Package ‘Rhtslib’

April 6, 2026

Title HTSlib high-throughput sequencing library as an R package

Description This package provides version 1.18 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", ``Rhtslib").

biocViews DataImport, Sequencing

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

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

Version 3.7.0

License LGPL (>= 2)

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Encoding UTF-8

Imports tools

Suggests knitr, rmarkdown, BiocStyle

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

StagedInstall no

VignetteBuilder knitr

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`Rhtslib-package` *An R packaged HTSlib 1.18*

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")`

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References

The HTSlib included in the package is based on release 1.18 of HTSlib found at `https://github.com/samtools/htslib/releases/`

See Also

pkgconfig

Examples

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

`pkgconfig` *Compiler configuration arguments for use of Rhtslib*

Description

This function prints 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

The function prints the `PKG_LIBS` or `PKG_CPPFLAGS` value and returns an invisible `NULL`.

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Examples

```
pkgconfig("PKG_LIBS")

pkgconfig("PKG_CPPFLAGS")
```

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