



Joint Modeling and Registration of Cell Populations in Cohorts of High-Dimensional Flow Cytometric Data

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In systems biomedicine, an experimenter encounters different potential sources of variation in data such as individual samples, multiple experimental conditions, and multi-variable network-level responses. In multiparametric cytometry, which is often used for analyzing patient samples, such issues are critical. While computational methods can identify cell populations in individual samples, without the ability to automatically match them across samples, it is difficult to compare and characterize the populations in typical experiments, such as those responding to various stimulations or distinctive of particular patients or time-points, especially when there are many samples. Joint Clustering and Matching (JCM) is a multi-level framework for simultaneous modeling and registration of populations across a cohort. JCM models every population with a robust multivariate probability distribution. Simultaneously, JCM fits a random-effects model to construct an overall batch template -- used for registering populations across samples, and classifying new samples. By tackling systems-level variation, JCM supports practical biomedical applications involving large cohorts.

Subjects: **Machine Learning (stat.ML)**

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