From Chaos to Chorus: Revealing disease phenotypes with computational analysis of high-dimensional flow cytometry data

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Advances in both cytometer capabilities and breadth of reagent availability have led to the expansion of individual flow cytometry panels; however, despite this newer ease in generation of high-parameter flow data, the proper extraction of results from larger panels is currently bottlenecked due the limitations of available analysis tools that cannot properly analyze such large datasets. Computational analysis is imperative for the proper investigation of high-dimensional flow and mass cytometry datasets. In this seminar, I will discuss several recent developments from the BUSM Flow Core and other sites that enable more efficient and comprehensive computational analysis of large flow cytometry datasets. Specifically, I will present flow and mass cytometry human immune-phenotyping data analyzed using our own adaptation of a classical t-SNE algorithm that can accommodate large datasets typical for flow cytometry but beyond reach for the traditional t-SNE implementations. To demonstrate the potency of various newer and adapted computational approaches, I will show an assembly of methods we used to characterize the inhibitory receptor (IR) landscape of various immune subsets in HIV individuals and to propose specific IR phenotypes to be investigated as potential biomarker readouts in HIV and aging.