individuals with a random traits

Author(s)

Patrick C.N. Martin

Examples

```
## by name
param <- c("N","lambda","PWMThreshold","CS1","CS2","CS3")

pop <- generateStartingPopulation(20,param, names = NULL)

# by range
paramValue <- list(c(10,1,1000),c(10,0,5),c(10,0,0.9),c(10,0,1),c(10,0,1),c(10,0,1))

pop <- generateStartingPopulation(20,paramValue,names= param)
```

---

genomicProfiles *Genomic Profile object*

Description

genomicProfiles is an S4 object serving two purposes: (i) storing internal computed data and (ii) storing paramter options. This object is parsed through the different steps of the pipeline to facilitate that parsing and changing of paramters.

Usage

```
genomicProfiles(..., parameterOptions = NULL, genomicProfiles = NULL, ChIPScore = NULL)
```

Arguments

...	Any of the user available slots in genomicProfiles.
parameterOptions	If some parameters were already previously computed or stored in a parameterOptions, parsing this object will use those values instead of the default ones.
genomicProfiles	If some parameters were already previously computed or stored in a genomicProfiles, parsing this object will use those values instead of the default ones.
ChIPScore	If some parameters were already previously computed or stored in a ChIPScore, parsing this object will use those values instead of the default ones.

Details

The genomicProfiles object serves the purpose of storing, and parsing paramters and computed data between the different steps of the pipeline. When creating a genomicProfiles object it is possible to use previously computed values by simply parsing the object to the constructor function.

Value

Returns a genomicsProfiles object with updated slots for all paramters parsed.

Author(s)

Patrick C. N. Martin <pm16057@essex.ac.uk>

References

Zabet NR, Adryan B (2015) Estimating binding properties of transcription factors from genome-wide binding profiles. Nucleic Acids Res., 43, 84–94. Patrick C.N. Martin and Nicolae Radu Zabe (2020) Dissecting the binding mechanisms of transcription factors to DNA using a statistical thermodynamics framework. CSBJ, 18, 3590-3605.

See Also

genomicProfiles

parameterOptions

Examples

```
PFM <- file.path(system.file("extdata",package="ChIPanalyser"),"BEAF-32.pfm")
genomicProfiles()
genomicProfiles(PFM=PFM,PFMFormat="JASPAR")
```

---

genomicProfiles-class *Class* "genomicProfiles"

Description

genomicProfiles is an S4 object serving two purposes: (i) storing internal computed data and (ii) storing paramter options. This object is parsed through the different steps of the pipeline to facilitate that parsing and changing of paramters.

Objects from the Class

Objects can be created by calls of the form genomicProfiles(ploidy, boundMolecules, backgroundSignal, maxSignal, lociWidth, chipMean, chipSd, chipSmooth, stepSize, noiseFilter, removeBackground, lambdaPWM, PWMpseudocount, naturalLog, noOfSites, PWMThreshold, strandRule, whichstrand, PFM, PWM, PFMFormat, BPFrequency, minPWMScore, maxPWMScore, profiles, DNASequenceLength, averageExpPWMScore).

Slots

PWM: Object of class "matrix": A Position Weight Matrix (either supplied or internally computed if PFM is provided)

PFM: Object of class "matrix": A Position Frequency Matrix (may also be a path to file containing PFM)

PFMFormat: Object of class "character": A character string of one of the following: raw, transfac,JASPAR or sequences

`BPFrequency`: Object of class `"vector"`: Base Pair Frequency in the genome (if a DNA sequence is provided (as a `DNAStringSet` or `BSgenome`), will be automatically computed internally). Default:c(0.25,0.25,0.25,0.25)

`minPWMScore`: Object of class `"vector"`: Lowest PWM score accros the genome (computed and updated internally)

`maxPWMScore`: Object of class `"vector"`: Highest PWM score across the genome (computed and updated internally)

`profiles`: Object of class `"GRList"`: Containins GRanges with sites above threshold and associated metrics (PWMscore and Occupancy) - Computed Internally

`DNASequenceLength`: Object of class `"vector"`: Length of the Genome (or accesible genome) - computed internally

`averageExpPWMScore`: Object of class `"vector"`: Average exponential PWM score across the genome (or accesible genome) - computed internally

`ZeroBackground`: Object of class `"vector"`: Internal background value (computed internally)

`drop`: Object of class `"vector"`: Stores Loci that do contain accesible DNA if it were to be the case (computed and updated internally)

`tags`: Object of class `"character"` ~Internal Tags~

`ploidy`: Object of class `"numeric"`: A numeric Value descibing the ploidy of the organism. Default: 2

`boundMolecules`: Object of class `"vector"`: A vector (or single value) containing the number of bound Molecules (bound Transcription Factors): Default: 1000

`backgroundSignal`: Object of class `"numeric"`: A numeric value descibing the ChIP-seq background Signal (average signal from real ChIP seq data). Default: 0

`maxSignal`: Object of class `"numeric"`: A numeric value describing the highest ChIP-seq signal (from real ChIP-seq data). Default: 1

`lociWidth`: Object of class `"numeric"` ~~

`chipMean`: Object of class `"numeric"`: A numeric value describing the mean width of a ChIP- seq peak. Default:150

`chipSd`: Object of class `"numeric"`: A numeric value describing the standard deviation of ChIP-seq peaks. Default: 150

`chipSmooth`: Object of class `"vector"`: A numeric value describing the width of the window used to smooth Occupancy profiles into ChIP profiles. Default:250

`stepSize`: Object of class `"numeric"`: A numeric value describing the step Size (in base pairs) between each ChIP-seq score. Default:10 (Scored every 10 base pairs)

`removeBackground`: Object of class `"numeric"`: A numeric value describing the value at which score should be removed. Defualt:0 (If negative scores then remove)

`noiseFilter`: Object of class `"character"` ~Describes the noiseFilter method that will be applied to ChIP data (Zero, mean, median, sigmoid)~

`PWMThreshold`: Object of class `"numeric"`: Threshold at which PWM Score should be selected (only sites above threshold will be selected - between 0 and 1)

`strandRule`: Object of class `"character"`: "mean", "max" or "sum" will dertermine how strand should be handle for computing PWM Scores. Default : "max"

`whichstrand`: Object of class `"character"`: "+","-" or "+-" on which strand should PWM Score be computed. Default: "+-"

`lambdaPWM`: Object of class `"vector"` A vector (or single value) contaning values for lambdaPWM Default:1

`naturalLog`: Object of class `"logical"`: A logical value describing if natural Log will be used to compute the PWM (if FALSE then log2 will be used). Default: TRUE

`noOfSites`: Object of class `"nos"` A Positive integer descibing number of sites (in base pair) should be used from the PFM to compute PWM. Default =0 (Full width of binding site will be used when set to 0)

`PWMpseudocount`: Object of class `"numeric"`: A numeric value describing a PWMpseudocount for PWM computation. Default:1

`paramTag`: Object of class `"character"` ~Internal~

Extends

Class `"genomicProfilesInternal"`, directly. Class `"parameterOptions"`, directly.

Methods

initialize `signature(.Object = "genomicProfiles")`: ...

show `signature(object = "genomicProfiles")`: ...

Author(s)

Partick C. N. Martin <p.martin@essex.ac.uk>

References

Zabet NR, Adryan B (2015) Estimating binding properties of transcription factors from genome-wide binding profiles. Nucleic Acids Res., 43, 84–94. Patrick C.N. Martin and Nicolae Radu Zabe (2020) Dissecting the binding mechanisms of transcription factors to DNA using a statistical thermodynamics framework. CSBJ, 18, 3590-3605.

See Also

`genomicProfiles` `parameterOptions`

Examples

```
showClass("genomicProfiles")
```

genomicProfilesInternal-class
Class "genomicProfilesInternal"

Description

Non exported class. Represents the stripped down version of genomicProfiles.

Objects from the Class

Created Internally.

Slots

PWM: Object of class "matrix" ~~

PFM: Object of class "matrix" ~~

PFMFormat: Object of class "character" ~~

BPFrequency: Object of class "vector" ~~

minPWMScore: Object of class "vector" ~~

maxPWMScore: Object of class "vector" ~~

profiles: Object of class "GRList" ~~

DNASequenceLength: Object of class "vector" ~~

averageExpPWMScore: Object of class "vector" ~~

ZeroBackground: Object of class "vector" ~~

drop: Object of class "vector" ~~

tags: Object of class "character" ~~

Methods

.averageExpPWMScore<- signature(object = "genomicProfilesInternal", value = "numeric"): ...

.DNASequenceLength<- signature(object = "genomicProfilesInternal", value = "vector"): ...

.drop<- signature(object = "genomicProfilesInternal", value = "vector"): ...

.generatePWM signature(object = "genomicProfilesInternal"): ...

.maxPWMScore<- signature(object = "genomicProfilesInternal", value = "vector"): ...

.minPWMScore<- signature(object = "genomicProfilesInternal", value = "vector"): ...

.profiles<- signature(object = "genomicProfilesInternal", value = "GRList"): ...

.tags signature(object = "genomicProfilesInternal"): ...

.tags<- signature(object = "genomicProfilesInternal", value = "character"): ...

averageExpPWMScore signature(object = "genomicProfilesInternal"): ...

BPFrequency `signature(object = "genomicProfilesInternal")`: ...

BPFrequency<- `signature(object = "genomicProfilesInternal", value = "DNAStringSet")`: ...

BPFrequency<- `signature(object = "genomicProfilesInternal", value = "vector")`: ...

DNASequenceLength `signature(object = "genomicProfilesInternal")`: ...

drop `signature(object = "genomicProfilesInternal")`: ...

maxPWMScore `signature(object = "genomicProfilesInternal")`: ...

minPWMScore `signature(object = "genomicProfilesInternal")`: ...

PFMFormat `signature(object = "genomicProfilesInternal")`: ...

PFMFormat<- `signature(object = "genomicProfilesInternal", value = "character")`: ...

PositionFrequencyMatrix `signature(object = "genomicProfilesInternal")`: ...

PositionFrequencyMatrix<- `signature(object = "genomicProfilesInternal", value = "character")`: ...

PositionFrequencyMatrix<- `signature(object = "genomicProfilesInternal", value = "matrix")`: ...

PositionWeightMatrix `signature(object = "genomicProfilesInternal")`: ...

PositionWeightMatrix<- `signature(object = "genomicProfilesInternal", value = "matrix")`: ...

profiles `signature(object = "genomicProfilesInternal")`: ...

Author(s)

Patrick C. N. Martin <pm16057@essex.ac.uk>

References

Zabet NR, Adryan B (2015) Estimating binding properties of transcription factors from genome-wide binding profiles. Nucleic Acids Res., 43, 84–94. Patrick C.N. Martin and Nicolae Radu Zabe (2020) Dissecting the binding mechanisms of transcription factors to DNA using a statistical thermodynamics framework. CSBJ, 18, 3590-3605.

See Also

genomicProfiles

parameterOptions

Examples

```
showClass("genomicProfilesInternal")
```

getHighestFitnessSolutions
Get Highest Fitness Solutions

Description

getHighestFitnessSolutions extract best solution from a ChIPanalyser GA/evolve Run.

Usage

```
getHighestFitnessSolutions(population,child=2,method="geometric")
```

Arguments

population	Population list as output by the evolve function.
child	numeric describing the number of solution to be extracted from Population list.
method	character string describing which scoring method should be used and selected from "geometric","ks","MSE","pearson","spearman","kendall", "recall","precesion","fscore","MCC","Ac or "AUC".

Details

This function only serves as a way of extracting data from the poppulation list. Ultimately - it is just a wrapper for some indexing.

Value

Return the index of the top "child" solutions.

Author(s)

Patrick C.N. Martin <pcnmartin@gmail.com>

Examples

```
library(ChIPanalyser)
data(ChIPanalyserData)
# See GA vignette for usage
```

getTestingData *Extract testing data from ChIPscore object*

Description

getTestingData extracts selected regions from ChIPscore object to be used as testing set.

Usage

```
getTestingData(ChIPscore,loci = 1)
```

Arguments

ChIPscore	ChIPscore object as returned by processingChIP
loci	numeric describing index of loci to be used as testing data.

Value

Returns ChIPscore object with the selected testing loci.

Author(s)

Patrick C.N. Martin <pcnmartin@gmail.com

Examples

```
library(ChIPanalyser)
data(ChIPanalyserData)
# See GA vignette for usage
test <- processingChIP(chip,top)
test <- getTestingData(test, 1:2)
```

getTrainingData *Extract training data from ChIPscore object*

Description

getTrainingData extracts selected regions from ChIPScore object to be used as training set.

