Package 'RBPSpliceMap'

May 20, 2015

Type Package

Title Summarize CLIPSeq data

Version 1.0

Date 2015-05-20

Author Laure Le Calvez

Maintainer Laure Le Calvez <laure.le-calvez@laposte.net>

Depends R (>= 2.10.0), GenomicRanges (>= 1.17.20), GenomicAlignments (>= 1.1.16)

Description This package is intended to manipulate CLIP data and summarize them along genomic regions. Typically it can be use to draw RNA splice map. It allows to select a chromosome, strand and interval of interest. It gives numerical and graphical results about the coverage of splice sites and their surroundings.

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R topics documented:

RBPSpliceMap-package *Summarize CLIPSeq data*

Description

This package is intended to manipulate CLIP data and summarize them along genomic regions. Typically it can be use to draw RNA splice map. It allows to select a chromosome, strand and interval of interest. It gives numerical and graphical results about the coverage of splice sites and their surroundings.

Details

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Type:	Package
Version:	1.0
Date:	2015-05-20
License:	GPL(>=2.0)

Author(s)

Laure Le Calvez <laure.le-calvez@laposte.net>

Examples

```
regulatedExons = system.file("extdata", "regulatedExons.bed", package="RBPSpliceMap", mustWork=TRUE)
iCLIPData = system.file("extdata", "iCLIPData.bam", package="RBPSpliceMap", mustWork=TRUE)
#Create GRanges from a bedFile with exons of interest
data <- read.table(regulatedExons, header = TRUE)
colnames(data) = c(chr, start, end, ProbeID, pval, strand)
exonInterest = with(data, GRanges(chr, IRanges(start, end), strand))
#Create a GRanges from a bam file
mapReadsGRanges = bamToGRanges(iCLIPData)
#Normalized mean of coverages of ranges of interest on the 3 splice site
spMapList3SS = spMap(exonInterest, mapReadsGRanges, spSite = "3SS", padding =  c(40, 200), goal = "normMean
#Mean of coverages of ranges of interest on the 5 splice site
spMapList5SS = spMap(exonInterest, mapReadsGRanges, spSite = "5SS", padding =  c(100, 50), goal = "mean")
#3 splice site representation
plotSpMap(spMapList3SS)
#5 splice site representation
plotSpMap(spMapList5SS)
```

bamToGRanges *bamToGRanges*

Description

This function transform a bam file into a GRanges object

Usage

```
bamToGRanges(bamFile)
```

Arguments

bamFile	bamFile is path of a bam file

Details

The return GRanges Object contain "seqnames", IRanges(start,end) and "strand". It is possible to have access to the different values vector with : - seqnames(<GRangesName>) - start(ranges(<GRangesName>) - end(ranges(<GRangesName>) - strand(<GRangesName>)

Value

GRanges object

Author(s)

Laure Le Calvez <laure.le-calvez@laposte.net>

See Also

readGAlignments from package GenomicAlignments as

Examples

```
iCLIPData = system.file("extdata", "iCLIPData.bam", package="RBPSpliceMap", mustWork=TRUE)
#Create a GRanges from a bam file
bamToGRanges(iCLIPData)
```

---

chromosomeSelect *chromosomeSelect*

Description

This function return the part of the GRanges object concerning the input "chromosome"

Usage

```
chromosomeSelect(objectGRanges, chromosome)
```

Arguments

objectGRanges	GRanges object from where we want to select the part concerning the strand of interest
chromosome	chromosome of interest as a string (ex: "7" or "chr7") /!\ Write it like it is written in the GRanges object

Value

GRanges object

Author(s)

Laure Le Calvez <laure.le-calvez@laposte.net>

See Also

strandSelect intervalSelect mapReadsTreatment

Examples

```
iCLIPData = system.file("extdata", "iCLIPData.bam", package="RBPSpliceMap", mustWork=TRUE)
#Create a GRanges from a bam file
mapReadsGRanges = bamToGRanges(iCLIPData)
#Select the chromosome of interest
chromosomeSelect(mapReadsGRanges, chromosome = "chr7")

regulatedExons = system.file("extdata", "regulatedExons.bed", package="RBPSpliceMap", mustWork=TRUE)
#Create GRanges from a bedFile with exons of interest
data <- read.table(regulatedExons, header = TRUE)
colnames(data) = c(chr, start, end, ProbeID, pval, strand)
exonInterest = with(data, GRanges(chr, IRanges(start, end), strand))
#Select the chromosome of interest
chromosomeSelect(mapReadsGRanges, chromosome = "chr7")
```

