

# Package ‘Rbwa’

November 1, 2025

**Version** 1.15.0

**Date** 2023-06-29

**Title** R wrapper for BWA-backtrack and BWA-MEM aligners

**Depends** R (>= 4.1)

**Suggests** testthat, BiocStyle, knitr, rmarkdown

**SystemRequirements** GNU make

**Description** Provides an R wrapper for BWA alignment algorithms.

Both BWA-backtrack and BWA-MEM are available.

Convenience function to build a BWA index from a reference genome is also provided. Currently not supported for Windows machines.

**License** MIT + file LICENSE

**URL** <https://github.com/Jfortin1/Rbwa>

**BugReports** <https://github.com/crisprVerse/Rbwa/issues>

**biocViews** Sequencing, Alignment

**VignetteBuilder** knitr

**RoxygenNote** 7.1.2

**OS\_type** unix

**git\_url** <https://git.bioconductor.org/packages/Rbwa>

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|         |                                                          |
|---------|----------------------------------------------------------|
| bwa_aln | <i>R wrapper to run BWA alignment tool BWA-backtrack</i> |
|---------|----------------------------------------------------------|

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Description

R wrapper to run BWA alignment tool BWA-backtrack.

Usage

```
bwa_aln(  
  type = c("single", "paired"),  
  index_prefix,  
  fastq_files,  
  sai_files,  
  ...  
)
```

Arguments

|              |                                                                                                                                                          |
|--------------|----------------------------------------------------------------------------------------------------------------------------------------------------------|
| type         | String specifying type of reads: "single" for single-end reads (default) or "paired" for paired-end reads.                                               |
| index_prefix | String specifying prefix of the BWA index.                                                                                                               |
| fastq_files  | Character vector specifying paths of fastq files. If type=="single", must be of length 1. If type=="paired", must be of length 2.                        |
| sai_files    | Character vector specifying filenames of the BWA alignment output files. If type=="single", must be of length 1. If type=="paired", must be of length 2. |
| ...          | Other arguments to pass to the bwa aln alignment.                                                                                                        |

Value

No return value. Output files from bwa aln alignment are produced as side effect.

Author(s)

Jean-Philippe Fortin

**Examples**

```
dir <- tempdir()
fasta <- system.file(package="Rbwa",
                     "fasta/chr12.fa")
fastq <- system.file(package="Rbwa",
                     "fastq/sequences.fastq")
index_prefix <- file.path(dir, "chr12")
bwa_build_index(fasta, index_prefix=index_prefix)

bwa_aln(index_prefix=index_prefix,
        fastq_files=fastq,
        sai_files=file.path(dir, "output.sai"))
```

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|                 |                                            |
|-----------------|--------------------------------------------|
| bwa_build_index | <i>R wrapper to create BWA index files</i> |
|-----------------|--------------------------------------------|

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**Description**

R wrapper to create BWA index files from a FASTA file.

**Usage**

```
bwa_build_index(fasta, index_prefix = NULL, ...)
```

**Arguments**

|              |                                                   |
|--------------|---------------------------------------------------|
| fasta        | String specifying path to a FASTA file.           |
| index_prefix | String specifying prefix of the output BWA index. |
| ...          | Other arguments to pass to bwa index.             |

**Value**

No return value. BWA index files are produced as a side-effect.

**Author(s)**

Jean-Philippe Fortin

**Examples**

```
dir <- tempdir()
fasta <- system.file(package="Rbwa",
                     "fasta/chr12.fa")
bwa_build_index(fasta,
                index_prefix=file.path(dir, "chr12"))
```

---

**bwa\_mem***R wrapper to run BWA alignment tool BWA-MEM*

---

**Description**

R wrapper to run BWA alignment tool BWA-MEM.

**Usage**

```
bwa_mem(type = c("single", "paired"), index_prefix, fastq_files, sam_file, ...)
```

**Arguments**

|                           |                                                                                                                                                               |
|---------------------------|---------------------------------------------------------------------------------------------------------------------------------------------------------------|
| <code>type</code>         | String specifying type of reads: "single" for single-end reads (default) or "paired" for paired-end reads.                                                    |
| <code>index_prefix</code> | String specifying prefix of the BWA index.                                                                                                                    |
| <code>fastq_files</code>  | Character vector specifying paths of fastq files. If <code>type=="single"</code> , must be of length 1. If <code>type=="paired"</code> , must be of length 2. |
| <code>sam_file</code>     | String specifying filename of the SAM alignment output.                                                                                                       |
| <code>...</code>          | Other arguments to pass to the <code>bwa aln</code> alignment.                                                                                                |

**Value**

No return value. Output SAM file is produced as side effect.

