

Package: Rhisat2 (via r-universe)

October 31, 2026

Type Package

Title R Wrapper for HISAT2 Aligner

Version 1.29.1

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

URL <https://github.com/fmicompbio/Rhisat2>

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

Config/roxygen2/version 8.0.0

Config/pak/sysreqs libglpk-dev make libbz2-dev libicu-dev liblzma-dev libpng-dev libxml2-dev libssl-dev xz-utils zlib1g-dev

Repository <https://bioc.r-universe.dev>

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extract_splice_sites	<i>Extract splice sites from annotation</i>
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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)
```

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 Sonesson, 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	<i>Print usage of hisat2-build</i>
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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	<i>Print usage of hisat2</i>
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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()`

<code>hisat2_version</code>	<i>Print HISAT2 version</i>
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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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