

# flowMerge: Merging mixture components for cell population identification in flow cytometry

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FlowMerge is a framework for automated gating of flow cytometry data [Finak 2009]. FlowMerge identifies distinct cell sub-populations in flow cytometry data based on merging mixture components from multivariate- $t$  mixtures under the Box-Cox transformation, implemented in the *flowClust* package [Lo 2008]. The cluster-merging algorithm under our framework improves model fit and provides a better estimate of the number of distinct cell sub-populations than either gaussian mixtures or multivariate- $t$  mixtures alone applied to flow cytometry data. Our framework allows the automated selection of the number of distinct cell sub-populations and allows for merged cell populations to be readily summarized in a simple manner that integrates with the existing flowClust framework and enables downstream data analysis. FlowMerge is implemented in R and is available through the BioConductor project.

## References:

Greg Finak, Ali Bashashati, Ryan Brinkman, Raphael Gottardo. Merging mixture components for cell population identification in flow cytometry. *Advances in Bioinformatics* (2009) pp. 247646

Kenneth Lo, Ryan Brinkman, Raphael Gottardo. Automated gating of flow cytometry data via robust model-based clustering. *Cytometry Part A* (2008) vol. 73 (4) pp. 321