**Author(s)**

Jean-Philippe Fortin

**Examples**

```
dir <- tempdir()
fasta <- system.file(package="Rbwa",
                     "fasta/chr12.fa")
fastq <- system.file(package="Rbwa",
                     "fastq/sequences.fastq")
index_prefix <- file.path(dir, "chr12")
bwa_build_index(fasta, index_prefix=index_prefix)

bwa_mem(index_prefix=index_prefix,
        fastq_files=fastq,
        sam_file=file.path(dir, "output.sam"))
```

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bwa\_sam*R wrapper to convert bwa aln output to SAM format*

---

**Description**

R wrapper to convert bwa aln output to SAM format.

**Usage**

```
bwa_sam(  
  type = c("single", "paired"),  
  index_prefix,  
  fastq_files,  
  sai_files,  
  sam_file,  
  ...  
)
```

**Arguments**

|              |                                                                                                                                                              |
|--------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------|
| type         | String specifying type of reads: "single" for single-end reads (default) or "paired" for paired-end reads.                                                   |
| index_prefix | String specifying prefix of the BWA index.                                                                                                                   |
| fastq_files  | Character vector specifying paths of fastq files. If type=="single", must be of length 1. If type=="paired", must be of length 2.                            |
| sai_files    | Character vector specifying filenames of the bwa aln alignment output files. If type=="single", must be of length 1. If type=="paired", must be of length 2. |
| sam_file     | String specifying paths of the SAM output file.                                                                                                              |
| ...          | Other arguments to pass to bwa_sam.                                                                                                                          |

**Value**

No return value. Output SAM files are produced as side effect.

**Author(s)**

Jean-Philippe Fortin

**Examples**

```
# Creating index:  
dir <- tempdir()  
fasta <- system.file(package="Rbwa",  
                      "fasta/chr12.fa")  
fastq <- system.file(package="Rbwa",
```

```

                                "fastq/sequences.fastq")
index_prefix <- file.path(dir,"chr12")
bwa_build_index(fasta, index_prefix=index_prefix)

# Creating alignments:
bwa_aln(index_prefix=index_prefix,
        fastq_files=fastq,
        sai_files=file.path(dir, "output.sai"))

# Generating SAM file:
bwa_sam(index_prefix=index_prefix,
        fastq_files=fastq,
        sai_files=file.path(dir, "output.sai"),
        sam_file=file.path(dir, "output.sam"))

# Reading in alignments from SAM file:
aln <- readLines(file.path(dir, "output.sam"))
aln

```

---

xa2multi

*Unpack multiple alignments stored in BWA output*


---

## Description

Unpack multiple alignments stored in BWA output

## Usage

```
xa2multi(input_sam_file, output_sam_file)
```

## Arguments

input\_sam\_file String specifying path of the input SAM file.

output\_sam\_file

String specifying path of the output SAM file.

## Details

Each row in the SAM file produced by `bwa_aln` corresponds to the best alignment hit for a given input query sequence. Other alignments (secondary alignments, or other loci in case of multiple alignments) are stored in the XA tag.

xa2multi conveniently extracts the alignments from the XA tags and represent them as additional rows in the SAM format.

## Value

Returns NULL invisibly. SAM file with multiple alignments is produced as a side effect.

**Author(s)**

Jean-Philippe Fortin

**Examples**

```
# Creating index:
dir <- tempdir()
fasta <- system.file(package="Rbwa",
                     "fasta/chr12.fa")
fastq <- system.file(package="Rbwa",
                     "fastq/sequences.fastq")
index_prefix <- file.path(dir, "chr12")
bwa_build_index(fasta, index_prefix=index_prefix)

# Creating alignments:
bwa_aln(index_prefix=index_prefix,
        fastq_files=fastq,
        sai_files=file.path(dir, "output.sai"))

# Generating SAM file:
bwa_sam(index_prefix=index_prefix,
        fastq_files=fastq,
        sai_files=file.path(dir, "output.sai"),
        sam_file=file.path(dir, "output.sam"))

# Generating multiple alignments:
xa2multi(input_sam_file=file.path(dir, "output.sam"),
        output_sam_file=file.path(dir, "output.multi.sam"))

#' Reading in:
aln <- readLines(file.path(dir, "output.multi.sam"))
aln
```

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