

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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Contents

| | |
|---------------------------|---|
| bwa_aln | 2 |
| bwa_build_index | 3 |
| bwa_mem | 4 |
| bwa_sam | 5 |
| xa2multi | 6 |

| | |
|--------------|----------|
| Index | 8 |
|--------------|----------|

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

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"))
```

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

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> |
|---------|--|

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
```

Index

bwa_aln, [2](#), [6](#)
bwa_build_index, [3](#)
bwa_mem, [4](#)
bwa_sam, [5](#)

xa2multi, [6](#)