

# Package ‘assorthead’

May 8, 2026

**Version** 1.7.2

**Date** 2026-05-05

**Title** Assorted Header-Only C++ Libraries

**Description** Vendors an assortment of useful header-only C++ libraries.

Bioconductor packages can use these libraries in their own C++ code by LinkingTo this package without introducing any additional dependencies.

The use of a central repository avoids duplicate vendoring of libraries across multiple R packages, and enables better coordination of version updates across cohorts of interdependent C++ libraries.

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**Suggests** knitr, rmarkdown, BiocStyle

**VignetteBuilder** knitr

**URL** <https://github.com/LTLA/assorthead>

**BugReports** <https://github.com/LTLA/assorthead/issues>

**Encoding** UTF-8

**biocViews** SingleCell, QualityControl, Normalization,  
DataRepresentation, DataImport, DifferentialExpression,  
Alignment

**RoxygenNote** 7.3.3

**git\_url** <https://git.bioconductor.org/packages/assorthead>

**git\_branch** devel

**git\_last\_commit** 3f30d63

**git\_last\_commit\_date** 2026-05-05

**Repository** Bioconductor 3.24

**Date/Publication** 2026-05-08

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assorthead-package     *assorthead: Assorted Header-Only C++ Libraries*

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**Description**

Vendors an assortment of useful header-only C++ libraries. Bioconductor packages can use these libraries in their own C++ code by `LinkingTo` this package without introducing any additional dependencies. The use of a central repository avoids duplicate vendoring of libraries across multiple R packages, and enables better coordination of version updates across cohorts of interdependent C++ libraries.

**Author(s)**

**Maintainer:** Aaron Lun <infinite.monkeys.with.keyboards@gmail.com>

**See Also**

Useful links:

- <https://github.com/LTLA/assorthead>
- Report bugs at <https://github.com/LTLA/assorthead/issues>

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