Usage

```
getTrainingData(ChIPscore,loci = 1)
```

Arguments

ChIPscore	ChIPscore object as returned by processingChIP
loci	numeric describing index of loci to be used as training data.

Value

Returns ChIPscore object with the selected training loci.

Author(s)

Patrick C.N. Martin <pcnmartin@gmail.com

Examples

```
library(ChIPanalyser)
data(ChIPanalyserData)
# See GA vignette for usage
test <- processingChIP(chip,top)
test <- getTrainingData(test, 1:2)
```

GRList-class *Class* "GRList"

Description

Virutal Class to handle multiple data types for one slot (profiles)

Objects from the Class

A virtual Class: No objects may be created from it.

Methods

GRList-class The purpose of this virtual classe is to store data of two different formats in one slot: GRangesList and Lists

Author(s)

Patrick C. N. Martin <p.martin@essex.ac.uk>

References

Zabet NR, Adryan B (2015) Estimating binding properties of transcription factors from genome-wide binding profiles. Nucleic Acids Res., 43, 84–94.

Examples

```
showClass("GRList")
```

initialize-methods ~~ *Methods for Function* initialize ~~

Description

~~ Methods for function initialize ~~

Methods:

signature(.Object = "ChIPScore") Initialize ChIPScore

signature(.Object = "genomicProfiles") Initialize genomicProfiles

signature(.Object = "parameterOptions") Initialize parameterOptions

---

lambdaPWM *Accessor Method for the* lambdaPWM *slot in a* parameterOptions *object*

Description

Accessor Method for the lambdaPWM slot in a parameterOptions object

Usage

```
lambdaPWM(object)
```

Arguments

object	object is parameterOptions object

Details

The model underlying ChIPanalyser internally infers two paramters: number of bound molecules and lambda. Lambda represents a scaling factor for the Position weight matrix (PWM). This can be described as how well does a TF discriminate between high affinity and very high affinity sites.

Value

Returns the value assigned to the lambdaPWM slot in a parameterOptions object.

Author(s)

Patrick C. N. Martin <p.martin@essex.ac.uk>

References

Zabet NR, Adryan B (2015) Estimating binding properties of transcription factors from genome-wide binding profiles. Nucleic Acids Res., 43, 84–94.

Examples

```
# Loading data
data(ChIPanalyserData)

#Building data objects
GPP <- parameterOptions(lambdaPWM=1)
#Setting new Value for lambdaPWM
lambdaPWM(GPP)
```

`lambdaPWM-methods` *~~ Methods for Function* `lambdaPWM` *~~*

Description

~~ Methods for function `lambdaPWM` ~~

Methods:

`lambdaPWM(object)`

`lambdaPWM<-` *Setter Method for the* `lambdaPWM` *slot in a* `parameterOptions` *object*

Description

Setter Method for the `lambdaPWM` slot in a `parameterOptions` object

Usage

```
lambdaPWM(object)<-value
```

Arguments

`object`	`object` is `parameterOptions` object
`value`	`value` is the numeric value to be assigned to the lambdaPWM slot. Default set at 1.

Details

The model underlying ChIPanalyser internally infers two paramters: number of bound molecules and lambda. Lambda represents a scaling factor for the Position weight matrix (PWM). This can be described as how well does a TF discriminate between high affinity and very high affinity sites.

Value

Returns the value assigned to the lambdaPWM slot in a parameterOptions object.

Author(s)

Patrick C. N. Martin <p.martin@essex.ac.uk>

References

Zabet NR, Adryan B (2015) Estimating binding properties of transcription factors from genome-wide binding profiles. Nucleic Acids Res., 43, 84–94.

Examples

```
# Loading data
data(ChIPanalyserData)

#Building data objects
GPP <- parameterOptions(lambdaPWM=1)
#Setting new Value for lambdaPWM
lambdaPWM(GPP) <- 2
```

---

lambdaPWM<-methods ~~ *Methods for Function* lambdaPWM<- ~~

Description

Setter method for the lambdaPWM slot in the parameterOptions

Methods:

lambdaPWM(object)<-value

---

loci *Accessor Method for the* loci *slot in a* ChIPScore *object*

Description

Setter Method for the loci slot in a ChIPScore object

Usage

```
loci(object)
```

Arguments

object	object is ChIPScore object

Details

When using the processingChIP, this functions will return a name GRanges with the loci of interest. These loci will either result from user input or extracted from the ChIP profiles (see processingChIP and lociWidth). This functions enalbles you to extract those loci from the ChIPScore object.

Value

Returns the value assigned to the loci slot in a ChIPScore object.

Author(s)

Patrick C. N. Martin <p.martin@essex.ac.uk>

References

Zabet NR, Adryan B (2015) Estimating binding properties of transcription factors from genome-wide binding profiles. Nucleic Acids Res., 43, 84–94.

Examples

```
# Loading data
data(ChIPanalyserData)

chip<-processingChIP(chip,top)
loci(chip)
```

---

loci-class *Class* "loci"

Description

Setter for Loci of interest parsed to or extracted from the ChIPScore object

Objects from the Class

A virtual Class: No objects may be created from it.

Methods

.loci<- signature(object = "ChIPScore", value = "loci"): ...

Author(s)

Patrick C. N. Martin <pm16057@essex.ac.uk>

References

Zabet NR, Adryan B (2015) Estimating binding properties of transcription factors from genome-wide binding profiles. Nucleic Acids Res., 43, 84–94. Patrick C.N. Martin and Nicolae Radu Zabe (2020) Dissecting the binding mechanisms of transcription factors to DNA using a statistical thermodynamics framework. CSBJ, 18, 3590-3605.

See Also

ChIPScore

Examples

```
showClass("loci")
```

`loci-methods` *~~ Methods for Function* `loci` *~~*

Description

Accessor method for the `loci` slot in ChIPScore

Methods:

`loci{Object}` Loci of interest parsed to or extracted from the ChIPScore object

---

`lociWidth` *Accessor Method for the* `lociWidth` *slot in a* `parameterOptions` *object*

Description

Setter Method for the `lociWidth` slot in a `parameterOptions` object

Usage

```
lociWidth(object)
```

Arguments

`object`	`object` is `parameterOptions` object

Details

When using the processingChIP function, the provided ChIP scores will be split into bins of a given size. lociWidth determines the Size of that bin. Default is set at 20 000 bp. This means that the ChIP profiles provided will be split into bins of 20 000 bp over the entire profile provided if no loci of interest is provided.

Value

Returns the value assigned to the lociWidth slot in a parameterOptions object.

Author(s)

Patrick C. N. Martin <p.martin@essex.ac.uk>

References

Zabet NR, Adryan B (2015) Estimating binding properties of transcription factors from genome-wide binding profiles. Nucleic Acids Res., 43, 84–94.

Examples

```
# Loading data
data(ChIPanalyserData)

#Building data objects
GPP <- parameterOptions(lociWidth=20000)
#Accessing new Value for lociWidth
lociWidth(GPP)
```

---

lociWidth-methods ~~ *Methods for Function* lociWidth ~~

Description

Accessor method for the loci slot in ChIPScore

Methods:

lociWidth(object) Setting width of regions when using the reduce argument and NOT providing your own loci when using the processingChIP function.

lociWidth<- *Setter Method for the* lociWidth *slot in a* parameterOptions *object*

Description

Setter Method for the lociWidth slot in a parameterOptions object

Usage

```
lociWidth(object)<-value
```

Arguments

object	object is parameterOptions object
value	value is the numeric value to be assigned to the lociWidth slot. Default set at 1.

Details

When using the processingChIP function, the provided ChIP scores will be split into bins of a given size. lociWidth determines the Size of that bin. Default is set at 20 000 bp. This mean that the ChIP profiles provided will be split into bins of 20 000 bp over the entire profile provided if no loci of interest is provided.

Value

Returns the value assigned to the lociWidth slot in a parameterOptions object.

Author(s)

Patrick C. N. Martin <p.martin@essex.ac.uk>

References

Zabet NR, Adryan B (2015) Estimating binding properties of transcription factors from genome-wide binding profiles. Nucleic Acids Res., 43, 84–94.

Examples

```
# Loading data
data(ChIPanalyserData)

#Building data objects
GPP <- parameterOptions(lociWidth=20000)
#Setting new Value for lociWidth
lociWidth(GPP) <- 30000
```

---

lociWidth<-methods *~~ Methods for Function* lociWidth<- *~~*

Description

Setter method for the loci slot in ChIPScore

Methods:

lociWidth(Object)<-value

---

maxPWMScore *Accessor function for* maxPWMScore *slot in a* genomicProfiles *object.*

Description

Accessor function for maxPWMScore slot in a genomicProfiles object.

Usage

```
maxPWMScore(object)
```

Arguments

object	object is a genomicProfiles object.

Details

maxPWMScore is a numerical value that can be described as the highest PWM score computed at a genome wide scale. This value is computed and updated in the genomicProfiles object after using the computeGenomeWideScores.

Value

Returns the value of assigned to the maxPWMScore slot in a genomicProfiles object.

Author(s)

Patrick C. N. Martin <p.martin@essex.ac.uk>

References

Zabet NR, Adryan B (2015) Estimating binding properties of transcription factors from genome-wide binding profiles. Nucleic Acids Res., 43, 84–94.

Examples

```
# Loading data
#Data extraction
data(ChIPanalyserData)
# path to Position Frequency Matrix
PFM <- file.path(system.file("extdata",package="ChIPanalyser"),"BEAF-32.pfm")
#As an example of genome, this example will run on the Drosophila genome

if(!require("BSgenome.Dmelanogaster.UCSC.dm6", character.only = TRUE)){
    if (!requireNamespace("BiocManager", quietly=TRUE))
        install.packages("BiocManager")
    BiocManager::install("BSgenome.Dmelanogaster.UCSC.dm6")
}
library(BSgenome.Dmelanogaster.UCSC.dm6)
DNASequenceSet <- getSeq(BSgenome.Dmelanogaster.UCSC.dm6)
#Building data objects
GPP <- genomicProfiles(PFM=PFM,PFMFormat="JASPAR")

# Computing Genome Wide
GenomeWide <- computeGenomeWideScores(DNASequenceSet = DNASequenceSet,
    genomicProfiles = GPP)
maxPWMScore(GenomeWide)
## If used before computeGenomeWidePWMScore, will return NULL
```

`maxPWMScore-methods` *~~ Methods for Function* `maxPWMScore` *~~*

Description

Accessor method for `maxPWMScore`

Methods:

`maxPWMScore(object)`

`maxSignal` *Accessor method for the* `maxSignal` *slot in a* `parameterOptions` *object.*

Description

Accessor method for the `maxSignal` slot in a `parameterOptions` object.

Usage

```
maxSignal(object)
```

Arguments

object	object is a parameterOptions object.

Details

In the context of ChIPanalyser, maxSignal represents the maximum normalised ChIP-Seq signal of a given Transcription factor (or DNA binding protein). Although, A default value of 1 has been assigned to this slot, we strongly recommend to tailor this value accordingly. We strongly encourage to set values when building a parameterOptions object.

Value

Returns the value assigned to the maxSignal slot in a parameterOptions object.

Author(s)

Patrick C.N. Martin <p.martin@essex.ac.uk>

References

Zabet NR, Adryan B (2015) Estimating binding properties of transcription factors from genome-wide binding profiles. Nucleic Acids Res., 43, 84–94. Patrick C.N. Martin and Nicolae Radu Zabe (2020) Dissecting the binding mechanisms of transcription factors to DNA using a statistical thermodynamics framework. CSBJ, 18, 3590-3605.

Examples

```
# Building parameterOptions object
OPP <- parameterOptions()
#Setting new Value for maxSignal
maxSignal(OPP)
```

---

maxSignal-methods ~~ *Methods for Function* maxSignal ~~

Description

Accessor method for maxSignal

Methods:

maxSignal(object) Maximum ChIP signal extracted from ChIP data (see processingChIP)

maxSignal<- *Setter method for* maxSignal *slot in a* parameterOptions *object.*

Description

Setter method for maxSignal slot in a parameterOptions object.

Usage

```
maxSignal(object) <- value
```

Arguments

object	object is a parameterOptions object.
value	value is a numerical value to be assigned to the maxSignal slot.

Details

In the context of ChIPanalyser, maxSignal represents the maximum normalised ChIP-Seq signal of a given Transcription factor (or DNA binding protein). Although, A default value of 1 has been assigned to this slot, we strongly recommend to tailor this value accordingly. We strongly encourage to set values when building a parameterOptions object.

Value

Returns a parameterOptions with an updated value for maxSignal.

Author(s)

Patrick C.N. Martin <p.martin@essex.ac.uk>

References

Zabet NR, Adryan B (2015) Estimating binding properties of transcription factors from genome-wide binding profiles. Nucleic Acids Res., 43, 84–94.

