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From Molecules to Cells to Organisms: Understanding Health and Disease with Multidimensional Single-Cell Methods

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The multidimensional nature of many single-cell measurements (e.g. multiple markers measured simultaneously using Fluorescence-Activated Cell Sorting (FACS) technologies) offers unprecedented opportunities to unravel emergent phenomena that are governed by the cooperative action of multiple elements across different scales, from molecules and proteins to cells and organisms. We will discuss an integrated analysis framework to investigate multicolor FACS data from different perspectives: Singular Value Decomposition to achieve an effective dimensional reduction in the data representation, machine learning techniques to separate different patient classes and improve diagnosis, as well as a novel cell-similarity network analysis method to identify cell subpopulations in an unbiased manner. Besides FACS data, this framework is versatile: in this vein, we will demonstrate an application to the multidimensional single-cell shape analysis of healthy and prematurely aged cells.