

# Package ‘crisprBwa’

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**Version** 1.13.0

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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

*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.      |

|                                  |                                                                                                      |
|----------------------------------|------------------------------------------------------------------------------------------------------|
| <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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