Examples

```
# Building parameterOptions object
OPP <- parameterOptions()
#Setting new Value for maxSignal
maxSignal(OPP) <- 1.8
```

maxSignal<-methods *~~ Methods for Function* maxSignal<- *~~*

Description

Setter method for maxSignal

Methods:

maxSignal(Object)<-value Maximum ChIP signal extracted from ChIP data (see processingChIP)

minPWMScore *Accessor method the* minPWMScore *slot in a* genomicProfiles *object*

Description

Accessor method the minPWMScore slot in a genomicProfiles object

Usage

```
minPWMScore(object)
```

Arguments

object	object is a genomicProfiles object.

Details

minPWMScore can be described as the lowest PWM score computed at a genome wide scale. Although it is possible to assigne a value to minPWMScore, we strongly advise to use the value computed and assigned internally. This value is computed in the computeGenomeWideScores function.

Value

Returns the value assigned to the minPWMScore slot in a genomicProfiles object.

Author(s)

Patrick C. N. Martin <p.martin@essex.ac.uk>

References

Zabet NR, Adryan B (2015) Estimating binding properties of transcription factors from genome-wide binding profiles. Nucleic Acids Res., 43, 84–94.

Examples

```
#Data extraction
data(ChIPanalyserData)
# path to Position Frequency Matrix
PFM <- file.path(system.file("extdata",package="ChIPanalyser"),"BEAF-32.pfm")
#As an example of genome, this example will run on the Drosophila genome

if(!require("BSgenome.Dmelanogaster.UCSC.dm6", character.only = TRUE)){
    if (!requireNamespace("BiocManager", quietly=TRUE))
        install.packages("BiocManager")
    BiocManager::install("BSgenome.Dmelanogaster.UCSC.dm6")
}
library(BSgenome.Dmelanogaster.UCSC.dm6)
DNASequenceSet <- getSeq(BSgenome.Dmelanogaster.UCSC.dm6)
#Building data objects
GPP <- genomicProfiles(PFM=PFM,PFMFormat="JASPAR")

# Computing Genome Wide
GenomceWide <- computeGenomeWideScores(DNASequenceSet = DNASequenceSet,
    genomicProfiles = GPP)
minPWMScore(GenomceWide)

## If used before computeGenomeWidePWMScore, will return NULL
```

---

minPWMScore-methods *~~ Methods for Function* minPWMScore *~~*

Description

Accessor for minPWMScore

Methods:

minPWMScore(object) Minimum PWM score computed during the computeGenomeWideScores step.

---

naturalLog *Accessor method the* naturalLog *slot in a* parameterOptions *object.*

Description

Accessor method the naturalLog slot in a parameterOptions object.

Usage

```
naturalLog(object)
```

Arguments

object	object is parameterOptions object.

Details

During the computation of a Postion Weight Matrix, the Position Probability Matrix (derived from a Position Frequency Matrix) is log transformed. This parameter provides whcih "log transform" will be used. If TRUE, the Natural Log will bu used (ln). If FALSE, log2 will be used. We strongly encourage to set values when building a parameterOptions object.

Value

Returns the value assigned to the naturalLog slot in a parameterOptions object.

Author(s)

Patrick C.N. Martin <p.martin@essex.ac.uk>

References

Zabet NR, Adryan B (2015) Estimating binding properties of transcription factors from genome-wide binding profiles. Nucleic Acids Res., 43, 84–94. Patrick C.N. Martin and Nicolae Radu Zabe (2020) Dissecting the binding mechanisms of transcription factors to DNA using a statistical thermodynamics framework. CSBJ, 18, 3590-3605.

Examples

```
# Loading data
data(ChIPanalyserData)

#Building data objects
GPP <- parameterOptions(naturalLog=TRUE)
#Setting new Value for naturalLog
naturalLog(GPP)
```

---

naturalLog-methods ~~ *Methods for Function* naturalLog ~~

Description

Accessor method for the naturalLog slot in a parameterOptions object.

Methods:

naturalLog(object)

naturalLog<- *Setter method for the* naturalLog *slot in a* parameterOptions *object.*

Description

Setter method for the naturalLog slot in a parameterOptions object.

Usage

```
naturalLog(object)<- value
```

Arguments

object	object is a parameterOptions object.
value	value is a logical value that will determine if the natural log or log2 should be used for the computation of the Position Weight Matrix.

Details

During the computation of a Postion Weight Matrix, the Position Probability Matrix (derived from a Position Frequency Matrix) is log transformed. This parameter provides whcih "log transform" will be used. If TRUE, the Natural Log will bu used (ln). If FALSE, log2 will be used. We strongly encourage to set values when building a parameterOptions object.

Value

Returns parameterOptions object with an updated value for the naturalLog slot.

Author(s)

Patrick C.N. Martin <p.martin@essex.ac.uk>

References

Zabet NR, Adryan B (2015) Estimating binding properties of transcription factors from genome-wide binding profiles. Nucleic Acids Res., 43, 84–94. Patrick C.N. Martin and Nicolae Radu Zabe (2020) Dissecting the binding mechanisms of transcription factors to DNA using a statistical thermodynamics framework. CSBJ, 18, 3590-3605.

Examples

```
# Loading data
data(ChIPanalyserData)

#Building data objects
OPP <- parameterOptions(naturalLog=TRUE)
#Setting new Value for naturalLog
naturalLog(OPP) <- FALSE
```

naturalLog<-methods *~~ Methods for Function* naturalLog<- *~~*

Description

Setter method for the naturalLog slot in a parameterOptions object.

Methods:

naturalLog(object)<-value

---

noiseFilter *Accessor Method for the* noiseFilter *slot in a* parameterOptions *object*

Description

Accessor Method for the noiseFilter slot in a parameterOptions object

Usage

```
noiseFilter(object)
```

Arguments

object	object is parameterOptions object

Details

Noise filtering method that should be used on ChIP-seq data. Four methods are available: Zero, Mean, Median and Sigmoid. Zero removes all ChIP-seq scores bellow zero, mean under the mean score, median under median score and sigmoid assignes a weight to each score based on a logistic regression curve. Mid point is set at 95 95 quantile of ChIP-seq scores. Below midpoint will receive a score between 0 and 1 , everything above will receive a score between 1 and 2

Value

Returns the value assigned to the noiseFilter slot in a parameterOptions object.

Author(s)

Patrick C. N. Martin <p.martin@essex.ac.uk>

References

Zabet NR, Adryan B (2015) Estimating binding properties of transcription factors from genome-wide binding profiles. Nucleic Acids Res., 43, 84–94.

Examples

```
# Loading data
data(ChIPanalyserData)

#Building data objects
GPP <- parameterOptions(noiseFilter="sigmoid")
#Setting new Value for noiseFilter
noiseFilter(GPP)
```

`noiseFilter-methods` *~~ Methods for Function* `noiseFilter` *~~*

Description

Accessor method for `noiseFilter`

Methods:

`noiseFilter(object)` Noise Filter that will be applied to ChIP scores

`noiseFilter<-` *Setter Method for the* `noiseFilter` *slot in a* `parameterOptions` *object*

Description

Setter Method for the `noiseFilter` slot in a `parameterOptions` object

Usage

```
noiseFilter(object) <- value
```

Arguments

`object`	`object` is `parameterOptions` object
`value`	`value` is the value to be assigned to the `noiseFilter` slot (zero - mean - median -sigmoid)

Details

Noise filtering method that should be used on ChIP-seq data. Four methods are available: Zero, Mean, Median and Sigmoid. Zero removes all ChIP-seq scores bellow zero, mean under the mean score, median under median score and sigmoid assignes a weight to each score based on a logistic regression curve. Mid point is set at 95 95 quantile of ChIP-seq scores. Below midpoint will receive a score between 0 and 1 , everything above will receive a score between 1 and 2

Value

Returns the value assigned to the noiseFilter slot in a parameterOptions object.

Author(s)

Patrick C. N. Martin <p.martin@essex.ac.uk>

References

Zabet NR, Adryan B (2015) Estimating binding properties of transcription factors from genome-wide binding profiles. Nucleic Acids Res., 43, 84–94.

Examples

```
# Loading data
data(ChIPanalyserData)

#Building data objects
GPP <- parameterOptions(noiseFilter="sigmoid")
#Setting new Value for noiseFilter
noiseFilter(GPP) <-"zero"
```

---

noiseFilter<-methods ~~ *Methods for Function* noiseFilter<- ~~

Description

Setter method for noiseFilter

Methods:

noiseFilter(object)<-value Noise Filter that will be applied to ChIP scores

---

noOfSites *Accessor Method for the* noOfSites *slot in a* parameterOptions *object*

Description

Accessor Method for the noOfSites slot in a parameterOptions object

Usage

```
noOfSites(object)
```

Arguments

object	object is parameterOptions object

Details

While computing Position Weight Matricies (PWM) from Position Frequency Matricies (PFM), it is possible to restrict the number of sites that will be used to compute the PWM. The default is set at "all". In this case, all sites will be used to compute the PWM.

Value

Returns the value assigned to the noOfSites slot in a parameterOptions object.

Author(s)

Patrick C. N. Martin <p.martin@essex.ac.uk>

References

Zabet NR, Adryan B (2015) Estimating binding properties of transcription factors from genome-wide binding profiles. Nucleic Acids Res., 43, 84–94.

Examples

```
# Loading data
data(ChIPanalyserData)

#Building data objects
GPP <- parameterOptions(noOfSites="all")
#Setting new Value for naturalLog
noOfSites(GPP)
```

---

noOfSites-methods ~~ *Methods for Function* noOfSites ~~

Description

~~ Methods for function noOfSites ~~

Methods:

signature(object = "parameterOptions")

noOfSites<- *Setter Method for the* noOfSites *slot in a* parameterOptions *object.*

Description

Setter Method for the noOfSites slot in a parameterOptions object.

Usage

```
noOfSites(object) <- value
```

Arguments

object	object is a parameterOptions object.
value	value is a positive integer that will be assigned to the noOfSites slot.

Details

While computing Position Weight Matricies (PWM) from Position Frequency Matricies (PFM), it is possible to restrict the number of sites that will be used to compute the PWM. The default is set at "all". In this case, all sites will be used to compute the PWM.

Value

Returns a parameterOptions object with an updated value for the noOfSites slot.

Author(s)

Patrick C.N. Martin <p.martin@essex.ac.uk>

References

Zabet NR, Adryan B (2015) Estimating binding properties of transcription factors from genome-wide binding profiles. Nucleic Acids Res., 43, 84–94. Patrick C.N. Martin and Nicolae Radu Zabe (2020) Dissecting the binding mechanisms of transcription factors to DNA using a statistical thermodynamics framework. CSBJ, 18, 3590-3605.

Examples

```
# Loading data
data(ChIPanalyserData)

#Building data objects
GPP <- parameterOptions(noOfSites=0)
#Setting new Value for naturalLog
noOfSites(GPP) <- 8
```

noOfSites<-methods ~~ *Methods for Function* noOfSites<- ~~

Description

Setter method for noOfSites

Methods:

noOfSites(object)<-"all"

noOfSites(object)<-value

nos-class *Class* "nos"

Description

Virtual class to handle Number of Sites

Objects from the Class

A virtual Class: No objects may be created from it.

Methods

No methods defined with class "nos" in the signature.

Author(s)

Patrick C. N. Martin <pm16057@essex.ac.uk>

References

Zabet NR, Adryan B (2015) Estimating binding properties of transcription factors from genome-wide binding profiles. Nucleic Acids Res., 43, 84–94. Patrick C.N. Martin and Nicolae Radu Zabe (2020) Dissecting the binding mechanisms of transcription factors to DNA using a statistical thermodynamics framework. CSBJ, 18, 3590-3605.

Examples

```
showClass("nos")
```

parameterOptions *parameter Options object*

Description

parameterOptions is an object used to store and parse the various parameters needed throughout this analysis pipeline.

