

# Package ‘cytolib’

October 14, 2021

**Type** Package

**Title** C++ infrastructure for representing and interacting with the gated cytometry data

**Version** 2.4.0

**Date** 2017-08-07

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**Description** This package provides the core data structure and API to represent and interact with the gated cytometry data.

**License** file LICENSE

**License\_restricts\_use** yes

**LazyLoad** yes

**Imports** RcppParallel, RProtoBufLib

**Depends** R (>= 3.4)

**Suggests** knitr

**LinkingTo** Rcpp, BH(>= 1.75.0.0), RProtoBufLib(>= 2.3.5),Rhdf5lib, RcppArmadillo, RcppParallel(>= 4.4.2-1)

**biocViews** ImmunoOncology, FlowCytometry, DataImport, Preprocessing, DataRepresentation

**VignetteBuilder** knitr

**SystemRequirements** GNU make, C++11

**RoxygenNote** 7.1.0

**Biarch** TRUE

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

**git\_branch** RELEASE\_3\_13

**git\_last\_commit** 652ea2c

**git\_last\_commit\_date** 2021-05-19

**Date/Publication** 2021-10-14

**R topics documented:**

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cytolib_LdFlags	<i>Output the LD flags for building against cytolib. These flags are propagated to sourceCxx via the inlineCxxPlugin (defined below) and to packages via a line in Makevars[.win] like this:</i>
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**Description**

```
PKG_LIBS += $(shell "$R_HOME/bin/$R_ARCH_BIN/Rscript.exe" -e "cytolib::cytolib_LdFlags()")
```

**Usage**

```
cytolib_LdFlags()
```

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