

# Package ‘Rhisat2’

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**Type** Package

**Title** R Wrapper for HISAT2 Aligner

**Version** 1.24.0

**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

**RoxygenNote** 7.3.1

**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>

**Archs** x64

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**Author** Charlotte Soneson [aut, cre] (ORCID:  
<<https://orcid.org/0000-0003-3833-2169>>)

**Maintainer** Charlotte Soneson <charlottesoneson@gmail.com>

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|                 |                         |
|-----------------|-------------------------|
| Rhisat2-package | <i>R hisat2 wrapper</i> |
|-----------------|-------------------------|

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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 Sonesson, 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 | <i>Create flags</i> |
|--------------|---------------------|

---

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**

|                       |                                                                                      |
|-----------------------|--------------------------------------------------------------------------------------|
| <code>flagList</code> | 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**

|                      |                                                                                                                 |
|----------------------|-----------------------------------------------------------------------------------------------------------------|
| <code>bin</code>     | The name of the binary, either <code>hisat2</code> or <code>hisat2-build</code> .                               |
| <code>args</code>    | A character string containing the arguments that will be passed to the binary.                                  |
| <code>execute</code> | Logical scalar, whether to execute the command. If <code>FALSE</code> , 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)
```

---

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 | <i>Print usage of hisat2-build</i> |
|--------------------|------------------------------------|

---

**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> |
|--------------|------------------------------|

---

**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 | <i>Print HISAT2 version</i> |
|----------------|-----------------------------|

---

**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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