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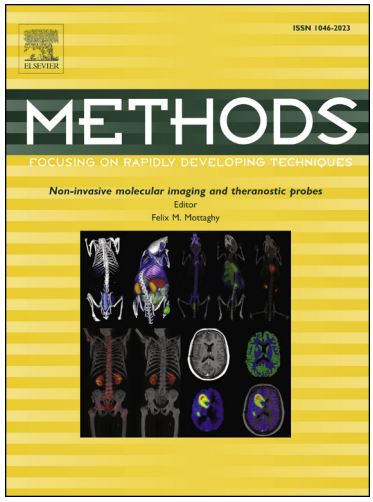

High Throughput Automated Analysis of Big Flow Cytometry Data

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ACCEPTED MANUSCRIPT

High Throughput Automated Analysis of Big Flow Cytometry Data

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Abstract

The rapid expansion of flow cytometry applications has outpaced the functionality of traditional manual analysis tools used to interpret flow cytometry data. Scientists are faced with the daunting prospect of manually identifying interesting cell populations in 50-dimensional datasets, equalling the complexity previously only reached in mass cytometry. Data can no longer be analyzed or interpreted fully by manual approaches. While automated gating has been the focus of intense efforts, there are many significant additional steps to the analytical pipeline (*e.g.*, cleaning the raw files, event outlier detection, extracting immunophenotypes). We review the components of a customized automated analysis pipeline that can be generally applied to large scale flow cytometry data. We demonstrate these methodologies on data collected by the International Mouse Phenotyping Consortium (IMPC).

Keywords:
flow cytometry, automated analysis, bioinformatics

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