

Special Issue on
**Single Cell Analysis: Technological Advances,
Bioinformatics Approaches, and Applications**

CALL FOR PAPERS

A growing body of evidence has been accumulating in the last few years, showing that a significant level of genomic variation can be found even among healthy cells of the same individual. This makes it possible for each cell to produce different transcripts or proteins to respond in different ways to stimuli. The analysis of such phenomenon clearly requires a shift in focus from whole tissues to their single components. In fact, whole tissue analysis gives only information about the average behavior of a population of cells and hides their internal heterogeneity for the most part. Assessing cell to cell variability is therefore crucial for understanding dynamic biological processes, such as embryo development and cancer.

Recent advances in transcriptome sequencing and protein quantification technologies have greatly lowered the amount of initial material that is necessary to obtain reliable measurements and have thus paved the way to the direct probing of single cells. In light of these technological improvements, it has become critical to develop proper statistical and computational methods specifically tailored to tackling the challenges posed by this type of data.

This special issue encourages the submission of papers describing the latest technological improvements in order to evaluate their advantages in the context of single-cell studies. We are also interested in the comparison of both published and novel approaches to the bioinformatic analysis of the resulting data. Discussions about improvement in the comprehension of tissue pathophysiological conditions providing single-cell analyses are encouraged. Finally, we will be considering reviews giving a broader overview of the state of the art and the challenges of this exciting new field of research.

Potential topics include but are not limited to the following:

- ▶ Cellular heterogeneity
- ▶ Single-cell genomics and epigenetics
- ▶ Technologies and application in single-cell analysis
- ▶ Single-cell transcriptomics (coding and noncoding RNAs)
- ▶ Single-cell proteomics
- ▶ Single-cell metabolomics
- ▶ Bioinformatic approaches to analyze single-cell genomics, transcriptomics, proteomics, and metabolomics data
- ▶ Single-cell analysis in pathological conditions and in health
- ▶ Single-cell analysis in animal models

Authors can submit their manuscripts through the Manuscript Tracking System at <https://mts.hindawi.com/submit/journals/ijg/staba/>.

Papers are published upon acceptance, regardless of the Special Issue publication date.

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Submission Deadline

Friday, 21 September 2018

Publication Date

February 2019