Package 'Rhisat2'

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Type Package

Title R Wrapper for HISAT2 Aligner

Version 1.28.1

SystemRequirements GNU make

Description An R interface to the HISAT2 spliced short-read aligner by Kim et al. (2015). The package contains wrapper functions to create a genome index and to perform the read alignment to the generated index.

License GPL-3

Encoding UTF-8

Depends R (>= 4.4.0)

Suggests testthat, knitr, rmarkdown, BiocStyle

VignetteBuilder knitr

biocViews Alignment, Sequencing, SplicedAlignment

Imports txdbmaker, SGSeq, GenomicRanges, methods, utils

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BugReports https://github.com/fmicompbio/Rhisat2/issues

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`Rhisat2-package` *R hisat2 wrapper*

Description

This package provides an R wrapper around the HISAT2 short read aligner. The package is used by the QuasR Bioconductor package. We recommend to use QuasR instead of calling Rhisat2 directly, since it covers the whole analysis workflow of typical high-throughput sequencing experiments.

Author(s)

Charlotte Soneson, based partly on code from Florian Hahne

References

Kim D, Langmead B and Salzberg SL. HISAT: a fast spliced aligner with low memory requirements. Nature Methods 12:357-360 (2015).

See Also

hisat2, hisat2_build, hisat2_build_usage, hisat2_usage

`.createFlags` *Create flags*

Description

Given a named list of argument values, generate a single character string containing all arguments and values, separated by single spaces. Logical values imply that the argument is either included (without a value) or excluded in the character string. For vector-valued arguments, the values will be comma separated in the final string.

Usage

```
.createFlags(flagList)
```

Arguments

flagList	A named list of argument values. Vectors will be collapsed and separated by a comma.

Details

Adapted from the Rbowtie package

Value

A character string with the arguments and their values.

.hisat2Bin *Call the HISAT2 binary with additional arguments.*

Description

Adapted from the Rbowtie package

Usage

```
.hisat2Bin(bin = c("hisat2", "hisat2-build"), args = "", execute = TRUE)
```

Arguments

bin	The name of the binary, either hisat2 or hisat2-build.
args	A character string containing the arguments that will be passed to the binary.
execute	Logical scalar, whether to execute the command. If FALSE, return a string with the shell command.

Value

If execute is TRUE, returns the console output of running the hisat2 command. If execute is FALSE, returns the shell command.

`extract_splice_sites` *Extract splice sites from annotation*

Description

This function extracts splice sites from an annotation object (a gtf/gff3 file, a `GRanges` object or a `TxDb` object) and saves them in a text file formatted such that it can be directly used with HISAT2, by providing it as the argument `known-splicesite-infile`.

Usage

```
extract_splice_sites(features, outfile, min_length = 5)
```

Arguments

`features`	Either the path to a gtf/gff3 file containing the genomic features, a GRanges object or a TxDb object.
`outfile`	Character scalar. The path to a text file where the extracted splice sites will be written.
`min_length`	Integer scalar. Junctions corresponding to introns below this size will not be reported. The default setting in HISAT2 is 5.

Value

Nothing is returned, but the splice junction coordinates are written to `outfile`.

Author(s)

Charlotte Soneson

References

Kim D, Langmead B and Salzberg SL. HISAT: a fast spliced aligner with low memory requirements. Nature Methods 12:357-360 (2015).

Examples

```
tmp <- tempfile()
extract_splice_sites(features=system.file("extdata/refs/genes.gtf",
                                          package="Rhisat2"),
                     outfile=tmp, min_length=5)
```

hisat2 *Align reads with HISAT2*

Description

The function can be used to call the `hisat2` binary.

Usage

```
hisat2(
  sequences,
  index,
  ...,
  type = c("single", "paired"),
  outfile,
  force = FALSE,
  strict = TRUE,
  execute = TRUE
)
```

Arguments

`sequences`	If `type` is `single`, a character vector of file names if the additional argument `c` is FALSE, otherwise a vector of read sequences. If `type` is `paired`, a length-2 list of file names or sequences, where the first list item corresponds to the first mate pair sequences, and the second list item to the second mate pair sequences.
`index`	Character scalar. The path+prefix of the HISAT2 index to align against (in the form `<path/to/index>/<prefix>`).
`...`	Additional arguments passed to the binaries.
`type`	Character scalar, either "single" or "paired". If `single`, the input sequences are interpreted as single-end reads. If `paired`, they are supposed to be paired reads.
`outfile`	(optional) Character scalar. The path to the output file. If missing, the alignments will be returned as an R character vector.
`force`	Logical scalar. Whether to force overwriting of `outdir`.
`strict`	Logical scalar. Whether strict checking of input arguments should be enforced.
`execute`	Logical scalar. Whether to execute the assembled shell command. If FALSE, return a string with the command.

