Package: minimapR (via r-universe)

October 31, 2024

Title R Wrapper for 'minimap2'

Version 0.0.0.96

Date 2024-03-28

Author Jake Reed [aut, cre] (<https://orcid.org/0000-0002-8384-3593>)

Maintainer Jake Reed <hreed.ga@gmail.com>

Description 'minimap2' is a very valuable long read aligner for the Pacbio and Oxford Nanopore Technologies sequencing platforms. minimapR is an R wrapper for 'minimap2' which was developed by Heng Li <me@liheng.org>. *SPECIAL NOTE Examples can only be run from 'GitHub' installation. *SPECIAL NOTE If using a Windows operating system, installation of the 'MSYS2' Linux emulator is required. *SPECIAL NOTE If using a Mac operating system, installation of 'Homebrew' is required.

License MIT + file LICENSE

Depends Rsamtools, git2r, pafr

URL https://github.com/jake-bioinfo/minimapR

Encoding UTF-8

Roxygen list(markdown = TRUE)

RoxygenNote 7.3.1

Repository https://jake-bioinfo.r-universe.dev

RemoteUrl https://github.com/jake-bioinfo/minimapr

RemoteRef HEAD

RemoteSha 741e5d25c6460c8ac9558e27d618adcaea4e5fe1

Contents

minimap2 2
minimap2_check 3
minimap2_install 4
samtools_check 5
samtools_install 5

Index 6

`minimap2` *minimap2*

Description

This function is a wrapper for the command line tool minimap2. minimap2 is a long read sequencing alignment tool that is used to align long reads to a reference genome.

Usage

```
minimap2(
  reference,
  query_sequences,
  output_file_prefix,
  a = TRUE,
  preset_string = "map-hifi",
  threads = 1,
  return = FALSE,
  verbose = TRUE,
  ...
)
```

Arguments

`reference`	Reference genome to align the query sequences
`query_sequences`	Query sequences to align to the reference genome
`output_file_prefix`	Output file to save the alignment results
`a`	Logical value to use the preset string with the -a flag
`preset_string`	Preset string to use with the -x flag
`threads`	Number of threads to use
`return`	Logical value to return the alignment results
`verbose`	Logical value to print progress of the installation
`...`	Additional arguments to pass to minimap2

Value

This function returns the line needed to add minimap2 to PATH

Examples

```
## Not run:
reference <- system.file("extdata/S288C_ref_genome.fasta", package = "minimapR")
query_sequences <- system.file("extdata/yeast_sample_hifi.fastq.gz", package = "minimapR")
out_dir <- system.file("extdata/test_out", package = "minimapR")
output_file_prefix <- paste0(out_dir, "/yeast_sample_hifi")
bam_out <- minimap2(reference,
 query_sequences,
 output_file_prefix,
 threads = 4,
 preset_string = "map-hifi",
 return = TRUE,
 verbose = TRUE)

## End(Not run)

## Not run:
reference <- system.file("extdata/GRCh38_chr1_50m.fa", package = "minimapR")
query_sequences <- system.file("extdata/ont_hs_sample.fastq.gz", package = "minimapR")
out_dir <- system.file("extdata/test_out", package = "minimapR")
output_file_prefix <- paste0(out_dir, "/ont_hs_sample")
bam_out <- minimap2(reference,
 query_sequences,
 output_file_prefix,
 threads = 4,
 preset_string = "map-hifi",
 return = TRUE,
 verbose = TRUE)

## End(Not run)
```

`minimap2_check` *minimap2_check*

Description

Check if minimap2 is installed

Usage

```
minimap2_check(return = TRUE)
```

Arguments

`return`	Logical value to return the path of minimap2

Value

This function returns the path of minimap2 if installed

Examples

```
minimap2_check(return = TRUE)
```

`minimap2_install` *minimap2_install*

Description

Install `minimap2` from Heng Li's github repository. If using a Windows operating system, installation of the MSYS2 Linux emulator is required.

Usage

```
minimap2_install(source_directory, verbose = TRUE, return = FALSE)
```

Arguments

`source_directory`	Source directory to install minimap2. Do not include minimap2 name in the source directory. Note that this must be entered as a full path location.
`verbose`	Logical value to print progress of the installation
`return`	This logical value causes the `minimap2_install` function to return the path of minimap2

Value

This function returns a character. source directoryro

Character value that is the path of the installed 'minimap2' tool. source directory

Examples

```
## Not run:
install_dir <- file.path("/dir/to/install")
minimap2_path <- minimap2_install(source_directory = install_dir, verbose = FALSE)

## End(Not run)
```

`samtools_check` *samtools_check*

Description

Check if samtools is installed

Usage

```
samtools_check(return = TRUE)
```

Arguments

`return`	Logical value to return the path of samtools

Value

This function returns the path of samtools if installed

Examples

```
samtools_check(return = TRUE)
```

`samtools_install` *samtools_install*

Description

Install samtools with conda

Usage

```
samtools_install(verbose = TRUE)
```

Arguments

`verbose`	Logical value to print progress of the installation

Examples

```
## Not run:
samtools_install()

## End(Not run)
```

Index

minimap2, 2
minimap2_check, 3
minimap2_install, 4

samtools_check, 5
samtools_install, 5