Package 'AlignmentView'

June 14, 2024

Title Show the CIGAR, read and reference genome sequences of a given read ID and BAM/SAM file with the AlignmentView package

Version 0.0.90

Description The AlignmentView package will take as input a BAM/SAM file , a specific read ID and a Genome provided by the user. The output will show the precise sequence alignment of the provided read ID to the reference genome according to the mapped read's CIGAR string. Nucleotides are given a color in order to have a clear visualization of the alignment.

Depends R(>= 4.4.0)

Imports Rsamtools, Biostrings, crayon, data.table, GenomicRanges, BSgenome

Suggests knitr, rmarkdown, BiocStyle, BSgenome.Hsapiens.UCSC.hg38

VignetteBuilder knitr

License GPL-2

URL https://github.com/annagrattagaliano

Encoding UTF-8

Roxygen list(markdown = TRUE)

RoxygenNote 7.3.1

biocViews ExperimentData, Alignment, DNASeqData

BugReports https://github.com/annagrattagliano/AlignmentView/issues

NeedsCompilation no

Author Anna Grattagliano [aut, cre]

Maintainer Anna Grattagliano <anna.grattagliano@mail.polimi.it>

Contents

`align_read` *Align a read to a reference sequence based on the CIGAR string*

Description

This function takes as input a reference sequence, a read sequence, and a CIGAR string, and returns the aligned reference and read sequences.

Usage

```
align_read(reference_seq, read_seq, cigar)
```

Arguments

`reference_seq`	A character string representing the reference sequence.
`read_seq`	A character string representing the read sequence.
`cigar`	A character string representing the CIGAR string of the read.

Value

A list with two elements, the reference sequence and the read sequence.

Author(s)

Anna Grattagliano
Politecnico di Milano
Maintainer: Anna Grattagliano
E-Mail: anna.grattagliano@mail.polimi.it

See Also

`show_alignment`

Examples

```
reference_seq <- "AGCTTAGCTAGCTACCTATATCTTGGTCTTG"
read_seq <- "AGCTTAGCTAGCTAC-TATCTTGGCCTTG"
cigar <- "14M1D11M1X6M"
align_read(reference_seq, read_seq, cigar)
```

`colorize_sequence` *Colorize a DNA sequence*

Description

This function takes a DNA sequence and returns a colorized version of the sequence where each base (A, C, G, T) is colored differently.

Usage

```
colorize_sequence(sequence)
```

Arguments

`sequence`	A character string representing the DNA sequence.

Value

A character string with HTML/CSS color codes applied to each base.

Examples

```
sequence <- 'AGCTTAGCTAGCTACCTATATCTTGGTCTTG'
colorize_sequence(sequence)
```

`extract_read` *extract a specific read ID's Information from a BAM/SAM file #' This function loads a BAM/SAM file and a specific read ID and will return-the necessary information*

Description

extract a specific read ID's Information from a BAM/SAM file #' This function loads a BAM/SAM file and a specific read ID and will returnthe necessary information

Usage

```
extract_read(file, read_id)
```

Arguments

`file`	the path to the BAM/SAM input file
`read_id`	is the identifier of the read

Value

the read information regarding the specifico read ID

Author(s)

Anna Grattagliano
Politecnico di Milano
Maintainer: Anna Grattagliano
E-Mail: anna.grattagliano@mail.polimi.it

See Also

show_alignment

Examples

```
library(Rsamtools)
library(data.table)
file <- system.file("extdata", "ERR188273_chrX.bam",
package = "AlignmentView")
read_id <- "ERR188273.11944385"
extract_read(file,read_id)
```

---

parse_cigar *Parse a CIGAR string This function takes as input the CIGAR string and finds the alphabetic and numeric parts and seperates them*

Description

Parse a CIGAR string This function takes as input the CIGAR string and finds the alphabetic and numeric parts and seperates them

Usage

```
parse_cigar(cigar)
```

Arguments

cigar	is the CIGAR string of the read

Value

a list with operations and their corresponding lengths

Author(s)

Anna Grattagliano
Politecnico di Milano
Maintainer: Anna Grattagliano
E-Mail: anna.grattagliano@mail.polimi.it

See Also

show_alignment

Examples

```
cigar <- "51M1D24M"
parse_cigar(cigar)
```

---

show_alignment *Show alignment of a read to the reference genome*

Description

This function takes a file containing read information, a read ID, and a reference genome,and prints the alignment of the specified read to the reference genome.

Usage

```
show_alignment(file, read_id, reference_genome)
```

Arguments

file	A character string representing the path to the file containing read information.
read_id	A character string representing the ID of the read to be aligned.
reference_genome	A BSgenome object representing the reference genome.

Value

Prints the alignment of the read to the reference genome.

See Also

parse_cigar, align_read, colorize_sequence

Examples

```
library(BSgenome.Hsapiens.UCSC.hg38)
file <- system.file("extdata", "ERR188273_chrX.bam",
package = "AlignmentView")
read_id <- "ERR188273.11944385"
genome <- BSgenome.Hsapiens.UCSC.hg38
show_alignment(file, read_id, genome)
```

Index