

Package ‘crisprBwa’

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Title BWA-based alignment of CRISPR gRNA spacer sequences

Depends methods

Imports BiocGenerics, BSgenome, crisprBase (>= 0.99.15), GenomeInfoDb, 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>

URL <https://github.com/crisprVerse/crisprBwa>

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runBwa	<i>Run BWA short-read aligner</i>
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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	<i>Find gRNA spacer alignments with bwa</i>
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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.

<code>n_mismatches</code>	Integer specifying maximum number of mismatches allowed between spacer and protospacer sequences.
<code>force_spacer_length</code>	Should the spacer length be overwritten in the <code>crisprNuclease</code> object? FALSE by default.
<code>verbose</code>	Should messages be printed to the console? 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("AGCTGTCCGTGGGGTCCGC",
          "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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