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: