

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. 'conda' or 'mamba' must be used to install 'minimapR' on your system.
3. For Windows users, 'minimap2' and 'samtools' can be installed via MSYS2, instructions are provided when 'minimap2_installation()' is run.

Li, Heng (2018) <[doi:10.1093/bioinformatics/bty191](https://doi.org/10.1093/bioinformatics/bty191)> ``Minimap2: pairwise alignment for nucleotide sequences".

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Depends R (>= 4.4.0), Rsamtools, 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	<i>minimap2</i>
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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 = "minimap2_out",
  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.gz", package = "minimapR")
query_sequences <- system.file("extdata/yeast_sample_hifi.fastq.gz", package = "minimapR")
# Warning: not setting output_file_prefix will generate the output in the current working directory
bam_out <- minimap2(reference,
  query_sequences,
  threads = 4,
  preset_string = "map-hifi",
  return = TRUE,
  verbose = TRUE)

## End(Not run)

## Not run:
reference <- system.file("extdata/GRCh38_chr1_130k.fa.gz", package = "minimapR")
query_sequences <- system.file("extdata/ont_hs_sample.fastq.gz", package = "minimapR")
# Warning: not setting output_file_prefix will generate the output in the current working directory
bam_out <- minimap2(reference,
  query_sequences,
  threads = 4,
  preset_string = "map-hifi",
  return = TRUE,
  verbose = TRUE)

## End(Not run)
```

minimap2_check	<i>minimap2_check</i>
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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(verbose = TRUE)
```

Arguments

verbose Logical value to print progress of the installation

Value

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

Examples

```
## Not run:  
minimap2_installation(verbose = FALSE)  
  
## End(Not run)
```

```
mm2_install            minimap2_install
```

Description

Install minimap2 using conda or mamba. Conda or mamba is required for installation.

Usage

```
mm2_install(verbose = TRUE)
```

Arguments

verbose Logical value to print progress of the installation. Default is TRUE. If set to FALSE, it will suppress the output messages during installation.

Value

If 'minimap2' is not installed, this function installs it on windows, linux or macOS.

Examples

```
## Not run:  
mm2_install(verbose = TRUE)  
  
## 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>
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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 returns the path of the installed 'samtools' tool (character).

Examples

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

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