---

coverageChr *coverageChr*

Description

This function, from the GRanges, give the coverage (number of reads) concerning the chromosome of interest

Usage

```
coverageChr(mapReadsGRanges, chromosome)
```

Arguments

mapReadsGRanges	GRanges object from where we want to select the part concerning the strand of interest
chromosome	chromosome of interest as a string (ex: "7" or "chr7") /!\ Write it like it is written in the GRanges object

Details

The return Rle (package S4Vectors) represent the coverage (number of reads) of the input chromosome

Value

Rle (package S4Vectors)

Author(s)

Laure Le Calvez <laure.le-calvez@laposte.net>

See Also

coverageVector coverage mapReadsTreatment

Examples

```
iCLIPData = system.file("extdata", "iCLIPData.bam", package="RBPSpliceMap", mustWork=TRUE)
#Create a GRanges from a bam file
mapReadsGRanges = bamToGRanges(iCLIPData)
#Calculate the coverage on a specified chromosome
coverageChr(mapReadsGRanges, chromosome = "chr7")
```

---

coverageVector *coverageVector*

Description

This function transform a coverage Rle (package S4Vector) into a coverage vector

Usage

```
coverageVector(cover, from = 0, to)
```

Arguments

cover	Rle (package S4Vector) with the coverage
from	If there is a part without any reads, from where do the reads appear. from = coordinate of the position just before the one with the first read DEFAULT = 0
to	The coordinate of the last read you want on the coverage

Details

/!\ ERROR if the from given correspond to a position with or after some reads of the input Rle from: only if you know how much nucleotides at the beggining of the sequence are not covered by reads The return vector contains the number of reads at each position (nucleotide)

Value

Vector

Author(s)

Laure Le Calvez <laure.le-calvez@laposte.net>

See Also

coverageChr coverage mapReadsTreatment

Examples

```
iCLIPData = system.file("extdata", "iCLIPData.bam", package="RBPSpliceMap", mustWork=TRUE)
#Create a GRanges from a bam file
mapReadsGRanges = bamToGRanges(iCLIPData)
#Calculate the coverage on a specified chromosome
cover = coverageChr(mapReadsGRanges, chromosome = "chr7")
#Transforme coverage Rle into a coverage vector
coverageVector(cover, from = 810695, to = 810796)
```

---

exonInterestTreatment *exonInterestTreatment*

Description

This function create a GRanges from another with modified coordinates given by the splice site chosen and the padding.

Usage

```
exonInterestTreatment(exonInterest, spSite, pE, pI)
```

Arguments

exonInterest	GRanges object containing coordinates of interest (thess coordinates match with exon ones)
spSite	Splice Site of interest ("5SS" or "3SS")
pE	padding exon. Number of nucleotides wanted around the splice site on the exon
pI	padding intron. Number of nucleotides wanted around the splice site on the intron

Details

If the input GRanges contain strand = "*", there are excluded, only strand = "+" or "-" are treated The return GRanges contain coordinates of nucleotides framing ranges of interest around the splice site.