Usage

```
parameterOptions(ploidy = 2, boundMolecules = 1000, backgroundSignal = 0, maxSignal = 1, lociWidth = 200
```

Arguments

ploidy	ploidy: A numeric Value descibing the ploidy of the organism. Default: 2
boundMolecules	boundMolecules: A vector (or single value) containing the number of bound Molecules (bound Transcription Factors): Default: 1000
backgroundSignal	backgroundSignal: A numeric value descibing the ChIP-seq background Signal (average signal from real ChIP seq data). Default: 0
maxSignal	maxSignal: A numeric value describing the highest ChIP-seq signal (from real ChIP-seq data). Default: 1
lociWidth	lociWidth: A numeric value describing the width of the bins used to split ChIP profiles parsed to processingChIP. Default = 20000
chipMean	chipMean: A numeric value describing the mean width of a ChIP- seq peak: Default:200
chipSd	chipSd: A numeric value describing the standard deviation of ChIP-seq peaks. Default: 200
chipSmooth	chipSmooth: A numeric value describing the width of the window used to smooth Occupancy profiles into ChIP profiles. Default:250
stepSize	stepSize: A numeric value describing the step Size (in base pairs) between each ChIP-seq score. Default:10 (Scored every 10 base pairs)
removeBackground	removeBackground: A numeric value describing the value at which score should be removed. Defualt:0 (If negative scores then remove)
noiseFilter	noiseFilter: A character string of one of the following: Zero, Mean, Median, or Sigmoid. Noise filter that will be applied to the ChIP Score during the processingChIP step.
naturalLog	naturalLog: A logical value describing if natural Log will be used to compute the PWM (if FALSE then log2 will be used). Default: TRUE
noOfSites	noOfSites: A Positive integer descibing number of sites (in base pair) should be used from the PFM to compute PWM. Default =0 (Full width of binding site will be used when set to 0)

PWMThreshold	PWMThreshold: Threshold at which PWM Score should be selected (only sites above threshold will be selected - between 0 and 1)
strandRule	strandRule: 'mean', 'max' or 'sum' will dertermine how strand should be handle for computing PWM Scores. Default : 'max'
whichstrand	whichstrand: '+','-' or '+-' on which strand should PWM Score be computed. Default: '+-'
PWMpseudocount	PWMpseudocount: A numeric value describing a PWMpseudocount for PWM computation. Default:1
lambdaPWM	A vector (or single value) contaning values for the ScalingFactorPWM (Also known as lambda).Default:1

Details

ChIPanalyser requires a lot of parameters. parameterOptions was created with the intent of storing and parsing these numerous arguments to the different functions. All parameters in this object are optional although strongly recommend. Some parameters are extracted and updated from function along the pipeline e.g. maxSignal and backgroundSignal are extracted during the processingChIP step. These paramters will be automatically parsed. If you do not which to use them (or any other parameter) simply parse a new parameterOptions object with your desired paramters.

Value

Returns a parameterOptions with updated values.

Author(s)

Patrick C. N. Martin <p.martin@essex.ac.uk>

References

Zabet NR, Adryan B (2015) Estimating binding properties of transcription factors from genome-wide binding profiles. Nucleic Acids Res., 43, 84–94.

See Also

genomicProfiles

Examples

```
#
parameterOptions(ploidy = 2, boundMolecules = 1000, backgroundSignal = 0,
    maxSignal = 1, lociWidth = 20000, chipMean = 200, chipSd = 200,
    chipSmooth = 250, stepSize = 10, removeBackground = 0, noiseFilter = "zero",
    naturalLog = TRUE, noOfSites = "all", PWMThreshold = 0.7,
    strandRule = "max", whichstrand = "+-", PWMpseudocount = 1,
    lambdaPWM = 1)
```

parameterOptions-class

Class "parameterOptions"

Description

parameterOptions is an object used to store and parse the various parameters needed throughout this analysis pipeline.

Objects from the Class

Objects can be created by calls of the form parameterOptions(ploidy, boundMolecules, backgroundSignal, maxSignal, lociWidth, chipMean, chipSd, chipSmooth, stepSize, noiseFilter, removeBackground, lambdaPWM, PWMpseudocount, naturalLog, noOfSites, PWMThreshold, strandRule, whichstrand).

Slots

ploidy: Object of class "numeric": A numeric Value descibing the ploidy of the organism. Default: 2

boundMolecules: Object of class "vector": A vector (or single value) containing the number of bound Molecules (bound Transcription Factors): Default: 1000

backgroundSignal: Object of class "numeric": A numeric value descibing the ChIP-seq background Signal (average signal from real ChIP seq data). Default: 0

maxSignal: Object of class "numeric": A numeric value describing the highest ChIP-seq signal (from real ChIP-seq data). Default: 1

lociWidth: Object of class "numeric": A numeric value describing bin size when splitting ChIP seq scores). Default: 20 000

chipMean: Object of class "numeric": A numeric value describing the mean width of a ChIP- seq peak. Default:150

chipSd: Object of class "numeric": A numeric value describing the standard deviation of ChIP-seq peaks. Default: 150

chipSmooth: Object of class "vector": A numeric value describing the width of the window used to smooth Occupancy profiles into ChIP profiles. Default:250

stepSize: Object of class "numeric": A numeric value describing the step Size (in base pairs) between each ChIP-seq score. Default:10 (Scored every 10 base pairs)

removeBackground: Object of class "numeric": A numeric value describing the value at which score should be removed. Defualt:0 (If negative scores then remove)

noiseFilter: Object of class "character" Describes noiseFilter method applied to ChIP scores

PWMThreshold: Object of class "numeric": Threshold at which PWM Score should be selected (only sites above threshold will be selected - between 0 and 1)

strandRule: Object of class "character": "mean", "max" or "sum" will dertermine how strand should be handle for computing PWM Scores. Default : "max"

whichstrand: Object of class "character": "+","-" or "+-" on which strand should PWM Score be computed. Default: "+-"

lambdaPWM: Object of class "vector" A vector (or single value) contaning values for lambdaPWM Default:1

naturalLog: Object of class "logical": A logical value describing if natural Log will be used to compute the PWM (if FALSE then log2 will be used). Default: TRUE

noOfSites: Object of class "nos" A Positive integer descibing number of sites (in base pair) should be used from the PFM to compute PWM. Default =0 (Full width of binding site will be used when set to 0)

PWMpseudocount: Object of class "numeric": A numeric value describing a PWMpseudocount for PWM computation. Default:1

paramTag: Object of class "character" ~Internal~

Methods

.paramTag signature(object = "parameterOptions"): ...

.paramTag<- signature(object = "parameterOptions", value = "character"): ...

.ZeroBackground signature(object = "parameterOptions"): ...

.ZeroBackground<- signature(object = "parameterOptions", value = "vector"): ...

backgroundSignal signature(object = "parameterOptions"): ...

backgroundSignal<- signature(object = "parameterOptions", value = "numeric"): ...

boundMolecules signature(object = "parameterOptions"): ...

boundMolecules<- signature(object = "parameterOptions", value = "vector"): ...

chipMean signature(object = "parameterOptions"): ...

chipMean<- signature(object = "parameterOptions", value = "numeric"): ...

chipSd signature(object = "parameterOptions"): ...

chipSd<- signature(object = "parameterOptions", value = "numeric"): ...

chipSmooth signature(object = "parameterOptions"): ...

chipSmooth<- signature(object = "parameterOptions", value = "vector"): ...

initialize signature(.Object = "parameterOptions"): ...

lambdaPWM signature(object = "parameterOptions"): ...

lambdaPWM<- signature(object = "parameterOptions", value = "vector"): ...

lociWidth signature(object = "parameterOptions"): ...

lociWidth<- signature(object = "parameterOptions", value = "numeric"): ...

maxSignal signature(object = "parameterOptions"): ...

maxSignal<- signature(object = "parameterOptions", value = "numeric"): ...

naturalLog signature(object = "parameterOptions"): ...

naturalLog<- signature(object = "parameterOptions", value = "logical"): ...

noiseFilter signature(object = "parameterOptions"): ...

noiseFilter<- signature(object = "parameterOptions", value = "character"): ...

noOfSites `signature(object = "parameterOptions")`: ...

noOfSites<- `signature(object = "parameterOptions", value = "character")`: ...

noOfSites<- `signature(object = "parameterOptions", value = "numeric")`: ...

ploidy `signature(object = "parameterOptions")`: ...

ploidy<- `signature(object = "parameterOptions", value = "numeric")`: ...

PWMpseudocount `signature(object = "parameterOptions")`: ...

PWMpseudocount<- `signature(object = "parameterOptions", value = "numeric")`: ...

PWMThreshold `signature(object = "parameterOptions")`: ...

PWMThreshold<- `signature(object = "parameterOptions", value = "numeric")`: ...

removeBackground `signature(object = "parameterOptions")`: ...

removeBackground<- `signature(object = "parameterOptions", value = "vector")`: ...

show `signature(object = "parameterOptions")`: ...

stepSize `signature(object = "parameterOptions")`: ...

stepSize<- `signature(object = "parameterOptions", value = "numeric")`: ...

strandRule `signature(object = "parameterOptions")`: ...

strandRule<- `signature(object = "parameterOptions", value = "character")`: ...

whichstrand `signature(object = "parameterOptions")`: ...

whichstrand<- `signature(object = "parameterOptions", value = "character")`: ...

Author(s)

Partick C. N. Martin <p.martin@essex.ac.uk>

References

Zabet NR, Adryan B (2015) Estimating binding properties of transcription factors from genome-wide binding profiles. Nucleic Acids Res., 43, 84–94. Patrick C.N. Martin and Nicolae Radu Zabe (2020) Dissecting the binding mechanisms of transcription factors to DNA using a statistical thermodynamics framework. CSBJ, 18, 3590-3605.

See Also

genomicProfiles

Examples

```
showClass("parameterOptions")
```

PFMFormat *Accesor method for the* PFMFormat *slot in a* genomicProfiles *object*

Description

Accesor method for the PFMFormat slot in a genomicProfiles object

Usage

```
PFMFormat(object)
```

Arguments

object	object is a genomicProfiles object

Details

If loading a PositionFrequencyMatrix from a file, the format of the file should be specified. Default is raw. Please keep in mind that this argument is used when parsing the PositionFrequencyMatrix file. IF this argument is changed after building the genomicProfiles with a PositionFrequencyMatrix file, this will not influence the parsing of the file. PFMFormat can be one of the following: "raw","transfac","JASPAR" or "sequences"

Value

Returns the value assigned to the PFMFormat slot a genomicProfiles

Author(s)

Patrick C. N. Martin <pm16057@essex.ac.uk>

References

Zabet NR, Adryan B (2015) Estimating binding properties of transcription factors from genome-wide binding profiles. Nucleic Acids Res., 43, 84–94. Patrick C.N. Martin and Nicolae Radu Zabe (2020) Dissecting the binding mechanisms of transcription factors to DNA using a statistical thermodynamics framework. CSBJ, 18, 3590-3605.

Examples

```
# Loading data
data(ChIPanalyserData)
#Loading PFM files
PFM <- file.path(system.file("extdata",package="ChIPanalyser"),"BEAF-32.pfm")
#Building data objects
#### THIS IS THE PREFFERED METHOD FOR SETTING PFMFormat
GPP <- genomicProfiles(PFM=PFM,PFMFormat="JASPAR")
```

```
#Setting New value for PFMFormat
PFMFormat(GPP)
```

PFMFormat-methods *~~ Methods for Function* PFMFormat *~~*

Description

Accesor method for the PFMFormat slot in a genomicProfiles object

Methods:

```
PFMFormat(object)
```

PFMFormat<- *Setter method for the* PFMFormat *slot in a* genomicProfiles *object*

Description

Setter method for the PFMFormat slot in a genomicProfiles object

Usage

```
PFMFormat(object) <- value
```

Arguments

object	object is a genomicProfiles object
value	value is character string of one of the following: "raw","transfac","JASPAR" or "sequences". If loading a PositionFrequencyMatrix from a file, the format of the file should specified. Default is JASPAR.

Details

If loading a PositionFrequencyMatrix from a file, the format of the file should be specified. Default is JASPAR. Please keep in mind that this argument is used when parsing the PositionFrequencyMatrix file. IF this argument is changed after building the genomicProfiles with a PositionFrequencyMatrix file, this will not influence the parsing of the file.

Value

Returns a genomicProfiles object with an updated value for the PFMFormat slot.

Author(s)

Patrick C. N. Martin <pm16057@essex.ac.uk>

References

Zabet NR, Adryan B (2015) Estimating binding properties of transcription factors from genome-wide binding profiles. Nucleic Acids Res., 43, 84–94. Patrick C.N. Martin and Nicolae Radu Zabe (2020) Dissecting the binding mechanisms of transcription factors to DNA using a statistical thermodynamics framework. CSBJ, 18, 3590-3605.

