Package: BasicSTARRseq (via r-universe)

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Type Package

Title Basic peak calling on STARR-seq data

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Imports S4Vectors,methods,IRanges,GenomeInfoDb,stats

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

biocViews PeakDetection, GeneRegulation, FunctionalPrediction, FunctionalGenomics, Coverage

NeedsCompilation no

Repository https://bioc.r-universe.dev

RemoteUrl https://github.com/bioc/BasicSTARRseq

RemoteRef HEAD

RemoteSha a4826874ccf4e3e9aafed6f7eb59a97b075014a7

Contents

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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