Analysis of Mass Cytometry Data

The CyTOF system produces single cell protein expression data similar to that from flow cytometry, but with an increased number of features measured. Traditionally, analysis of these data is carried out using manual gating, but with the increased dimensionality, manual gating becomes a suboptimal analysis strategy in some cases. To address this, a number of data analysis tools for tasks such as clustering, differential abundance analysis, and visualization have been developed and made freely available. We here introduce some of the more popular tools for CyTOF analysis and exemplify their utility in a common analysis workflow.

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