Examples

```
# Loading data
data(ChIPanalyserData)
#Loading PFM files
PFM <- file.path(system.file("extdata",package="ChIPanalyser"),"BEAF-32.pfm")
#Building data objects
#### THIS IS THE PREFFERED METHOD FOR SETTING PFMFormat
GPP <- genomicProfiles(PFM=PFM,PFMFormat="JASPAR")
#Setting New value for PFMFormat
PFMFormat(GPP) <- "JASPAR"
```

`PFMFormat<-methods` *~~ Methods for Function* `PFMFormat<-` *~~*

Description

Setter method for the `PFMFormat` slot in a `genomicProfiles` object

Methods:

`PFMFormat(object)<-value`

`ploidy` *Accessor method for the* `ploidy` *slot in a* `parameterOptions` *object*

Description

Accessor method for the `ploidy` slot in a `parameterOptions` object

Usage

```
ploidy(object)
```

Arguments

`object`	`object` is a `parameterOptions` object

Details

Default value for ploidy is set a 2. It should be mentioned that ChIPanalyser is based on a model that also considers the ploidy of the organism of interest however this only considers simple polyploidy (or haploidy). The model does not consider hybrids such as wheat.

Value

Returns the value assigned to the ploidy slot in a parameterOptions object

Author(s)

Patrick C. N. Martin <pm16057@essex.ac.uk>

References

Zabet NR, Adryan B (2015) Estimating binding properties of transcription factors from genome-wide binding profiles. Nucleic Acids Res., 43, 84–94.

Examples

```
# Building parameterOptions object
OPP <- parameterOptions()
#Setting new Value for maxSignal
ploidy(OPP)
```

---

ploidy-methods ~~ *Methods for Function* ploidy ~~

Description

Accessor method for the ploidy slot in a parameterOptions object

Methods:

ploidy(object)

ploidy<- *Setter Method for the* ploidy *slot in an* parameterOptions *object*

Description

Setter Method for the ploidy slot in an parameterOptions object

Usage

```
ploidy(object)<- value
```

Arguments

object	object is a parameterOptions object
value	value is a positive integer that describes the ploidy of the organism of interest.

Details

Default value for ploidy is set a 2. It should be mentioned that ChIPanalyser is based on a model that also considers the ploidy of the organism however this only considers simple polyploidy (or haploidy). T he model does not consider hybrids such as wheat.

Value

Returns a parameterOptions object with an updated value for the ploidy slot.

Author(s)

Patrick C. N. Martin <pm16057@essex.ac.uk>

References

Zabet NR, Adryan B (2015) Estimating binding properties of transcription factors from genome-wide binding profiles. Nucleic Acids Res., 43, 84–94.

Examples

```
# Building parameterOptions object
OPP <- parameterOptions()
#Setting new Value for maxSignal
ploidy(OPP) <- 2
```

---

ploidy<-methods ~~ *Methods for Function* ploidy<- ~~

Description

Setter Method for the ploidy slot in an parameterOptions object

Methods:

ploidy(object)<-value

---

plotOccupancyProfile *Plot Occupancy Profiles*

Description

plotOccupancyProfile plots the predicted profiles. If provided, this functions will also plot ChIP-seq profiles, PWMScores (or Occupancy), chromatin States, Goodness of Fit estimates and gene information.

Usage

```
plotOccupancyProfile(predictedProfile, ChIPScore = NULL,chromatinState = NULL,
  occupancy = NULL,goodnessOfFit = NULL,PWM=FALSE,
  geneRef = NULL,addLegend = TRUE,...)
```

Arguments

predictedProfile	predictedProfile is a either GRanges containing the predicted profiles for one loci, all loci selected for one paramter, or all loci selected for all parameter combinations selected. (see searchSites)
ChIPScore	ChIPScore is a ChIPscore object containing ChIPscore (or a list of numeric values representing ChIP scores (Experimental ChIP))
chromatinState	chromatinState is a GRanges containing accesible DNA sites or chromatin States.
occupancy	occupancy is a GRanges or a genomicProfiles object contaning PWM scores and Occupancy (see computeOccupancy)
goodnessOfFit	goodnessOfFit results of the profileAccuracyEstimate function.
PWM	PWM is a logical value that in the case occupancy is provided which of occupancy scores of PWM scores hsould be plotted. Default set at FALSE
geneRef	geneRef is a GRanges containing gene information on exons,introns, UTR's, enhancers or any other genetic element to be plotted.

addLegend — addLegend is a logical value defining if the legend should be added. The legend will add all elements provided. See details.

... — Any other graphical Parameter of the following : cex, cex.lab, cex.main, densityCS , densityGR , ylab, xlab, main, colPred, colChIP, colOccup, colCS, colGR, n_axis_ticks. See details.

Details

Once the predicted ChIP-seq like profiles have been computed, it is possible to plot these profiles.

This functions allows to control graphical parameters. In short:

* col = color values - exact number of colors or colors that will be used in a colorRampPalettte.

* cex = font sizes - for text, axis labels and main

* Density = fill density for chromatin state and/or geneRef blocks

Pred = predictedProfile ChIP = ChIP score (Experimental ChIP data) CS = Chromatin States GR = Gene reference Occup = Occupnacy locations

Value

Returns a profile plot with "Occupancy" on the y axis and DNA position on the the X- axis.

Author(s)

Patrick C.N. Martin <pcnmartin@gmail.com>

References

Zabet NR, Adryan B (2015) Estimating binding properties of transcription factors from genome-wide binding profiles. Nucleic Acids Res., 43, 84–94. Patrick C.N. Martin and Nicolae Radu Zabe (2020) Dissecting the binding mechanisms of transcription factors to DNA using a statistical thermodynamics framework. CSBJ, 18, 3590-3605.

Examples

```
#Data extraction
data(ChIPanalyserData)
# path to Position Frequency Matrix
PFM <- file.path(system.file("extdata",package="ChIPanalyser"),"BEAF-32.pfm")
#As an example of genome, this example will run on the Drosophila genome

if(!require("BSgenome.Dmelanogaster.UCSC.dm6", character.only = TRUE)){
    if (!requireNamespace("BiocManager", quietly=TRUE))
        install.packages("BiocManager")
    BiocManager::install("BSgenome.Dmelanogaster.UCSC.dm6")
    }
library(BSgenome.Dmelanogaster.UCSC.dm6)
DNASequenceSet <- getSeq(BSgenome.Dmelanogaster.UCSC.dm6)
#Building data objects
GPP <- genomicProfiles(PFM=PFM,PFMFormat="JASPAR", BPFrequency=DNASequenceSet)
```

```
# Computing Genome Wide
GenomeWide <- computeGenomeWideScores(DNASequenceSet = DNASequenceSet,
    genomicProfiles = GPP)

#Compute PWM Scores
PWMScores <- computePWMScore(DNASequenceSet = DNASequenceSet,
    genomicProfiles = GenomeWide,
    loci = top, chromatinState = Access)
#Compute Occupnacy
Occupancy <- computeOccupancy(genomicProfiles = PWMScores)

#Compute ChIP profiles
chipProfile <- computeChipProfile(loci = top,
    genomicProfiles = Occupancy)


#Plotting Profile
plotOccupancyProfile(predictedProfile=chipProfile,
    ChIPScore = chip,
    chromatinState = Access,
    occupancy = Occupancy,
    geneRef =geneRef)

plotOccupancyProfile(predictedProfile=chipProfile,
    ChIPScore = chip,
    chromatinState = Access,
    occupancy = Occupancy,
    geneRef = geneRef,
    colCS = c("red","blue"),
    densityGR = 60)
```

`plotOptimalHeatMaps` *Heat Map of optimal Parameters*

Description

`plotOptimalHeatMaps` will plot heat maps of optimal Parameters and highlight the optimal combination of `lambdaPWM` and `boundMolecules`

Usage

```
plotOptimalHeatMaps(optimalParam,contour=TRUE,col=NULL,main=NULL,layout=TRUE,overlay=FALSE)
```

Arguments

optimalParam	optimalParam is a list containing containing optimal matricies (or only one if only one paramter was selected). These matricies are the result of the computeOptimal function
contour	parameter is logical. Should contour lines be plotted?
col	col vector of colours to be used for each heat map. If none are specified, rainbow colours will be used. NOTE: colour vector will be recyled if not enough colours are provided.
main	main title.
layout	layout is either TRUE or FALSE specifying if stadard layout should be used or not. If TRUE, each heat map will be plotted on an individual page with a heat map scale of the right side.
overlay	overlay is either TRUE or FALSE specifying if an overlay plot should be produced. The overlay plot takes the top 10 percent of best performing parameters per scoring metric and overlays them in a single plot. The resulting plots shows the optimal set of paramters for all metrics combined.

Details

Once the optimal set of Parameters (lambdaPWM and boundMolecules), it is possible to plot the results in the form of a heat map. Each heat map will be plotted in a seperate page if layout = TRUE, If layout= FALSE, it is up to the user to define how they wish to layout there heat maps.

Value

Returns a heat map of optimal combinations of lambdaPWM and boundMolecules. The x axis represents the different value assigned to lambda (lambdaPWM) and the y axis represents the different values to boundMolecules (boundMolecules).

Author(s)

Patrick C. N. Martin <pm16057@essex.ac.uk>

References

Zabet NR, Adryan B (2015) Estimating binding properties of transcription factors from genome-wide binding profiles. Nucleic Acids Res., 43, 84–94.

Examples

```
#Data extraction
data(ChIPanalyserData)
# path to Position Frequency Matrix
PFM <- file.path(system.file("extdata",package="ChIPanalyser"),"BEAF-32.pfm")
#As an example of genome, this example will run on the Drosophila genome

if(!require("BSgenome.Dmelanogaster.UCSC.dm6", character.only = TRUE)){
    if (!requireNamespace("BiocManager", quietly=TRUE))
```

```
        install.packages("BiocManager")
    BiocManager::install("BSgenome.Dmelanogaster.UCSC.dm6")
    }
library(BSgenome.Dmelanogaster.UCSC.dm6)
DNASequenceSet <- getSeq(BSgenome.Dmelanogaster.UCSC.dm6)

#Building data objects
GPP <- genomicProfiles(PFM=PFM,PFMFormat="JASPAR",BPFrequency=DNASequenceSet)

#Computing Optimal set of Parameters
optimalParam <- computeOptimal(genomicProfiles = GPP,
    DNASequenceSet = DNASequenceSet,
    ChIPScore = chip,
    chromatinState = Access,
    parameterOptions = OPP,
    parameter = "all",
    peakMethod="moving_kernel")
plotOptimalHeatMaps(optimalParam)
```

`PositionFrequencyMatrix`

Accessor method for the `PFM` *slot in a* `genomicProfiles` *object*

Description

Accessor method for the `PFM` slot in a `genomicProfiles` object

Usage

```
PositionFrequencyMatrix(object)
```

Arguments

`object`	`object` is a `genomicProfiles` object

Details

After creating a `genomicProfiles` object, it is possible to access the Position Frequency Matrix slot. However this slot will be empty if the `genomicProfiles` object was built using directly a Position Weight Matrix. See `genomicProfiles`

Value

Returns the Position Frequency Matrix (`PFM` slot) used to compute the `PositionWeightMatrix` in a `genomicProfiles` object

Author(s)

Patrick C. N. Martin <pm16057@essex.ac.uk>

References

Zabet NR, Adryan B (2015) Estimating binding properties of transcription factors from genome-wide binding profiles. Nucleic Acids Res., 43, 84–94. Patrick C.N. Martin and Nicolae Radu Zabe (2020) Dissecting the binding mechanisms of transcription factors to DNA using a statistical thermodynamics framework. CSBJ, 18, 3590-3605.

Examples

```
#Loading data
data(ChIPanalyserData)
#Loading PFM files
PFM <- file.path(system.file("extdata",package="ChIPanalyser"),"BEAF-32.pfm")
#Building genomicProfiles object
GPP<-genomicProfiles(PFM=PFM,PFMFormat="JASPAR")
# Accessing Slot
PositionFrequencyMatrix(GPP)
```

PositionFrequencyMatrix-methods

~~ Methods for Function PositionFrequencyMatrix *~~*

Description

Accessor method for the PFM slot in a genomicProfiles object

Methods:

PositionFrequencyMatrix(object)

PositionFrequencyMatrix<-

Setter method for the PFM *slot in a* genomicProfiles *object*

Description

Setter method for the PFM slot in a genomicProfiles object

Usage

```
PositionFrequencyMatrix(object)<- value
```

Arguments

object	object is a genomicProfiles object
value	value can be of two forms. Either a matrix in the form of a Position Frequency Matrix or a path/to/file character string.

Details

The Position Frequency Matrix is one of the fundamental object that needs to be supplied to a genomicProfiles. If after building a genomicProfiles, only the Position Frequency Matrix needs to be modified then it is possible to manually update the value of this matrix using the function above. There are two options for the type of data that may be supplied to the PFM slot: a matrix in the form of a Position Frequency Matrix (matrix with four rows - one for each base pair (ACTG) and a number of columns equal to the number of sites in the binding site), or it is possible (also recommended) to provide a path to the file containing the Position Frequency Matrix. This Position Frequency Matrix file may come in multiple form such as RAW, Transfac or JASPAR. WARNING: if a genomicProfiles object has already been created and only the PFM is supplied/updated , then the Positon Weight Matrix will automatically updated as well.

