Package 'BasicSTARRseq'

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Type Package

Title Basic peak calling on STARR-seq data

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Depends GenomicRanges,GenomicAlignments

Description Basic peak calling on STARR-seq data based on a method introduced in ``Genome-Wide Quantitative Enhancer Activity Maps Identified by STARR-seq" Arnold et al. Science. 2013 Mar 1;339(6123):1074-7. doi: 10.1126/science. 1232542. Epub 2013 Jan 17.

License LGPL-3

LazyData TRUE

Suggests knitr

VignetteBuilder knitr

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getPeaks *Peak calling on STARR-seq data*

Description

Performs basic peak calling on STARR-seq data based on a method introduced in "Genome-Wide Quantitative Enhancer Activity Maps Identified by STARR-seq" Arnold et al. [1]

Usage

```
getPeaks(object, minQuantile = 0.9, peakWidth = 500, maxPval = 0.001,
            deduplicate = TRUE, model = 1)
```

Arguments

object	A STARRseqData object for which the peaks should be calculated.
minQuantile	Which quantile of coverage height should be considered as peaks.
peakWidth	The width (in base pairs) that the peaks should have.
maxPval	The maximal p-value of peaks that is desired.
deduplicate	Wether the sequences should be deduplicated before calling peaks or not.
model	Which binomial model should be applied to calculate the p-values.

Details

The peak calling works the following way: All genomic positions having a STARR-seq coverage over the quantile minQuantile are considered to be the center of a peak with width peakWidth. If then two ore more peaks overlap, the lower one is discarded. If then the binomial p-Value of the peak is higher than maxPval the peak is discarded as well.

The binomial model 1 for calculating the p-Value is: number of trials = total number of STARR-seq sequences, number of successes = STARR-seq coverage, estimated sucess probability in each trial = input coverage/total number of input sequences.

The binomial model 2 for caculating the p-Value is: number of trials = STARR-seq coverage plus input coverage, number of successes = STARR-seq coverage, estimated success probability in each trial = total number of STARR-seq sequences/(total number of STARR-seq sequences plus total number of input sequences). This model is used in [1].

The enrichment of STARR-seq over input coverage is then calculated as follows: (STARR-seq coverage of peak/total number of STARR-seq sequences)/(input coverage of peak/total number of input sequences), the numinator and denuminator corrected conservatively to the bounds of the 0.95 binomial confidence inverval corresponding to model 1.

Value

The method getPeaks return a GRanges object. The contained ranges are the found peaks with desired width peakWidth. The metadata columns of the ranges contain four elements:

sampleCov	The maximal and central STARR-seq coverage of the peak.
controlCov	The maximum of the central and the median input coverage of the peak.
pVal	The binomial p-Value of the coverage height of the peak normalised to toal number of sequences in STARR-seq and input.

`enrichment` The enrichment of STARR-seq over input coverage height normalised to total number of sequences in STARR-seq and input corrected conservatively to the bounds of a confidence interval.

Author(s)

Annika Buerger

References

[1] *Genome-Wide Quantitative Enhancer Activity Maps Identified by STARR-seq*. Arnold et al. Science. 2013 Mar 1;339(6123):1074-7. doi: 10.1126/science.1232542. Epub 2013 Jan 17.

See Also

`GRanges` `STARRseqData-class`

Examples

```
# create a small sample STARRseqData object
starrseqFileName <- system.file("extdata", "smallSTARR.bam",
                                package="BasicSTARRseq")
inputFileName <- system.file("extdata", "smallInput.bam",
                                package="BasicSTARRseq")
data <- STARRseqData(sample=starrseqFileName, control=inputFileName,
                        pairedEnd=TRUE)

# call peaks with default parameters
peaks = getPeaks(data)

# call peaks with no deduplication and no restriction concerning p-value
peaks = getPeaks(data, maxPval = 1, deduplicate = FALSE)

# call peaks with other binomial model and width 700
peaks = getPeaks(data, peakWidth = 700, model = 2)

# call peaks assuming less regions as potential peaks
peaks = getPeaks(data, minQuantile = 0.99)
```

`STARRseqData-class` *Class* "STARRseqData"

Description

The STARR-seq data class is a container for STARR-sequencing data.

Details

STARRseqData contains two GRanges objects that store the STARR-seq sequences and the input sequences respectively of an STARR-seq experiment.

Slots

`sample`: Object of class `"GRanges"` which contains STARR-seq sequences.

`control`: Object of class `"GRanges"` which contains input sequences.

Constructor

`STARRseqData(sample, control)`: Create a STARRseqData object.

`sample`: An GRanges object.

`control`: An GRanges object.

Accessors

In the following code snippets, x is an STARRseqData object.

`sample(x)`, `sample(x) <- value`: Get or set the STARR-seq sequences.

`control(x)`, `control(x) <- value`: Get or set the input sequences.

Methods

getPeaks `signature(object = "STARRseqData")`: Performs basic peak calling on data.

Author(s)

A. Buerger

References

Genome-Wide Quantitative Enhancer Activity Maps Identified by STARR-seq. Arnold et al. Science. 2013 Mar 1;339(6123):1074-7. doi: 10.1126/science.1232542. Epub 2013 Jan 17.

See Also

`GRanges` `getPeaks`

Examples

```
# create small sample dataset
starrseqFileName <- system.file("extdata", "smallSTARR.bam", package="BasicSTARRseq")
inputFileName <- system.file("extdata", "smallInput.bam", package="BasicSTARRseq")
STARRseqData(sample=starrseqFileName, control=inputFileName, pairedEnd=TRUE)
```

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