Value

GRanges object

Author(s)

Laure Le Calvez <laure.le-calvez@laposte.net>

Examples

```
regulatedExons = system.file("extdata", "regulatedExons.bed", package="RBPSpliceMap", mustWork=TRUE)
#Create GRanges from a bedFile with exons of interest
data <- read.table(regulatedExons, header = TRUE)
colnames(data) = c(chr, start, end, ProbeID, pval, strand)
exonInterest = with(data, GRanges(chr, IRanges(start, end), strand))
#Treatment of the GRanges with exons of Interest
exonInterestTreatment(exonInterest, spSite = "3SS", pE = 40, pI = 200)
```

`intervalSelect` *intervalSelect*

Description

This function return the part of the GRanges object concerning the input ranges

Usage

```
intervalSelect(objectGRanges, from, to)
```

Arguments

`objectGRanges`	GRanges object from where we want to select the part concerning the strand of interest
`from`	Coordinate from where you want the coverage
`to`	Coordinate where you want the coverage to end

Value

GRanges object

Author(s)

Laure Le Calvez <laure.le-calvez@laposte.net>

See Also

`strandSelect` `chromosomeSelect` `mapReadsTreatment`

Examples

```
iCLIPData = system.file("extdata", "iCLIPData.bam", package="RBPSpliceMap", mustWork=TRUE)
#Create a GRanges from a bam file
mapReadsGRanges = bamToGRanges(iCLIPData)
#Select the interval of interest
intervalSelect(mapReadsGRanges, from = 134621217, to = 134681857)
```

`mapReadsTreatment` *mapReadsTreatment*

Description

This function, from a GRanges object, give the coverage (number of reads) on a "chromosome", a "strand" and a range of interest ("from" and "to")

Usage

```
mapReadsTreatment(mapReadsGRanges, chromosome, strand, from, to)
```

Arguments

mapReadsGRanges	GRanges object containing mapped reads (generally from a bam file) (see bamToGRanges())
chromosome	chromosome of interest as a string (ex: "7" or "chr7") /!\ Write it like it is written in the GRanges object
strand	strand of interest as a string ("+", "-", "*") "*" correspond to the 2 strands
from	Coordinate from where you want the coverage
to	Coordinate where you want the coverage to end

Details

The return coverage vector indicate the number of reads per nucleotide

Value

Coverage Vector

Author(s)

Laure Le Calvez <laure.le-calvez@laposte.net>

See Also

strandSelect intervalSelect coverageChr coverageVector

Examples

```
iCLIPData = system.file("extdata", "iCLIPData.bam", package="RBPSpliceMap", mustWork=TRUE)
#Create a GRanges from a bam file
mapReadsGRanges = bamToGRanges(iCLIPData)
#Treatment of the GRanges with mapped reads
mapReadsTreatment(mapReadsGRanges, chromosome = "chr7", strand = "+", from = 810695, to = 810796)
```

---

plotSpMap *plotSpMap*

Description

This function is a way to represent the coverage in reads of a splice Site and its surrondings

Usage

```
plotSpMap(spMapList)
```

Arguments

spMapList	List of 4 vectors spMapList[[1]] : coverage vector spMapList[[2]] : splice site ("3SS" or "5SS") spMapList[[3]] : paddingExon (number) spMapList[[4]] : paddingIntron (number)

Details

padding : - paddingExon and paddingIntron correspond to the number of nucleotides wanted around the splice site on the exon and the intron - This function create a representation of the coverage of a "splice site" (x=0) between paddingIntron (x= pI-1) and paddingExon (x=pE) - paddingIntron is used with -1 because x=0 is the splice site and it is included in the Intron - The return graph represent the coverage of the part of interest of the exon (or multiple exon if you used spMap() with multiple regions)

Value

Graph

Author(s)

Laure Le Calvez <laure.le-calvez@laposte.net>

See Also

spMap coverageVector

Examples

```
iCLIPData = system.file("extdata", "iCLIPData.bam", package="RBPSpliceMap", mustWork=TRUE)
regulatedExons = system.file("extdata", "regulatedExons.bed", package="RBPSpliceMap", mustWork=TRUE)
#Create GRanges from a bedFile with exons of interest
data <- read.table(regulatedExons, header = TRUE)
colnames(data) = c(chr, start, end, ProbeID, pval, strand)
exonInterest = with(data, GRanges(chr, IRanges(start, end), strand))
#Create a GRanges from a bam file
mapReadsGRanges = bamToGRanges(iCLIPData)
#Normalized mean of coverages of ranges of interest on the 3 splice site
spMapList3SS = spMap(exonInterest, mapReadsGRanges, spSite = "3SS", padding =  c(40, 200), goal = "normMean
#Mean of coverages of ranges of interest on the 5 splice site
spMapList5SS = spMap(exonInterest, mapReadsGRanges, spSite = "5SS", padding =  c(100, 50), goal = "mean")
#3 splice site representation
plotSpMap(spMapList3SS)
#5 splice site representation
plotSpMap(spMapList5SS)
```

---

spMap *spMap*

Description

This function return a coverage calculate from all coverage vectors of ranges described in the GRanges object "exonInterest" given.

