

# Package ‘cytolib’

August 15, 2018

**Type** Package

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

**Version** 1.2.0

**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** Artistic-2.0

**LazyLoad** yes

**Collate** 'zzz.R'

**Depends** R (>= 3.4)

**Suggests** knitr

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

**LinkingTo** BH(>= 1.62.0-1), RProtoBufLib(>= 1.1.2)

**VignetteBuilder** knitr

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

**RoxygenNote** 6.0.1

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

**git\_branch** RELEASE\_3\_7

**git\_last\_commit** 26a0ea

**git\_last\_commit\_date** 2018-04-30

**Date/Publication** 2018-08-15

**R topics documented:**