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# Flow cytometry data analysis using Bioconductor.

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## Abstract

Flow cytometry has benefited from the advent of high throughput techniques and now enables high content screening (FH-HCS), in both basic and clinical research, generating large complex data sets with many covariates. To model multiple covariates and interpret such FH-HCS experiment, rigorous workflow must be followed. Along with the task of acquiring the data come the tasks of storing, managing, assessing quality, analyzing, and summarizing to a condensed form that can be interpreted by researchers. Open source Bioconductor packages for analysis of flow cytometry data provide a unified framework for researchers to manage such workflow. Additionally they offer a research platform which bioinformaticians, computer scientists, and statisticians can use to develop novel methods. Currently, 12 Bioconductor packages are relevant to flow cytometry. In this presentation, I will first give an overview of their functionalities and then I will focus on the packages flowCore (infrastructure), flowViz (visualization), flowQ (quality assessment), and flowClust (clustering) to illustrate an analysis workflow of flow cytometry data using Bioconductor.

**Keywords:** R, Bioconductor, FlowCytometry, Analysis, Visualization

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