Package 'crisprBwa'

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Title BWA-based alignment of CRISPR gRNA spacer sequences

Depends methods

Imports BiocGenerics, BSgenome, crisprBase (>= 0.99.15), Seqinfo, Rbwa, readr, stats, stringr, utils

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

biocViews CRISPR, FunctionalGenomics, Alignment

Description Provides a user-friendly interface to map on-targets and off-targets of CRISPR gRNA spacer sequences using bwa. The alignment is fast, and can be performed using either commonly-used or custom CRISPR nucleases. The alignment can work with any reference or custom genomes. Currently not supported on Windows machines.

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Encoding UTF-8

RoxygenNote 7.1.2

VignetteBuilder knitr

BugReports https://github.com/crisprVerse/crisprBwa/issues

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Contents

`runBwa` *Run BWA short-read aligner*

Description

Return BWA alignments for a list of short sequences for a prebuilt BWA index.

Usage

```
runBwa(sequences, bwa_index = NULL, n_mismatches = 3)
```

Arguments

`sequences`	Character vector of DNA sequences.
`bwa_index`	String specifying path to the BWA index.
`n_mismatches`	Integer specifying maximum number of mismatches allowed between the query sequences and the index sequences.

Details

`runBwa` can be used to map short DNA sequences to a reference genome. To search for sequences while imposing constraints on PAM sequences (such as gRNA spacer sequences), see `runCrisprBwa` instead.

Value

A data.frame of the alignments with the following columns:

- `query` — string specifying query DNA sequence
- `chr` - string specifying chromosome name
- `pos` - string specifying genomic coordinate of the start of the target DNA sequence
- `strand` - string specifying strand ("+" or "-")
- `n_mismatches` - integer specifying number of mismatches between query and target sequences

Author(s)

Jean-Philippe Fortin

See Also

`link{runCrisprBwa}` to map gRNA spacer sequences.

Examples

```
fasta <- system.file(package="crisprBwa", "example/chr12.fa")
outdir <- tempdir()
index <- file.path(outdir, "chr12")
Rbwa::bwa_build_index(fasta,
                      index_prefix=index)

seqs <- c("GGAAGTTG",
          "GTGGACAC",
          "GTGTGCAA")

aln <- runBwa(seqs,
              n_mismatches=1,
              bwa_index=index)
```

`runCrisprBwa` *Find gRNA spacer alignments with bwa*

Description

Return bwa alignments for a list of gRNA spacer sequences.

Usage

```
runCrisprBwa(
  spacers,
  bwa_index = NULL,
  bsgenome = NULL,
  crisprNuclease = NULL,
  canonical = TRUE,
  ignore_pam = FALSE,
  n_mismatches = 0,
  force_spacer_length = FALSE,
  verbose = TRUE
)
```

Arguments

`spacers`	Character vector of DNA sequences corresponding to gRNA spacer sequences. Must all be of equal length.
`bwa_index`	Path to the bwa index to be used for alignment.
`bsgenome`	BSgenome object.
`crisprNuclease`	`CrisprNuclease` object.
`canonical`	Should only canonical PAM sequences be considered? TRUE by default.
`ignore_pam`	If TRUE, will return all matches regardless of PAM sequence. FALSE by default.
`n_mismatches`	Integer specifying maximum number of mismatches allowed between spacer and protospacer sequences.

force_spacer_length
: Should the spacer length be overwritten in the crisprNuclease object? FALSE by default.

verbose
: Should messages be printed to the consolde? TRUE by default.

Details

runCrisprBwa is similar to runBwa, with the addition of imposing constraints on PAM sequences such that the query sequences are valid protospacer sequences in the searched genome.

Value

runBwa returns spacer alignment data, including genomic coordinates and sequence.

Author(s)

Jean-Philippe Fortin

See Also

link{runBwa} to map general DNA sequences.

Examples

```
# Building BWA index first:
fasta <- system.file(package="crisprBwa", "example/chr12.fa")
outdir <- tempdir()
index <- file.path(outdir, "chr12")
Rbwa::bwa_build_index(fasta,
                      index_prefix=index)


# Aligning Cas9 gRNA
library(BSgenome.Hsapiens.UCSC.hg38)
seqs <- c("AGCTGTCCGTGGGGGTCCGC",
          "CCCCTGCTGCTGTGCCAGGC")
data(SpCas9, package="crisprBase")
bsgenome <- BSgenome.Hsapiens.UCSC.hg38
results <- runCrisprBwa(seqs,
                        bsgenome=bsgenome,
                        bwa_index=index,
                        n_mismatches=2,
                        crisprNuclease=SpCas9)
```

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