flowMeans: Rapid Cell Population Identification in Flow Cytometry Data

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The K-means clustering algorithm was the first automated data analysis approaches applied to FCM data. However, the adoption of K-means has been restricted, because it requires the number of populations to be pre-identified, it is sensitive to its initialization, and it is limited to modelling spherical cell populations. We have developed flowMeans, a time-efficient and accurate method for automated identification of cell populations in flow cytometry (FCM) data based on K-means clustering. Unlike traditional K-means, flowMeans can identify concave cell populations by modelling a single population with multiple clusters. Our framework uses a change point detection algorithm to determine the number of sub-populations, enabling the method to be used in high throughput FCM data analysis pipelines. flowMeans is publicly available as an open source R package through Bioconductor.

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