

# Package ‘cytolib’

October 17, 2020

**Type** Package

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

**Version** 2.0.3

**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(>= 1.72.0-2), RProtoBufLib(>= 1.99.8), 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\_11

**git\_last\_commit** 9437bc4

**git\_last\_commit\_date** 2020-06-08

**Date/Publication** 2020-10-16

## R topics documented:

cytolib\_LdFlags . . . . . 2

**Index** . . . . . 3

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cytolib_LdFlags	<i>Output the LD flags for building against cytolib. These flags are propagated to sourceCpp 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()
```

# Index

cytolib\_LdFlags, [2](#)