Details

All additional arguments in `...` are interpreted as additional arguments to the HISAT2 binaries. Any flags are supposed to be represented as logical values (e.g., `quiet=TRUE` will be translated into `--quiet`). Parameters with additional input are supposed to be character or numeric vectors, and the individual elements are collapsed into a single comma-separated string (e.g., `k=2` is translated into `-k 2`, `bmax=100` into `--bmax 100`). Some arguments to the HISAT2 binaries will be ignored if they are already handled as explicit function arguments. See the output of `hisat2_usage()` for details about available parameters.

Value

If `execute` is TRUE, the output generated by calling the `hisat2` binary. If `execute` is FALSE, the `hisat2` command.

Author(s)

Charlotte Soneson, based on code from Florian Hahne.

References

Kim D, Langmead B and Salzberg SL. HISAT: a fast spliced aligner with low memory requirements. Nature Methods 12:357-360 (2015).

Examples

```
tmp <- tempdir()
refs <- list.files(system.file("extdata/refs", package="Rhisat2"),
                   full.names=TRUE, pattern="\\.fa$")
hisat2_build(references=refs, outdir=file.path(tmp, "index"),
             force=TRUE, prefix="index")
reads <- list.files(system.file("extdata/reads", package="Rhisat2"),
                    full.names=TRUE, pattern="\\.fastq$")
hisat2(sequences=as.list(reads), index=file.path(tmp, "index/index"),
       type="paired", outfile=file.path(tmp, "out.sam"), force=TRUE)
```

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hisat2_build *Generate HISAT2 index*

Description

This function can be used to call the `hisat2-build` binary.

Usage

```
hisat2_build(
  references,
  outdir,
  ...,
  prefix = "index",
  force = FALSE,
  strict = TRUE,
  execute = TRUE
)
```

Arguments

references	Character vector. The path to the files containing the reference sequences from which to build the HISAT2 index.
outdir	Character scalar. The path to the output directory in which to store the HISAT2 index. If the directory already exists, the function will throw an error, unless force=TRUE.
...	Additional arguments passed to the binaries.
prefix	Character scalar. The prefix to use for the HISAT2 index files.
force	Logical scalar. Whether to force overwriting of outdir.
strict	Logical scalar. Whether strict checking of input arguments should be enforced.
execute	Logical scalar. Whether to execute the assembled shell command. If FALSE, return a string with the command.

Details

All additional arguments in ... are interpreted as additional arguments to the HISAT2 binaries. Any flags are supposed to be represented as logical values (e.g., quiet=TRUE will be translated into --quiet). Parameters with additional input are supposed to be character or numeric vectors, and the individual elements are collapsed into a single comma-separated string (e.g., k=2 is translated into -k 2, bmax=100 into --bmax 100). Some arguments to the HISAT2 binaries will be ignored if they are already handled as explicit function arguments. See the output of hisat2_build_usage() for details about available parameters.

Value

If execute is TRUE, the output generated by calling the hisat2-build binary. If execute is FALSE, the hisat2-build command.

Author(s)

Charlotte Soneson, based on code from Florian Hahne.

References

Kim D, Langmead B and Salzberg SL. HISAT: a fast spliced aligner with low memory requirements. Nature Methods 12:357-360 (2015).

Examples

```
tmp <- tempdir()
refs <- list.files(system.file(package="Rhisat2", "extdata/refs"),
                   full.names=TRUE, pattern="\\.fa$")
x <- hisat2_build(references=refs, outdir=file.path(tmp, "index"),
                  force=TRUE)
head(x)
list.files(file.path(tmp, "index"))
```

hisat2_build_usage *Print usage of hisat2-build*

Description

Print usage of hisat2-build

Usage

```
hisat2_build_usage()
```

Value

No value is returned, the usage of `hisat2_build` is printed to the console.

Author(s)

Charlotte Soneson

Examples

```
hisat2_build_usage()
```

hisat2_usage *Print usage of hisat2*

Description

Print usage of hisat2

Usage

```
hisat2_usage()
```

Value

No value is returned, the usage of `hisat2` is printed to the console.

Author(s)

Charlotte Soneson

Examples

```
hisat2_usage()
```

hisat2_version *Print HISAT2 version*

Description

Print HISAT2 version

Usage

```
hisat2_version()
```

Value

No value is returned, the version information for `hisat2` is printed to the console.

Author(s)

Charlotte Soneson

Examples

```
hisat2_version()
```

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