

Package ‘cytolib’

May 25, 2026

Type Package

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

Version 2.25.0

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

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License_restricts_use no

LazyLoad yes

Imports RProtoBufLib

Depends R (>= 3.4)

Suggests knitr, rmarkdown

LinkingTo BH(>= 1.84.0.0), RProtoBufLib(>= 2.13.1), Rhdf5lib

biocViews ImmunoOncology, FlowCytometry, DataImport, Preprocessing, DataRepresentation

VignetteBuilder knitr

SystemRequirements GNU make, C++11

RoxygenNote 7.1.2

Biarch TRUE

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

git_branch devel

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Contents

| | |
|---------------------------|----------|
| 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> |
|-----------------|--|

Description

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

Usage

```
cytolib_LdFlags()
```

Index

cytolib_LdFlags, [2](#)