Package ‘Rbwa’

August 26, 2024

Version 1.8.0

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.

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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

git_branch RELEASE_3_19

git_last_commit 7f23b4f

git_last_commit_date 2024-04-30

Repository Bioconductor 3.19

Date/Publication 2024-08-25

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Contents

`bwa_aln` *R wrapper to run BWA alignment tool BWA-backtrack*

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 aligmment 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"))
```

`bwa_build_index` *R wrapper to create BWA index files*

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

`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.
`sam_file`	String specifying filename of the SAM aligmment output.
`...`	Other arguments to pass to the `bwa aln` 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"))
```

`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` aligmment 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
```

Index