Package 'Rbwa'

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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

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Author Jean-Philippe Fortin [aut, cre]

Maintainer Jean-Philippe Fortin <fortin946@gmail.com>

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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

`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
```

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