

Package: Rbwa (via r-universe)

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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

Repository <https://bioc.r-universe.dev>

RemoteUrl <https://github.com/bioc/Rbwa>

RemoteRef HEAD

RemoteSha 27c701763afaf2f35e22dbe3e3901c97820b5e0b

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`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

<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>sai_files</code>	Character vector specifying filenames of the BWA alignment output files. If <code>type=="single"</code> , must be of length 1. If <code>type=="paired"</code> , must be of length 2.
<code>...</code>	Other arguments to pass to the <code>bwa aln</code> 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)
```

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

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"))
```

bwa_sam	<i>R wrapper to convert bwa aln output to SAM format</i>
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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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