

Preface

High-dimensional cytometry has ushered in a new era of single-cell analysis. High-end flow cytometers are now capable of 15-parameter analysis and the mass cytometer is routinely used for 34 parameter experiments and is capable of analyzing 100 unique parameters on single cells.

These technological advances have enabled a comprehensive panel of surface markers to be analyzed in tandem with intracellular protein states, allowing researchers to disentangle complex signaling networks in heterogeneous tissues such as blood, bone marrow, and tumors in ways that were previously impossible. Mass cytometry and high-dimensional flow cytometry have been employed in transformative studies in diverse disciplines including hematopoiesis, immunology, and drug profiling. The rapid increase in dimensionality has also spurred the development of novel analytics allowing researchers to probe and visualize high-parameter, single-cell datasets.

In this volume we will address the most interesting questions and applications enabled by high-dimensional technologies, review current practical approaches used to perform high-dimensional experiments, and address the key bioinformatic techniques developed to facilitate analysis of datasets involving dozens of parameters in millions of single cells.

High-dimensional cytometry has made it possible to systematically measure mechanisms of tumor initiation, progression, and therapy resistance on millions of individual cells from human tumors. This has ushered in a “single-cell systems biology” view of cancer ([“High-Dimensional Single-Cell Cancer Biology”](#)). High-dimensional cytometry has facilitated a similar paradigm shift in immunology and provided a view of the human “immunome” with unprecedented breadth ([“Studying the Human Immunome: The Complexity of Comprehensive Leukocyte Immunophenotyping”](#)) and allowed for the exploration of immunological cell types, such as CD8⁺ T cells with increasing depth ([“High-Dimensional Analysis of Human CD8⁺ T Cell Phenotype, Function, and Antigen Specificity”](#)). Mass cytometry has provided an increasingly sophisticated view of intracellular signaling and acted as an ideal tool to pry open the signaling processes of cancer ([“Mass Cytometry to Decipher the Mechanism of Nongenetic Drug Resistance in Cancer”](#)).

New techniques have emerged to maximize the power of high-dimensional cytometry. Mass cell barcoding greatly increases the throughput, reduces antibody consumption, and increases data quality for mass cytometry experiments

(“[A Practical Guide to Multiplexed Mass Cytometry](#)”). Proximity ligation assays greatly expand the number of possible processes that can be targeted, allowing for the detection of protein–protein interactions, post-translational modifications, and interactions of proteins with nucleic acids (“[Analysis of Protein Interactions in situ by Proximity Ligation Assays](#)”).

A host of new analytical approaches and platforms have been developed to analyze increasingly complex high-dimensional single-cell datasets. Cytobank, an analysis platform leveraging recent advances in cloud computing and virtualization, lets researchers annotate, analyze, and share results along with the underlying single-cell data (“[Cytobank: Providing an Analytics Platform for Community Cytometry Data Analysis and Collaboration](#)”). Advances in unsupervised discovery allow for biological insights to be gleaned from large datasets without *a priori* knowledge or intensive manual intervention (“[Computational Analysis of High-Dimensional Flow Cytometric Data for Diagnosis and Discovery](#)”). In order to deal with intricate intracellular data, computational deconvolution approaches have been developed to reconstruct and describe signaling dynamics (“[Shooting Movies of Signaling Network Dynamics with Multiparametric Cytometry](#)”).

Finally, looking into the future, new technologies such as hyperspectral cytometry may be poised to increase parameterization capabilities of single-cell measurement and expand the capabilities of high-dimensional cytometry (“[Hyperspectral Cytometry](#)”).

Harris G. Fienberg
Garry P. Nolan

High-Dimensional Single Cell Analysis
Mass Cytometry, Multi-parametric Flow Cytometry and
Bioinformatic Techniques
Fienberg, H.G.; Nolan, G.P. (Eds.)
2014, X, 215 p. 68 illus., 67 illus. in color., Hardcover
ISBN: 978-3-642-54826-0