

Package: minimapR (via r-universe)

August 21, 2024

Title Wrapper for 'minimap2'

Version 0.0.1.0

Date 2024-07-11

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

Description Wrapper for 'Minimap2'. '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 NOTES
1. Examples can only be run from 'GitHub' installation. 2. If using a Windows operating system, installation of the 'MSYS2' Linux emulator is required. 3. If using a Mac operating system, installation of 'Homebrew' is required. Li, Heng (2018) <doi:10.1093/bioinformatics/bty191> ``Minimap2: pairwise alignment for nucleotide sequences".

License MIT + file LICENSE

Depends R (>= 4.0.0), Rsamtools, git2r, pafr

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

Encoding UTF-8

RoxygenNote 7.3.2

Suggests knitr, rmarkdown

VignetteBuilder knitr

NeedsCompilation no

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

Repository CRAN

Date/Publication 2024-07-21 10:10:02 UTC

Contents

minimap2	2
--------------------	---

minimap2_check	3
minimap2_installation	4
mm2_install	5
samtools_check	5
samtools_install	6

Index	7
--------------	----------

minimap2	<i>minimap2</i>
----------	-----------------

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

If minimap2 is installed, this function returns the path of minimap2 (character).

Examples

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

```
minimap2_installation minimap2_installation
```

Description

This function prints installation instructions specific to the user's operating system.

Usage

```
minimap2_installation(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 <code>minimap2_install</code> function to return the path of minimap2

Value

This function returns the path of the installed 'minimap2' tool (character).

Examples

```
## Not run:  
install_dir <- file.path("/dir/to/install")  
minimap2_path <- minimap2_installation(source_directory = install_dir, verbose = FALSE)  
  
## End(Not run)
```

mm2_install	<i>minimap2_install</i>
-------------	-------------------------

Description

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

Usage

```
mm2_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

If 'minimap2' is not installed, this function installs it on linux and returns the path of the installed 'minimap2' tool (character).

Examples

```
## Not run:  
install_dir <- file.path("/dir/to/install")  
minimap2_path <- mm2_install(source_directory = install_dir, verbose = FALSE)  
  
## End(Not run)
```

samtools_check	<i>samtools_check</i>
----------------	-----------------------

Description

Check if samtools is installed

Usage

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

Arguments

return Logical value to return the path of samtools

Value

If 'samtools' is installed, this function returns the path of samtools (character).

Examples

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

samtools_install	<i>samtools_install</i>
------------------	-------------------------

Description

Install samtools with conda

Usage

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

Arguments

verbose Logical value to print progress of the installation

Value

If 'samtools' is not installed, this function installs it on linux and returns the path of the installed 'samtools' tool (character).

Examples

```
## Not run:  
samtools_install()  
  
## End(Not run)
```

Index

minimap2, [2](#)
minimap2_check, [3](#)
minimap2_installation, [4](#)
mm2_install, [5](#)

samtools_check, [5](#)
samtools_install, [6](#)