

Package ‘cytolib’

October 11, 2022

Type Package

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

Version 2.8.0

Date 2017-08-07

Author Mike Jiang

Maintainer Mike Jiang <mike@ozette.ai>

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, rmarkdown

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_15

git_last_commit 733543e

git_last_commit_date 2022-04-26

Date/Publication 2022-10-11

R topics documented:

cytolib_LdFlags 2

Index 3

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>
-----------------	--

Description

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

Usage

```
cytolib_LdFlags()
```

Index

cytolib_LdFlags, [2](#)