

Package ‘Rhtslib’

October 12, 2021

Title HTSlib high-throughput sequencing library as an R package

Description This package provides version 1.7 of the 'HTSlib' C library for high-throughput sequence analysis. The package is primarily useful to developers of other R packages who wish to make use of HTSlib. Motivation and instructions for use of this package are in the vignette, `vignette(package = "Rhtslib")`.

biocViews DataImport, Sequencing

URL <https://bioconductor.org/packages/Rhtslib>, <http://www.htslib.org/>

BugReports <https://github.com/Bioconductor/Rhtslib/issues>

Version 1.24.0

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Imports zlibbioc

LinkingTo zlibbioc

Suggests BiocStyle, knitr

SystemRequirements libbz2 & liblzma & libcurl (with header files), GNU make

StagedInstall no

VignetteBuilder knitr

git_url <https://git.bioconductor.org/packages/Rhtslib>

git_branch RELEASE_3_13

git_last_commit 28051cc

git_last_commit_date 2021-05-19

Date/Publication 2021-10-12

Author Nathaniel Hayden [led, aut],
Martin Morgan [aut],
Bioconductor Package Maintainer [cre]

Maintainer Bioconductor Package Maintainer <maintainer@bioconductor.org>

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Rhtslib-package	<i>An R packaged HTSlib 1.7</i>
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Description

This package is interesting to package developers only, and provides a compiled HTSlib for developers to use in their own packages. See the vignette for instructions on use.

Details

Instructions for use are in the vignette, available with `browseVignettes(package="Rhtslib")`

Author(s)

Nathaniel Hayden nhayden@fredhutch.org

References

The HTSlib included in the package is based on release 1.7 of HTSlib found in the GitHub repository at <https://github.com/samtools/htslib>

See Also

[pkgconfig](#)

Examples

```
packageDescription('Rhtslib')
Rhtslib:::htsVersion()
```

pkgconfig

Compiler configuration arguments for use of Rhtslib

Description

This function returns values for PKG_LIBS and PKG_CPPFLAGS variables for use in Makevars files. See vignette("Rhtslib") for details. The environment variable RHTSLIB_RPATH can be used to over-ride the inferred location of the installed package.

Usage

```
pkgconfig(opt = c("PKG_LIBS", "PKG_CPPFLAGS"))
```

Arguments

opt A scalar character from the list of available options; default is PKG_LIBS.

Value

NULL; prints the corresponding value to stdout.

Author(s)

Nathaniel Hayden <mailto:nhayden@fredhutch.org>

Examples

```
pkgconfig("PKG_LIBS")
pkgconfig("PKG_CPPFLAGS")
```

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