Value

Returns a genomicProfiles with an updated PFM slot (as described above this will lead to an updated PositionWeightMatrix).

Author(s)

Patrick C. N. Martin <pm16057@essex.ac.uk>

References

Zabet NR, Adryan B (2015) Estimating binding properties of transcription factors from genome-wide binding profiles. Nucleic Acids Res., 43, 84–94.

Examples

```
#Loading data
data(ChIPanalyserData)
#Loading PFM files
PFM <- file.path(system.file("extdata",package="ChIPanalyser"),"BEAF-32.pfm")
#Building genomicProfiles object
# NOT ADVISED!!!! PLEASE PARSE PFM AND PFMFormat together
GPP<-genomicProfiles(PFMFormat = "JASPAR")
#Setting PFM
PositionFrequencyMatrix(GPP) <- PFM
```

PositionFrequencyMatrix<-methods

~~ *Methods for Function* PositionFrequencyMatrix<- ~~

Description

Setter method for the PFM slot in a genomicProfiles object

Methods:

```
PositionFrequencyMatrix(object)<-"path/to/file/"
PositionFrequencyMatrix(object)<-value
```

PositionWeightMatrix *Accessor Method for the* PWM *slot in a* genomicProfiles *object*

Description

Accessor Method for the PWM slot in a genomicProfiles object

Usage

```
PositionWeightMatrix(object)
```

Arguments

object	object is a genomicProfiles

Details

After creating a genomicProfiles object, it is possible to access the Position Weight Matrix stored in this slot. This slot should always contain something. This slot is either supplied by user or directly computed from a Position Frequency Matrix when supplied.

Value

Returns a matrix in the form of a Position Weight Matrix

Author(s)

Patrick C. N. Martin <pm16057@essex.ac.uk>

References

Zabet NR, Adryan B (2015) Estimating binding properties of transcription factors from genome-wide binding profiles. Nucleic Acids Res., 43, 84–94. Patrick C.N. Martin and Nicolae Radu Zabe (2020) Dissecting the binding mechanisms of transcription factors to DNA using a statistical thermodynamics framework. CSBJ, 18, 3590-3605.

Examples

```
#Loading data
data(ChIPanalyserData)
#Loading PFM files
PFM <- file.path(system.file("extdata",package="ChIPanalyser"),"BEAF-32.pfm")
#Building genomicProfiles object
GPP<-genomicProfiles(PFM=PFM,PFMFormat="JASPAR")
# Accessing Slot
PositionWeightMatrix(GPP)
```

PositionWeightMatrix-methods

~~ *Methods for Function* PositionWeightMatrix ~~

Description

Accessor Method for the PWM slot in a genomicProfiles object

Methods:

PositionWeightMatrix(object)

PositionWeightMatrix<-

Setter Method for the PositionWeightMatrix *slot in a* genomicProfiles *object*

Description

Setter Method for the PositionWeightMatrix slot in a genomicProfiles object

Usage

```
PositionWeightMatrix(object) <- value
```

Arguments

object	object is a genomicProfiles object
value	value is a matrix in the form of a Position Weight Matrix.

Details

If a Position Weight Matrix is readily available, it is possible to directly assign this matrix to the PWM slot. However, this is only possible if a genomicProfiles object has already been created. In that case, we advise to first create a genomicProfiles object. It should be noted that this Position Weight Matrix will be automatically computed from a Position Frequency Matrix. If no Position Frequency Matrix are available, then a Position Weight Matrix can be directly assigned to this slot.

Value

Returns a genomicProfiles object with an updated value for the PWM slot

Author(s)

Patrick C. N. Martin <pm16057@essex.ac.uk>

References

Zabet NR, Adryan B (2015) Estimating binding properties of transcription factors from genome-wide binding profiles. Nucleic Acids Res., 43, 84–94. Patrick C.N. Martin and Nicolae Radu Zabe (2020) Dissecting the binding mechanisms of transcription factors to DNA using a statistical thermodynamics framework. CSBJ, 18, 3590-3605.

Examples

```
#Building genomicProfiles object
GPP <- genomicProfiles()
#Setting PWM to PositionWeightMatrix slot
PWM <- matrix(runif(32,-10,20), ncol=8)
rownames(PWM) <- c("A","C","T","G")
PositionWeightMatrix(GPP) <- PWM
```

`PositionWeightMatrix<-methods` *~~ Methods for Function* `PositionWeightMatrix<-` *~~*

Description

Setter Method for the `PositionWeightMatrix` slot in a `genomicProfiles` object

Methods:

`PositionWeightMatrix(object)<-value`

`processingChIP` *Pre-processing ChIP-seq data*

Description

`processingChIP` will process and extract ChIP scores at a set of loci of interest.

Usage

```
processingChIP(profile,loci=NULL,reduce=NULL,
     peaks=NULL,chromatinState=NULL,parameterOptions=NULL,
     cores=1)
```

Arguments

profile	profile is a path to a UCSC format file, a GRanges or data frame. The input data should contain 4 columns:chromosome, start , end and score.
loci	loci is GRanges describing the loci at which ChIP scores should be extracted. If NULL, a set of Loci will extracted from profile. The data provided will then be split into bins of width equal to lociWidth (Default 20kbp) Default=NULL
reduce	reduce is a the top regions to select based on the mean ChIP score. If peaks are provided, regions overlappling with known peaks will be selected based on highest ChIP score. If NULL, all regions will be considered. Default=NULL
parameterOptions	parameterOptions is an parameterOptions object containing chip Parameters to be parsed for ChIP score extraction. If NULL, parameterOptions will be built internally with default ChIP extraction parameters (see chipSmooth, chipSd and chipMean) Default=NULL
peaks	peaks is a path to UCSC format file or a GRanges object containing location of ChIP peaks. Default=NULL
chromatinState	chromatinState is a GRanges containing Accessible DNA or chromatin States If provided, regions will be selected only if they contain accessible DNA. Default=NULL
cores	cores is the number of cores used to extract ChIP scores. Default = 1

Details

When using computeOptimal, it is required to supply real ChIP data in order to have a point of comparison. The corralation and MSE Scores are computed based of how well the model fits biological data. processingChIP will extract this data from ChIP data at loci of interest. When using the reduce option, this function will only select the top regions based on peak height or mean ChIP score. processingChIP will also extract maxSignal and backgroundSignal from ChIP data and parse it to an parameterOptions object.

Value

Returns a ChIPScore object containing extracted (and normalised) ChIP scores, the loci of interest and newly extracted Parameters(e.g. maxSignal)

Author(s)

Patrick C.N. Martin <pcnmartin@gmail.com>

References

Zabet NR, Adryan B (2015) Estimating binding properties of transcription factors from genome-wide binding profiles. Nucleic Acids Res., 43, 84–94. Patrick C.N. Martin and Nicolae Radu Zabe (2020) Dissecting the binding mechanisms of transcription factors to DNA using a statistical thermodynamics framework. CSBJ, 18, 3590-3605.

Examples

```
#Data extraction
data(ChIPanalyserData)

## Extracting ChIP scores at loci of interest

ChIP<-processingChIP(profile=chip, loci=top)
```

`profileAccuracyEstimate`

Estimating Accuracy of predicted Profiles

Description

`profileAccuracyEstimate` will compare the predicted ChIP-seq-like profile to real ChIP-seq data and return a set of metrics describing how accurate the predicted model is compared to real data.

Usage

```
profileAccuracyEstimate(genomicProfiles,ChIPScore,
    parameterOptions=NULL,method="all",cores=1)
```

Arguments

`genomicProfiles`	`genomicProfiles` is the result of `computeChIPProfile`
`ChIPScore`	`ChIPScore` is the result of `processingChIP`. Extracted/Normalised experimental ChIP scores.
`parameterOptions`	`parameterOptions` is a `parameterOptions` object for paramter specification.
`method`	`method` is the method that will be used to assess model quality agianst ChIP-seq data. Method can be one of the following: pearson, spearman, kendall, ks, geometric,fscore, MSE,or all.Fscore contains f-score, precision,recall, MCC, Accuracy and AUC ROC.
`cores`	`cores` is the number of cores used to extract ChIP scores. Default = 1

Details

In order to assess the quality of the model against experimental ChIP-seq data, ChIPanalyser offers a wide range of method to choose from. These methods are also used when computing optimal paramters.

Value

Returns list of goodness of fit metrics for each loci and each parameter selected.

Author(s)

Patrick C. N. Martin <pm16057@essex.ac.uk>

References

Zabet NR, Adryan B (2015) Estimating binding properties of transcription factors from genome-wide binding profiles. Nucleic Acids Res., 43, 84–94. Patrick C.N. Martin and Nicolae Radu Zabe (2020) Dissecting the binding mechanisms of transcription factors to DNA using a statistical thermodynamics framework. CSBJ, 18, 3590-3605.

Examples

```
#Data extraction
data(ChIPanalyserData)
# path to Position Frequency Matrix
PFM <- file.path(system.file("extdata",package="ChIPanalyser"),"BEAF-32.pfm")
#As an example of genome, this example will run on the Drosophila genome

  if(!require("BSgenome.Dmelanogaster.UCSC.dm6", character.only = TRUE)){
      if (!requireNamespace("BiocManager", quietly=TRUE))
          install.packages("BiocManager")
      BiocManager::install("BSgenome.Dmelanogaster.UCSC.dm6")
      }
  library(BSgenome.Dmelanogaster.UCSC.dm6)
  DNASequenceSet <- getSeq(BSgenome.Dmelanogaster.UCSC.dm6)
  # Building genomicProfiles object
  GPP <- genomicProfiles(PFM=PFM,PFMFormat="JASPAR", BPFrequency=DNASequenceSet)


  # Computing Genome Wide
  GenomeWide <- computeGenomeWideScore(genomicProfiles = GPP,
      DNASequenceSet = DNASequenceSet)

  #Compute PWM Scores
  PWMScores <- computePWMScore(genomicProfiles = GenomeWide,
       DNASequenceSet = DNASequenceSet, loci = top, chromatinState = Access)
  #Compute Occupnacy
  Occupancy <- computeOccupancy(genomicProfiles = PWMScores)

  #Compute ChIP profiles
  chipProfile <- computeChIPProfile(genomicProfiles=Occupancy,loci=top)
#Estimating accuracy estimate
AccuracyEstimate <- profileAccuracyEstimate(genomicProfiles = chipProfile,
    ChIPScore = chip,
    occupancyProfileParameters = OPP)
```

profiles-methods ~~ *Methods for Function* profiles ~~

Description

Accessor method for profiles in a genomicProfiles object

Methods:

profiles(oject) Computed PWM scores, Occupancy or ChIP-seq like profiles for loci of interest and paramter combination of interest.

PWMpseudocount *Accessor Method for a* PWMpseudocount *slot in a* parameterOptions

Description

Accessor Method for a PWMpseudocount slot in a parameterOptions

Usage

```
PWMpseudocount(object)
```

Arguments

object	object is a parameterOptions object.

Details

In the context of Position Weight Matricies, the pseudocount is used to avoid 0 probabilities during the transformation of Position Frequency Matrix to a Position Probability Matrix and finally to a Postion Weight Matrix. It is essentially a sample correction that is added in the case of small sample size. The effect of the base pair to which a pseudocount was assigned will not influence the model nor will create mathematical issues such as infinities or zero division. Default is set at 1.

Value

Returns the value assigned to a PWMpseudocount slot in a parameterOptions object

Author(s)

Patrick C. N. Martin <pm16057@essex.ac.uk>

References

Zabet NR, Adryan B (2015) Estimating binding properties of transcription factors from genome-wide binding profiles. Nucleic Acids Res., 43, 84–94. Patrick C.N. Martin and Nicolae Radu Zabe (2020) Dissecting the binding mechanisms of transcription factors to DNA using a statistical thermodynamics framework. CSBJ, 18, 3590-3605.

Examples

```
# Loading data
data(ChIPanalyserData)

#Building data objects
GPP <- parameterOptions(PWMpseudocount=0)
#Accessing slot value
PWMpseudocount(GPP)
```

PWMpseudocount-methods

~~ Methods for Function PWMpseudocount *~~*

Description

Accessor Method for a PWMpseudocount slot in a parameterOptions

Methods:

PWMpseudocount(object)

PWMpseudocount<- *Setter Method for the* pseudocount *slot in a* parameterOptions *object*

Description

Setter Method for the pseudocount slot in a parameterOptions object

Usage

```
PWMpseudocount(object) <- value
```

Arguments

object	object is a parameterOptions object
value	value is a numeric value that will be assigned to the pseudocount slot. Defualt is set at 1

Details

In the context of Position Weight Matricies, the pseudocount is used to avoid 0 probabilities during the transformation of Position Frequency Matrix to a Position Probability Matrix and finally to a Postion Weight Matrix. It is essentially a sample correction that is added in the case of small sample size. The effect of the base pair to which a pseudocount was assigned will not influence the model nor will create mathematical issues such as infinities or zero division.

