

# Package ‘crisprBwa’

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**Version** 1.10.0

**Date** 2022-10-17

**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)

```

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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.
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 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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