

# flowpipe

## An R Package for Automating the Analysis of Flow- & Mass-Cytometry Event Data

Jim Java<sup>1\*</sup>   Matt Cochran<sup>1</sup>   Tim Bushnell<sup>1</sup>  
Wojciech Wojciechowski<sup>1</sup>

<sup>1</sup>Shared Resource Laboratories, Department of Pediatrics,  
University of Rochester Medical Center<sup>†</sup>

[github.com/priscian/flowpipe](https://github.com/priscian/flowpipe)

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\*james\_java@urmc.rochester.edu

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# Reproducibility in Flow Data Analysis

- ▶ Reproducible analysis in flow cytometry not a new concern
- ▶ CYTO 2018<sup>‡</sup>: “Key features [SRL managers] would like to see . . . are automatic data clean-up, automatic gating, guided cluster analysis, and 3D visualizations.”

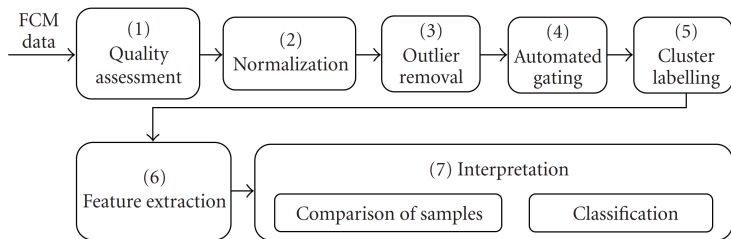


Figure: Fig. 2, Bashashati and Brinkman 2009<sup>§</sup>, Proposed FCM analysis framework.

<sup>‡</sup>Czechowska K, Lannigan J, Wang L, et al. Cyt-Geist: Current and Future Challenges in Cytometry: Reports of the CYTO 2018 Conference Workshops. *Cytometry Part A* 2019;95:598–644, 10.1002/cyto.a.23777.

<sup>§</sup>Bashashati A and Brinkman RR. Recent Bioinformatics Advances in the Analysis of High Throughput Flow Cytometry Data. *Advances in Bioinformatics* 2009;2009:1–19, 10.1155/2009/584603.

# Desired Requirements of an Analysis Pipeline

- ▶ As automatic as possible (point to FCS files & go), but:
  - accommodates uncommon prelim gating
  - readily uses clinical data in differential analysis etc.
- ▶ Supports any needful preprocessing steps
  - ... e.g. normalization, debarcoding, compensation, live gating
- ▶ Supplies diagnostic plots & summaries
- ▶ Uses well-tested, reproducible analysis methods¶
- ▶ Provides a summary report to investigators
- ▶ Readily configurable & expandable as necessary

**flowPipe** implements this framework. . . .

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¶For an instructive full CyTOF analysis, v. [Nowicka M, Krieg C, Weber LM, et al. CyTOF Workflow: Differential Discovery in High-Throughput High-Dimensional Cytometry Datasets. F1000Research 2017;6, 10.12688/f1000research.11622.4.](#)

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**flowpipe**<sup>||</sup>, an R package for automating the analysis of flow- & mass-cytometry event data. Features:

- ▶ Configurable pipeline to give investigators prelim analyses
- ▶ Based on **flowCore**<sup>\*\*</sup> data structures & functions
- ▶ IDs neg/dim/pos/bright events by silhouette-scanning<sup>††</sup>
- ▶ Automatic<sup>‡‡</sup> & user-defined clustering
- ▶ Differential abundance analysis by cluster based on user-supplied clinical metadata
- ▶ Gives template-generated prelim report & spreadsheets

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<sup>||</sup>[github.com/priscian/flowpipe](https://github.com/priscian/flowpipe)

<sup>\*\*</sup>Hahne F, LeMeur N, Brinkman RR, et al. flowCore: A Bioconductor Package for High Throughput Flow Cytometry. *BMC Bioinformatics* 2009;10:1–8, 10.1186/1471-2105-10-106.

<sup>††</sup>Hu Z, Jujjavarapu C, Hughey JJ, et al. MetaCyto: A Tool for Automated Meta-Analysis of Mass and Flow Cytometry Data. *Cell Reports* 2018;24:1377–88, 10.1016/j.celrep.2018.07.003.

<sup>‡‡</sup>Via X-shift: Samusik N, Good Z, Spitzer MH, Davis KL, and Nolan GP. Automated Mapping of Phenotype Space with Single-Cell Data. *Nature Methods* 2016;13:493–6, 10.1038/nmeth.3863.