Value

Returns a `parameterOptions` object with an updated value for the `pseudocount` slot.

Author(s)

Patrick C. N. Martin <pm16057@essex.ac.uk>

References

Zabet NR, Adryan B (2015) Estimating binding properties of transcription factors from genome-wide binding profiles. Nucleic Acids Res., 43, 84–94. Patrick C.N. Martin and Nicolae Radu Zabe (2020) Dissecting the binding mechanisms of transcription factors to DNA using a statistical thermodynamics framework. CSBJ, 18, 3590-3605.

Examples

```
# Loading data
data(ChIPanalyserData)

#Building data objects
GPP <- parameterOptions( PWMpseudocount=0)
#Setting Value for new PWMpseudocount
PWMpseudocount(GPP) <- 1
```

`PWMpseudocount<-methods`

~~ Methods for Function `PWMpseudocount<-` *~~*

Description

Setter Method for the `pseudocount` slot in a `parameterOptions` object

Methods:

`PWMpseudocount(object)<-value`

PWMThreshold *Accessor method for the* PWMThreshold *slot in a* parameterOptions *object*

Description

Accessor method for the PWMThreshold slot in a parameterOptions object

Usage

```
PWMThreshold(object)
```

Arguments

object	object is a parameterOptions object

Details

The computePWMScore function requires a so-called PWM Threshold. This threshold represents the Threshold at which PWM Score should be selected. The PWMThreshold is a positive numeric value (between 0 and 1. If set at 0, all sites will be selected. If set at 0.7 (Default value), then 70 % of PWM Score (and by extension binding sites) will be IGNORED. The top 30 % will be selected.

Value

Returns the value assinged to the PWMThreshold slot in a parameterOptions object

Author(s)

Patrick C. N. Martin <pm16057@essex.ac.uk>

References

Zabet NR, Adryan B (2015) Estimating binding properties of transcription factors from genome-wide binding profiles. Nucleic Acids Res., 43, 84–94. Patrick C.N. Martin and Nicolae Radu Zabe (2020) Dissecting the binding mechanisms of transcription factors to DNA using a statistical thermodynamics framework. CSBJ, 18, 3590-3605.

Examples

```
# Loading data
data(ChIPanalyserData)

#Building data objects
GPP <- parameterOptions(PWMThreshold=0.7)
#Accessing Value for  PWMThreshold
PWMThreshold(GPP)
```

PWMThreshold-methods ~~ *Methods for Function* PWMThreshold ~~

Description

Accessor method for the PWMThreshold slot in a parameterOptions object

Methods:

PWMThreshold(object)

PWMThreshold<- *Setter Method for the* PWMThreshold *slot in a* parameterOptions *object*

Description

Setter Method for the PWMThreshold slot in a parameterOptions object

Usage

```
PWMThreshold(object) <- value
```

Arguments

object	object is a parameterOptions object
value	value is a numeric value (between 0 and 1) to be assigned to the PWMThreshold slot in parameterOptions object. Default is set at 0.7

Details

The computePWMScore function requires a so-called PWM Threshold. This threshold represents the Threshold at which PWM Score should be selected. The PWMThreshold is a positive numeric value (between 0 and 1. If set at 0, all sites will be selected. If set at 0.7 (Default value), then 70 % of PWM Score (and by extension binding sites) will be IGNORED. The top 30 % will be selected.

Value

Returns parameterOptions objetc with an updated value for the PWMThreshold slot

Author(s)

Patrick C. N. Martin <pm16057@essex.ac.uk>

References

Zabet NR, Adryan B (2015) Estimating binding properties of transcription factors from genome-wide binding profiles. Nucleic Acids Res., 43, 84–94. Patrick C.N. Martin and Nicolae Radu Zabe (2020) Dissecting the binding mechanisms of transcription factors to DNA using a statistical thermodynamics framework. CSBJ, 18, 3590-3605.

Examples

```
# Loading data
data(ChIPanalyserData)

#Building data objects
GPP <- parameterOptions(PWMThreshold=0.7)
#Setting Value for new PWMThreshold
PWMThreshold(GPP) <- 0.8
```

`PWMThreshold<-methods` *~~ Methods for Function* `PWMThreshold<-` *~~*

Description

Setter Method for the `PWMThreshold` slot in a `parameterOptions` object

Methods:

`PWMThreshold(object)<-value`

`removeBackground` *Accessor Method for the* `removeBackground` *slot in a* `parameterOptions` *object*

Description

Accessor Method for the `removeBackground` slot in a `parameterOptions` object

Usage

```
removeBackground(object)
```

Arguments

`object`	`object` is a `parameterOptions` object

Details

A numeric value describing a threshold at which Occupancy signals must be removed (Default is set at 0). The removal of Occupancy signals will occur when computing `computeOccupancy` (see `computeOccupancy` function)

Value

Returns the value assigned to the removeBackground slot in a parameterOptions object

Author(s)

Patrick C. N. Martin <pm16057@essex.ac.uk>

References

Zabet NR, Adryan B (2015) Estimating binding properties of transcription factors from genome-wide binding profiles. Nucleic Acids Res., 43, 84–94. Patrick C.N. Martin and Nicolae Radu Zabe (2020) Dissecting the binding mechanisms of transcription factors to DNA using a statistical thermodynamics framework. CSBJ, 18, 3590-3605.

Examples

```
#Building parameterOptions object
OPP <- parameterOptions()
#Accessing  Value for removeBackground
removeBackground(OPP)
```

---

removeBackground-methods

~~ *Methods for Function* removeBackground ~~

Description

Accessor Method for the removeBackground slot in a parameterOptions object

Methods:

removeBackground(object)

---

removeBackground<- *Setter Method for the* removeBackground *slot in a* parameterOptions *object*

Description

Setter Method for the removeBackground slot in a parameterOptions object

Usage

```
removeBackground(object) <-value
```

Arguments

object	object is an parameterOptions object
value	value is positive numerical value to be assigned to the removeBackground slot in a parameterOptions object. Default is set a 0.

Details

A numeric value describing a threshold at which Occupancy signals must be removed (Default is set at 0). The removal of Occupancy signals will occur when computing computeOccupancy (see computeOccupancy function)

Value

Returns an parameterOptions object with an updated value for the removeBackground slot

Author(s)

Patrick C. N. Martin <pm16057@essex.ac.uk>

References

Zabet NR, Adryan B (2015) Estimating binding properties of transcription factors from genome-wide binding profiles. Nucleic Acids Res., 43, 84–94. Patrick C.N. Martin and Nicolae Radu Zabe (2020) Dissecting the binding mechanisms of transcription factors to DNA using a statistical thermodynamics framework. CSBJ, 18, 3590-3605.

Examples

```
#Building parameterOptions object
OPP <- parameterOptions()
#Setting new Value for removeBackground
removeBackground(OPP) <- 0.1
```

---

removeBackground<–methods

~~ *Methods for Function* removeBackground<- ~~

Description

Setter Method for the removeBackground slot in a parameterOptions object

Methods:

removeBackground(object)<-value

scores *Accessor Method for the* scores *slot in a* ChIPScore *object*

Description

Setter Method for the scores slot in a ChIPScore object

Usage

```
scores(object)
```

Arguments

object	object is ChIPScore object

Details

When using the processingChIP, this functions will return a name list of normalised ChIP scores at loci of interest. This functions enalbles you to extract those scores from the ChIPScore object.

Value

Returns the value assigned to the scores slot in a ChIPScore object.

Author(s)

Patrick C. N. Martin <p.martin@essex.ac.uk>

References

Zabet NR, Adryan B (2015) Estimating binding properties of transcription factors from genome-wide binding profiles. Nucleic Acids Res., 43, 84–94.

Examples

```
# Loading data
data(ChIPanalyserData)

chip<-processingChIP(chip,top)
str(scores(chip))
```

---

scores-methods ~~ *Methods for Function* scores ~~

Description

Accessor method for scores slot in a ChIPScore object.

Methods:

scores(object) Extracted and normalised ChIP scores at loci of interest.

---

searchSites *Searching function for Sites above threshold and predicted ChIP-seq Profiles*

Description

searchSites is function enabling quick extraction and search for parameter combinations and/or loci in any genomicProfiles object from computeOccupancy onwards.

Usage

```
searchSites(Sites,lambdaPWM="all",BoundMolecules="all", Locus="all")
```

Arguments

Sites	Sites is either a genomicProfiles or the result of computeOptimal
lambdaPWM	lambdaPWM is a numeric vector describing the ScalingFactors that should be searched within Sites.
BoundMolecules	BoundMolecules is a numeric vector describing the BoundMolecules that should be searched within Sites.
Locus	Locus is a character vector describing the Loci that should be searched within Sites.

Details

When testing numerous combinations of lambdaPWM and boundMolecules on top of many loci, it can become challenging to navigate the large data output searchSites will make searching in this slot a lot easier. If all arguments are left at their default value of "all", then all Parameters will be searched thus returning the full list of Sites above threshold. If a value for lambdaPWM is user provided then only this lambdaPWM will be selected (all boundMolecules and loci will also be selected). searchSites also works on the result of computeOptimal.

Value

Returns object of same time as parsed to this function with only the parameters and/or loci selected.

Author(s)

Patrick C. N. Martin <pm16057@essex.ac.uk>

References

Zabet NR, Adryan B (2015) Estimating binding properties of transcription factors from genome-wide binding profiles. Nucleic Acids Res., 43, 84–94. Patrick C.N. Martin and Nicolae Radu Zabe (2020) Dissecting the binding mechanisms of transcription factors to DNA using a statistical thermodynamics framework. CSBJ, 18, 3590-3605.

Examples

```
#Data extraction
data(ChIPanalyserData)
# path to Position Frequency Matrix
PFM <- file.path(system.file("extdata",package="ChIPanalyser"),"BEAF-32.pfm")
#As an example of genome, this example will run on the Drosophila genome

  if(!require("BSgenome.Dmelanogaster.UCSC.dm6", character.only = TRUE)){
      if (!requireNamespace("BiocManager", quietly=TRUE))
          install.packages("BiocManager")
      BiocManager::install("BSgenome.Dmelanogaster.UCSC.dm6")
      }
  library(BSgenome.Dmelanogaster.UCSC.dm6)
  DNASequenceSet <- getSeq(BSgenome.Dmelanogaster.UCSC.dm6)
  # Building genomicProfiles object
  GPP <- genomicProfiles(PFM=PFM,PFMFormat="JASPAR", BPFrequency=DNASequenceSet)


  # Computing Genome Wide
  GenomeWide <- computeGenomeWideScore(genomicProfiles = GPP,
      DNASequenceSet = DNASequenceSet)

  #Compute PWM Scores
  PWMScores <- computePWMScore(genomicProfiles = GenomeWide,
       DNASequenceSet = DNASequenceSet, loci = top, chromatinState = Access)
  #Compute Occupnacy
  Occupancy <- computeOccupancy(genomicProfiles = PWMScores)
  searchSites(Occupancy,ScalingFactor=c(1,4), BoundMolecules = c(1,100),
      Locus="eve")

  #Compute ChIP profiles
  chipProfile <- computeChIPProfile(genomicProfiles=Occupancy,loci=top)
  searchSites(chipProfile,ScalingFactor=c(1,4), BoundMolecules = c(1,100),
      Locus="eve")

optimalParam <- computeOptimal(genomicProfiles = GPP,
        DNASequenceSet = DNASequenceSet,
        ChIPScore = chip,
        chromatinState = Access,
        parameterOptions = OPP,
        parameter = "all",
```

```
        peakMethod="moving_kernel")

searchSites(optimalParam,ScalingFactor=c(1,4), BoundMolecules = c(1,100),
    Locus="eve")
```

---

setChromatinStates *setChromatinStates*

Description

setChromatinStates sets chromatin state affinity values to a GRanges object.

Usage

```
setChromatinStates(population,chromatinStates)
```

Arguments

population	Population list containing all individuals and associated parameter. Must contain chromatin state affinity values. See generateStartingPopulation.
chromatinStates	GRanges object containing chromatin state locations.

Details

Chromatin states can be loaded into R as a GRanges object. Each range represents the extent of a certain chromatin state and the chromatin state type should be assigned to a meta data column called "name". The affinity values names should be set accordingly.

