The anatomy of single cell mass cytometry data

Mass cytometry enables the measurement of up to 50 features on single cell. This has catalyzed a shift toward multidimensional data analysis methods, rather than the manual gating strategies as traditionally for in flow cytometry data. This shift means that data scientists are involved in the analysis process to an increasing degree. As the data is analyzed in a more unbiased fashion, where noisy or uninformative observations are not easily excluded, a deeper knowledge of the origin, noise, and modalities of the data is therefore needed to embark on useful data analysis. In this primer, we introduce the idiosyncrasies of mass cytometry data with a focus on the technical properties of how data generated with the CyTOF® system, and the characteristics of protein expression in the cells of the hematopoietic continuum, specifically targeted toward data scientists. We also provide a comprehensive online repository of scripts, tutorials, and example data.

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