Package ‘RbowtieCuda’

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Type Package

Title An R Wrapper for nvBowtie and nvBWT, a rewritten version of Bowtie2 for cuda

Version 1.2.0

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Description This package provides an R wrapper for the popular Bowtie2 sequencing read aligner, optimized to run on NVIDIA graphics cards. It includes wrapper functions that enable both genome
indexing and alignment to the generated indexes, ensuring high performance and ease of use within the R environment.

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Depends R (>= 4.5.0)

Encoding UTF-8

Imports methods

Suggests knitr, rmarkdown, RUnit, BiocGenerics

SystemRequirements C++20, GNU make, cmake, CUDA Toolkit(>=10), MSVC, libthrust-dev, libcub-dev, gcc, g++

Archs x64

RoxygenNote 7.3.2

biocViews Sequencing, Alignment, Preprocessing, Coverage

VignetteBuilder knitr

Config/testthat/edition 3

NeedsCompilation yes

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BugReports `https://github.com/FranckRICHARD01/RbowtieCuda/issues`

URL `https://github.com/FranckRICHARD01/RbowtieCuda`,
`https://belacqua-labo.ovh/bioinformatic/RbowtieCuda`

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`.callbinary2` *Make system call for binaries*

Description

Function that makes a system call for the RbowtieCuda binaries. Note that it is not designed to be used outside the package.

Usage

```
.callbinary2(bin1, args1, path = NULL)
```

Arguments

`bin1`	`Character`. The binary used for the system call.
`args1`	`Character`. The arguments to pass to the binary.
`path`	`Character` Optional: If passed to function, returns the path.

Value

An invisible `Integer` of call status. The value is 0 when there is not any mistakes.

Author(s)

Franck RICHARD

Examples

```
.callbinary2(bin1 = "nvBowtie", args1 = "--version")
```

`nvbio_tests` *Print unit tests*

Description

Calling nvbio_tests() performs alignment tests

Usage

```
nvbio_tests()
```

Value

The return value is the string "nvbio test passed." when there is not any mistakes.

Author(s)

Franck RICHARD

Examples

```
nvbio_tests()
```

`nvBowtie` *nvBowtie align function*

Description

nvBowtie is a GPU-accelerated re-engineering of Bowtie2, a very widely used short-read aligner.

Usage

```
nvBowtie(index, output_file, options, seq1, seq2 = NULL)
```

Arguments

`index`	`Character` vector. Index file created by nvBWT.
`output_file`	`Character` vector. The alignment output file (.sam o .bam)
`options`	`Character` vector. Specify additional options here to customize the processing. For a complete list of available options, type `nvBowtie_usage()`.
`seq1`	`Character` vector. For single-end sequencing, it contains sequence file paths. For paired-end sequencing, it can be file path with #1 mates paired with file paths in seq2.
`seq2`	`Character` vector. It contains file paths with #2 mates paired with file path in seq1. For single-end sequencoing files, it must be `NULL`.

Details

We've introduced several new features to nvBowtie. You can now perform alignments using the WFA method by including the `--wfa` (or `--scoring wfa`) parameter. The WFA method requires a large amount of RAM on the graphics card. We therefore recommend using an Nvidia card with 8GB or more. Please note that this feature is still experimental; it currently supports only end-to-end alignments and does not yet allow customization of scoring parameters. By default, it uses the following scoring: `match:0`, `mismatch:1`, `gap_open:1` and `gap_ext:1`. Additionally, the `--cache-writes` parameter optimizes disk write operations, resulting in faster alignments. This functionality requires 4GB of RAM and is limited to paired-end alignments.

Value

An invisible `Integer` of call status. The value is 0 when there is not any mistakes Otherwise the value is non-zero.

References

Langmead, B., & Salzberg, S. L. (2012). Fast gapped-read alignment with Bowtie 2. Nature methods, 9(4), 357-359.

Examples

```
td <- tempdir()

## Building index
fa_file <- system.file(package='RbowtieCuda', 'extdata', 'bt2', 'refs', 'lambda_virus.fa')
nvBWT(myinput=fa_file, output=file.path(td, 'index'), options='')

## Alignments
read_1 <- system.file(package='RbowtieCuda', 'extdata', 'bt2', 'reads', 'reads_1.fastq')
read_2 <- system.file(package='RbowtieCuda', 'extdata', 'bt2', 'reads', 'reads_2.fastq')

## Sam file created with paired-end files (paired mates are here reverse-forward)
nvBowtie(file.path(td, 'index'), file.path(td, 'my_result.sam'), options='--rf', seq1=read_1, seq2=read_2)

## Bam file created with single-end file
nvBowtie(file.path(td, 'index'), file.path(td, 'my_result.bam'), options='', seq1=read_1)
```

`nvBowtie_usage` *Print available arguments that can be passed to nvBowtie()*

Description

Calling nvBowtie_usage() prints available arguments that can be passed to the nvBowtie() function.

Usage

```
nvBowtie_usage()
```

Value

An invisible Integer of call status. The value is 0 when there is not any mistakes Otherwise the value is non-zero.

Author(s)

Franck RICHARD

References

Langmead, B., & Salzberg, S. L. (2012). Fast gapped-read alignment with Bowtie 2. Nature methods, 9(4), 357-359.

Examples

```
nvBowtie_usage()
```

`nvBowtie_version` *Print version information*

Description

Calling nvBowtie_version() displays the version information of the RbowtieCuda package in use.

Usage

```
nvBowtie_version()
```

Value

An invisible `Integer` of call status. The value is 0 when there is not any mistakes.

Author(s)

Franck RICHARD

Examples

```
nvBowtie_version()
```

`nvBWT` *nvBWT : builds the BWT indices of the reference FASTA files*

Description

This function can be use to call wrapped `nvBWT` binary.

Usage

```
nvBWT(myinput, output, options = NULL)
```

Arguments

`myinput`	`Character` vector. A path to a .fa file
`output`	`Character` vector. A path to a index file used for the alignment output.
`options`	`Character` vector. Options Example: `--verbosity`

Details

Available options:

```
-v       | --verbosity     int (0-6) [5]     // select the verbosity level
-m       | --max-length    int       [inf]   // clamp input length
-b       | --byte-packing  [default]         // output a byte-encoded .pac file
-w       | --word-packing                   // output a word-encoded .wpac file
                                             // (more efficient)
-c       | --crc                             // compute CRCs
-d       | --device                          // select a cuda device
```

Value

An invisible `Integer` of call status. The value is 0 when there is not any mistakes Otherwise the value is non-zero.

Author(s)

Franck RICHARD

References

Langmead, B., & Salzberg, S. L. (2012). Fast gapped-read alignment with Bowtie 2. Nature methods, 9(4), 357-359.

Examples

```
td <- tempdir()
fa_file <- system.file(package='RbowtieCuda', 'extdata', 'bt2', 'refs', 'lambda_virus.fa')
nvBWT(myinput=fa_file, output=file.path(td, 'index'), options='')
```

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