Value

Returns a GRange object with affinity scores for each chromatin state range. Affinity scores are placed in the DNAAffinity meta data column.

Author(s)

Patrick C.N. Martin

Examples

```
library(ChIPanalyser)
# Input data
data(ChIPanalyserData)

pop <- 10
params <- c("N","lambda","PWMThreshold", paste0("CS",seq(1:11)))
start_pop <- generateStartingPopulation(pop, params)
```

```
cs <- setChromatinStates(start_pop,cs)
```

---

show-methods ~~ *Methods for Function* show ~~

Description

Show methods for various objects

Methods:

signature(object = "ChIPScore")

signature(object = "genomicProfiles")

signature(object = "parameterOptions")

---

singleRun *singleRun*

Description

singleRun runs ChIPanalyser after optimal paramters have been found by the evolve function.

Usage

```
singleRun(indiv,DNAAffinity,
          genomicProfiles,DNASequenceSet,
          ChIPScore,fitness="all")
```

Arguments

indiv	Population list containing the top scoring individual. Note that this should be a list of length 1 containing another list with all parameter values.
DNAAffinity	GRanges object as outputed by the setchromatinStates.
genomicProfiles	genomicProfiles object containing PWM scores and other desired metrics. Note that PWMThreshold, lambda and N will be overwritten using values from indiv.
DNASequenceSet	DNA string set object containing DNA sequence of interest.
ChIPScore	ChIPScore object as outputed by the processingChIP function.
fitness	character string describing which metric should be used to assess fitness and should be one of the following:"geometric","ks","MSE","pearson","spearman","kendall", "recall","precesion","fscore","MCC","Accuracy" or "AUC".

Details

Once the genetic algorithm has been optimised, the top individual may be run on its own to get predicted ChIP profiles. The use of this function requires a few extract steps in order to predict ChIP profiles.

First, the index of the top individual should be extracted (see `getHighestFitnessSolutions`). Second, using this index, subset top individual from GA population. Note this should be done using "[]" single bracket notation as, a list of length 1 containing another list with all parameter values is required for the next steps. Yes, this is might seem annoying but the functions were design for list structures... Third, setchromatinStates using the top individual list. This will add chromatin affinity values to your chromatinState GRanges. Use this new chromatinState object as your new chromatinState object. Fourth, parse your indiv list object to `singleRun`.

Value

Return a list with three elements. First element contains a genomicProfiles object with occupancy scores. Second element contains a genomicProfiles objecy with ChIP profile scores. Third element contains a goodness of fit metrics.

Author(s)

Patrick C.N. Martin <pcnmartin@gmail.com

Examples

```
library(ChIPanalyser)
data(ChIPanalyserData)
# See GA vignette for usage
```

`splitData` *Get Training and Testing data from ChIPscore objects*

Description

`splitData` splits processed ChIP data into training and testing sets.

Usage

```
splitData(ChIPscore,dist = c(80,20), as.proportion = TRUE)
```

Arguments

`ChIPscore`	ChIPscore object as returned by `processingChIP`
`dist`	If `as.proportion` is to TRUE, split the data into desired proportions. Default sets 80% training and 20% testing. If `as.proportion` is to FALSE,a vector of 4 numeric values describing start and end of training and testing respectively.
`as.proportion`	Logical describing if values provided to `dist` should be treated as % of training and testing or if `dist` should be considered as start and end of loci selected for training and testing respectively.

Value

Returns a named list of ChIPScore objects

* trainingSet = ChIPscore containing training set * testingSet = ChIPscore containing testing set.

Author(s)

Patrick C.N. Martin <pcnmartin@gmail.com

Examples

```
library(ChIPanalyser)
data(ChIPanalyserData)
# See GA vignette for usage
test <- processingChIP(chip,top)
usingDist <- splitData(test, dist = c(50,50),as.proportion = TRUE )
usingIndex <- splitData(test, dist = c(1,2,3,4),as.proportion = FALSE )
```

---

stepSize *Accessor method of the* stepSize *slot in* parameterOptions *object*

Description

Accessor method of the stepSize slot in parameterOptions object

Usage

```
stepSize(object)
```

Arguments

object	object is a parameterOptions object.

Details

It possible to restrict the size of the ChIP-seq-like profile produced by computeChIPProfile. Instead of returning ChIP-seq like score for each base pair, it is possible to skip base pairs and only return the predicted enrichement score for every "n" base pair (n is the value assigned to stepSize). This will reduce the size of the output data (unless step size is very large, this will not affect the accuracy of the model). Default is set at 10 base pairs.

Value

Returns the value assigned to the stepSize slot in a parameterOptions

Author(s)

Patrick C. N. Martin <pm16057@essex.ac.uk>

References

Zabet NR, Adryan B (2015) Estimating binding properties of transcription factors from genome-wide binding profiles. Nucleic Acids Res., 43, 84–94. Patrick C.N. Martin and Nicolae Radu Zabe (2020) Dissecting the binding mechanisms of transcription factors to DNA using a statistical thermodynamics framework. CSBJ, 18, 3590-3605.

Examples

```
# Building parameterOptions  object
OPP <- parameterOptions()
#Setting new Value for maxSignal
stepSize(OPP)
```

`stepSize-methods` *~~ Methods for Function* `stepSize` *~~*

Description

Accessor method of the `stepSize` slot in `parameterOptions` object

Methods:

`stepSize(object)`

`stepSize<-` *Setter Method for the* `stepSize` *slot in a* `parameterOptions`

Description

Setter Method for the `stepSize` slot in a `parameterOptions`

Usage

```
stepSize(object) <- value
```

Arguments

`object`	`object` is a `parameterOptions` object
`value`	`value` is a positive numeric value that will be assigned to the `stepSize` slot in a `parameterOptions` object. Default is set at 10 base pairs.

Details

It possible to restrict the size of the ChIP-seq-like profile produced by `computeChIPProfile`. Instead of returning ChIP-seq like score for each base pair, it is possible to skip base pairs and only return the predicted enrichement score for every "n" base pair (n is the value assigned to stepSize). This will reduce the size of the output data (unless step size is very large, this will not affect the accuracy of the model). Default is set at 10 base pairs.

Value

Returns a parameterOptions object with an updated value for the stepSize slot.

Author(s)

Patrick C. N. Martin <pm16057@essex.ac.uk>

References

Zabet NR, Adryan B (2015) Estimating binding properties of transcription factors from genome-wide binding profiles. Nucleic Acids Res., 43, 84–94. Patrick C.N. Martin and Nicolae Radu Zabe (2020) Dissecting the binding mechanisms of transcription factors to DNA using a statistical thermodynamics framework. CSBJ, 18, 3590-3605.

Examples

```
# Building parameterOptions  object
OPP <- parameterOptions()
#Setting new Value for maxSignal
stepSize(OPP) <- 20
```

---

stepSize<-methods *~~ Methods for Function* stepSize<- *~~*

Description

Setter Method for the stepSize slot in a parameterOptions

Methods:

stepSize(object)<-value

---

strandRule *Accessor Method for the* strandRule *slot in a* parameterOptions *object*

Description

Accessor Method for the strandRule slot in a parameterOptions object

Usage

```
strandRule(object)
```

Arguments

object	object is a parameterOptions object

Details

When computing the PWM Scores and if whichstrand is set to "+-", strandRule will determine how to handle both strands (one of three options : "mean", "max", "sum"). If set to "mean", the average PWM Score of both strand will be computed. If set to "max", the highest PWM score between each strand will be selected and finally "sum" will sum both score together. Default set at "max"

Value

Returns the value assigned to strandRule slot (one of three options : "mean", "max", "sum") in a parameterOptions object

Author(s)

Patrick C. N. Martin <pm16057@essex.ac.uk>

References

Zabet NR, Adryan B (2015) Estimating binding properties of transcription factors from genome-wide binding profiles. Nucleic Acids Res., 43, 84–94. Patrick C.N. Martin and Nicolae Radu Zabe (2020) Dissecting the binding mechanisms of transcription factors to DNA using a statistical thermodynamics framework. CSBJ, 18, 3590-3605.

Examples

```
# Loading data
data(ChIPanalyserData)

#Building data objects
GPP <- parameterOptions( strandRule="max")
#Accesssing Value for strandRule
strandRule(GPP)
```

---

strandRule-methods ~~ *Methods for Function* strandRule ~~

Description

Accessor Method for the strandRule slot in a parameterOptions object

Methods:

strandRule(object)

strandRule<- *Setter method for the* strandRule *slot in a* parameterOptions *object.*

Description

Setter method for the strandRule slot in a parameterOptions object.

Usage

```
strandRule(object) <- value
```

Arguments

object	object is a parameterOptions object
value	value is a character string and can be one of the following 'mean', 'max', 'sum'. This will only apply if whichstrand is '+-'. Default set at 'max'

Details

When computing the PWM Scores and if whichstrand is set to '+-', strandRule will determine how to handle both strands (one of three options : 'mean', 'max', 'sum'). If set to 'mean', the average PWM Score of both strand will be computed. If set to 'max', the highest PWM score between each strand will be selected and finally 'sum' will sum both score together. Default set at 'max'

Value

Returns a parameterOptions object with an updated value for the strandRule slot

Author(s)

Patrick C. N. Martin <pm16057@essex.ac.uk>

References

Zabet NR, Adryan B (2015) Estimating binding properties of transcription factors from genome-wide binding profiles. Nucleic Acids Res., 43, 84–94. Patrick C.N. Martin and Nicolae Radu Zabe (2020) Dissecting the binding mechanisms of transcription factors to DNA using a statistical thermodynamics framework. CSBJ, 18, 3590-3605.

Examples

```
# Loading data
data(ChIPanalyserData)

#Building data objects
GPP <- parameterOptions(strandRule="max")
#Setting New Value for strandRule
strandRule(GPP) <- "mean"
```

`strandRule<-methods` ~~ *Methods for Function* `strandRule<-` ~~

Description

Setter method for the `strandRule` slot in a `parameterOptions` object.

Methods:

`strandRule(object)<-value`

`whichstrand` *Accessor method for the* `whichstrand` *slot in a* `parameterOptions` *object*

Description

Accessor method for the `whichstrand` slot in a `parameterOptions` object

Usage

```
whichstrand(object)
```

Arguments

`object`	`object` is a `parameterOptions` object

Details

PWM Score may be computed on either the positive strand ("+"), the negative strand ("-") or on both strands ("+-").

Value

Returns on which strand PWM Scores should be computed (`whichstrand` in a `parameterOptions` object)

Author(s)

Patrick C. N. Martin <pm16057@essex.ac.uk>

References

Zabet NR, Adryan B (2015) Estimating binding properties of transcription factors from genome-wide binding profiles. Nucleic Acids Res., 43, 84–94. Patrick C.N. Martin and Nicolae Radu Zabe (2020) Dissecting the binding mechanisms of transcription factors to DNA using a statistical thermodynamics framework. CSBJ, 18, 3590-3605.

Examples

```
# Loading data
data(ChIPanalyserData)

#Building data objects
GPP <- parameterOptions( whichstrand="+-")
#Setting New Value for whichstrand
whichstrand(GPP)
```

---

whichstrand-methods *~~ Methods for Function* whichstrand *~~*

Description

Accessor method for the whichstrand slot in a parameterOptions object

Methods:

whichstrand(object)

---

whichstrand<- *Setter method for the* whichstrand *slot in a* parameterOptions *object*

Description

Setter method for the whichstrand slot in a parameterOptions object

Usage

```
whichstrand(object) <- value
```

Arguments

object	object is a parameterOptions object
value	value is a character string specifying which strand should be used to compute PWM Scores. The three available options are the following: "+","-" or "+-". Default is "+-"

Details

PWM Score may be computed on either the positive strand ("+"), the negative strand ("-") or on both strands ("+-").

Value

Returns a parameterOptions object with an updated value for the whichstrand slot

Author(s)

Patrick C. N. Martin <pm16057@essex.ac.uk>

References

Zabet NR, Adryan B (2015) Estimating binding properties of transcription factors from genome-wide binding profiles. Nucleic Acids Res., 43, 84–94. Patrick C.N. Martin and Nicolae Radu Zabe (2020) Dissecting the binding mechanisms of transcription factors to DNA using a statistical thermodynamics framework. CSBJ, 18, 3590-3605.

Examples

```
# Loading data
data(ChIPanalyserData)

#Building data objects
GPP <- parameterOptions( whichstrand="+-")
#Setting New Value for whichstrand
whichstrand(GPP) <- "+"
```

`whichstrand<-methods` ~~ *Methods for Function* `whichstrand<-` ~~

Description

Setter method for the `whichstrand` slot in a `parameterOptions` object

Methods:

`whichstrand(object)<-value`

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