
Handbook of Single-Cell Technologies

Tuhin Subhra Santra • Fan-Gang Tseng
Editors

Handbook of Single-Cell Technologies

With 296 Figures and 38 Tables

 Springer

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Preface

The cell is the fundamental unit of biological organisms. It plays a significant role in coordinating with each other to perform systemic functions. Numerous bioanalytical techniques depend on the whole sample's analysis while performing a study on bio-entities existing in a very low concentration. Thus, the outcome of the study reflects merely an average. Though the approach is best suited for whole bio-samples (blood, saliva, urine, and other bodily fluids), where quantity is not a limiting factor, there is also increasing need for extreme small-quantity sample analysis on the single cell or subcellular level. Such needs in the case of limited number of cells, for example, circulating tumor cells (CTCs), early-stage embryos or rare cells, or even when differences among the cells in the cell population, are of interest. Despite the apparent synchrony in cellular systems, single cell analysis (SCA) is important due to its capability to reveal the environmental and developmental changes in the chemical content of individual cell. The fundamental principle of cell biology is cellular heterogeneity that arises from stochastic expression of genes, proteins, and metabolites. Thus, the natural cellular heterogeneity is manifested not only in the structure and composition of cells but also in their functionality. SCA plays an important role in the system biology, where the interactions of molecular components are studied at different molecular levels, from genome to cellular functions. Individual cell or cell organelle analysis can reveal an effect of different life conditions, surrounding environment on the genome, cell cycle, and also transcriptome, proteome, peptidome, metabolome, etc. In this respect, single-cell-omics promote system biology to investigate cellular heterogeneities and their reasons.

Initial basic techniques mainly focus on single modalities, such as DNA sequence, RNA expression, or chromatin accessibility. These technologies have yielded transformative insights into cellular development and diversity. But the cellular segregation is driven by methodological convenience and limits the ability to derive a deep understanding of the relationship between biomolecules in single cell. To understand these interactions is the key to derive deep understanding of the cellular state and remains a challenge for the field of SCA. Moreover, the availability and scale of the data sets are rapidly growing, which requires new computational methods for normalization and joint analysis across samples, even for the presence of significant batch effects or interindividual variation. Approximately, 5 years ago, flow cytometry, patch-clamping electrophysiology methods, fluorescence in situ

hybridization, and enzyme-linked immunospot assays were among few single cell molecular analysis tools available. From a given cell, most of these methods could analyze only between 1 and 3 molecules, while multicolor flow cytometry has been successful in capturing approximately 12 cell surface protein markers. This scenario is rapidly changing. Recently, single-cell sequencing technologies have been mainly led by the recent advances observed in the field of molecular biology, microfluidics, and nanotechnology. Several new technologies have emerged for the comprehensive analysis of single molecules. Some single cell methods are capable to assay about >40 secreted proteins, elements of phosphoprotein signaling pathways, and large number of cell surface markers. Even single cells genome can be analyzed at high coverage or focused, whereas transcriptome at sparse coverage at moderate or high cell statistics.

In the last two decades, due to the rapid development of sophisticated micro-/nanofluidic devices, we now have Bio-MEMS, Lab on a Chip (LOC), and micro total analysis systems (μ TAS) that enable more complex manipulations of chemicals and biological agents in fluidic environments. Microfluidics methods enable single cell or molecular analysis correlated with measurement of cellular functionality. These devices permit single cell analysis within custom environment, highly controlled, or even allow nondestructive cell analysis to identify cell of interest, for example, B cells producing specific antibodies to be harvested for further use. In situ RNA profiling via sequential hybridization and proteomic analysis via ion beam profiling are the two recent tissue staining methods. These techniques enable single cell analysis within fixed and intact tissues, with multiplexing level that significantly exceeds traditional immunohistochemical staining methods. Thus, generate new types of data and which has been integrated with new computational tools. With these novel devices, technology has become a pioneer in omics analysis and an integral part of medical biotechnology, such as diagnostics, prognostics, and cancer therapy.

This book comprises eight parts broadly covering several aspects of single cell analysis using different technologies. **Part one** emphasizes in detail about single cell therapy and analysis using different physical methods such as optoporation or photoporation, mechanoporation, electroporation, and microinjection. Most of these techniques use micro-/nanofluidic devices to induce different physical energy such as optical, electrical, and mechanical stress. These energies can deform cellular membrane, create hydrophilic transient membrane pores, deliver exogenous biomolecules into cells, and perform different cellular analysis. **Part two** broadly covers micro-/nanofluidic devices design, fabrication, and their operation for cellular analysis. The devices not only perform single cell manipulation, separation, isolation, cultivation, and lysis, but also electrical, mechanical, and biochemical characterization and analysis. **Part three** covers different chemical methods for single cell analysis. The part covers in detail about liposome-mediated molecular delivery into cells, antibody discovery using single cell analysis, and antibody discovery for detection, diagnosis, and treatment of infectious diseases. Moreover, this part demonstrates high-throughput screening of antigen-specific antibody-secreting cells and secreted molecules from individual cells. This can offer a valid approach

towards understanding and treatment of various diseases, disorders, and syndromes. **Part four** elaborates in detail about single cell genomics, proteomics, transcriptomics, and high-throughput transcriptome sequencing. **Part five** demonstrates single cell analysis in system biology and biocatalysis and covers the adult bovine intervertebral disc model system, which anatomically and histologically reflects the situation in human. The primary cell lineages were repeatedly isolated from the annulus fibrosus and the nucleus pulposus tissues of bovine intervertebral disc, and the isolation was typically heterogeneous in culture. Moreover, the part covers rapid cell process, with a focus on receptor signal transduction within the cell membrane. Also, it covers how large-scale single cell assays provide an efficient route for the identification of biocatalysts with novel or improved function.

Part six broadly discusses single cell adhesion in cancer progression, single cell technologies for cancer therapy, analytical tool for single cancer cell analysis, and transmembrane receptor dynamics as biophysical markers for cancer cells analysis.

Part seven briefly emphasizes flow cytometry-based high-throughput single cell electrical characterization and single cell cytometry for the application in biology and medicine.

Part eight discusses spectrum analysis, methods, targets, imaging, and applications. The part broadly covers single cell electrophysiology, analytical techniques for single cell study in microbiology, microwave and mechanical resonators for sensing and sizing of single cells, molecular force spectroscopy to measure the physiological function of cell adhesion, mass spectrometry for single cell analysis, micro-tweezers and force microscopy techniques for single cell mechanobiological analysis, acoustic tweezers for single cell manipulation, and **single cell pull down for characterization of protein complexes**.

We hope this book will be fascinating to the readers, especially undergraduate and graduate students, and it will be efficient for scientists in academic and industrial research who are performing various aspects of single cell analysis.

Chennai, India
Hsinchu, Taiwan
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Tuhin Subhra Santra
Fan-Gang Tseng
Editors

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