Usage

```
spMap(exonInterest, mapReadsGRanges, spSite, padding, goal)
```

Arguments

exonInterest	GRanges object containing coordinates of interest (these coordinates match with exon ones)
mapReadsGRanges	GRanges object containing mapped reads (generally from a bam file) (see bamToGRanges())
spSite	Splice Site of interest ("5SS" or "3SS")
padding	Vector with the padding exon (pE) and the padding intron (pI) in the form of c(pE,pI) (pE and pI correspond to the number of nucleotides wanted around the splice site on the exon and the intron)
goal	Function, applied between the different coverage vectors to get the wanted result into the return coverage vector. This function can be "normMean" to get a normalized mean or a basic R function. - "normMean" : normalized mean - "sum" - "mean" - "median" - "max" - ...

Details

The coverage vector represent the number of reads (depending on the chosen function "goal") at each nucleotide. This function return a list containing the coverage vector, splice site, padding exon (pE) and padding intron (pI) in this order You can access differents elements with : <listName>[[i]] (i = 1, 2, 3 or 4)

Value

list(coverage vector, splice site, pE, pI)

Author(s)

Laure Le Calvez <laure.le-calvez@laposte.net>

See Also

exonInterestTreatment mapReadsTreatment

Examples

```
iCLIPData = system.file("extdata", "iCLIPData.bam", package="RBPSpliceMap", mustWork=TRUE)
regulatedExons = system.file("extdata", "regulatedExons.bed", package="RBPSpliceMap", mustWork=TRUE)
#Create GRanges from a bedFile with exons of interest
data <- read.table(regulatedExons, header = TRUE)
colnames(data) = c(chr, start, end, ProbeID, pval, strand)
exonInterest = with(data, GRanges(chr, IRanges(start, end), strand))
#Create a GRanges from a bam file
mapReadsGRanges = bamToGRanges(iCLIPData)
#Normalized mean of coverages of ranges of interest on the 3 splice site
spMapList3SS = spMap(exonInterest, mapReadsGRanges, spSite = "3SS", padding =  c(40, 200), goal = "normMean")
#Mean of coverages of ranges of interest on the 5 splice site
spMapList5SS = spMap(exonInterest, mapReadsGRanges, spSite = "5SS", padding =  c(100, 50), goal = "mean")
```

strandSelect *strandSelect*

Description

This function return the part of the GRanges object about the input "strand"

Usage

```
strandSelect(objectGRanges, strand)
```

Arguments

objectGRanges	GRanges object from where we want to select the part concerning the strand of interest
strand	strand of interest as a string ("+", "-", "*") "*" correspond to the 2 strands -> return the entire GRanges object

Value

GRanges object

Author(s)

Laure Le Calvez <laure.le-calvez@laposte.net>

See Also

intervalSelect chromosomeSelect mapReadsTreatment

Examples

```
iCLIPData = system.file("extdata", "iCLIPData.bam", package="RBPSpliceMap", mustWork=TRUE)
#Create a GRanges from a bam file
mapReadsGRanges = bamToGRanges(iCLIPData)
#Select the strand of interest
strandSelect(mapReadsGRanges, strand = "+")

regulatedExons = system.file("extdata", "regulatedExons.bed", package="RBPSpliceMap", mustWork=TRUE)
#Create GRanges from a bedFile with exons of interest
data <- read.table(regulatedExons, header = TRUE)
colnames(data) = c(chr, start, end, ProbeID, pval, strand)
exonInterest = with(data, GRanges(chr, IRanges(start, end), strand))
#Select the strand of interest
strandSelect(regulatedExons, strand = "+")
```

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