Package 'minimapR'

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Title Wrapper for 'minimap2'

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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".

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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

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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

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 minimap2_install 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 *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

```
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 *samtools_check*

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   *samtools_install*

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)
```

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