Journal of Nucleic Acids

Hindawi

Special Issue on

Defining Cancer Heterogeneity by Single-Cell RNA Sequencing

CALL FOR PAPERS

According to World Health Organization estimates, cancer claims more than 8.8 million lives globally every year. Cancer drugs do not deliver optimal clinical benefits to all patients and a significant contribution of the variable treatment response can be attributed to the lack of cellular homogeneity in cancers. The battle against cancer has thus witnessed the natural convergence of the biomedical community for oncological research, engineers involved in technology design, and computer scientists for Big Data analysis. Recent advances in single-cell RNA sequencing (scRNA-seq) present unprecedented opportunities to characterize cancer heterogeneity and may therefore help in designing more efficacious treatment strategies.

Over the last decade sc-RNA-seq has been performed on malignant neoplastic tissue, distal metastatic sites, and circulating tumor cells (CTCs) derived from liquid biopsy, providing valuable insights on intratumoral hierarchies, microenvironment, and detection of rare/cancer-stem cells. However, despite the remarkable growth in terms of transcript evaluation and experimental throughput, adoption of scRNA-seq technology in clinics is considered impractical at this stage. Maturation of this field will require a concerted effort on the part of scientific community in establishing the merits of how scRNA-seq can best be applied as a state-of-the-art cancer diagnostic tool and not be a burden on public health expenditure.

The goal of this special issue is to broaden the interdisciplinary understanding of the potential of scRNA-seq in discerning cancer's vulnerabilities and the contributions we expect for this issue should endeavor to address the translational challenges in the format of Review, and Original Research.

Potential topics include but are not limited to the following:

- Clinical sample collection, processing, single-cell isolation, and RNA capture
- Library generation, sequencing technology, and bioinformatics pipelines
- Innovative platforms to analyze publicly available sc-RNA-seq data
- Comparisons with complimentary single-cell technologies and bulk RNA-seq
- Integration with single cell multiomics and Machine Learning (ML) interface
- Debate the urgency of sc-RNAseq for personalized cancer management

Authors can submit their manuscripts through the Manuscript Tracking System at https://mts.hindawi.com/submit/journals/jna/dch/.

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

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