Single Cell and Spatial Transcriptomics: A Beginners Viewpoint from the Conceptual Pipeline

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Abstract : Messenger ribooxynucleic acid (mRNA) molecules are compositional, protein-based. These proteins, encoding mRNA molecules (which collectively connote the transcriptome), when analyzed by RNA sequencing (RNAseq), unveils the nature of gene expression in the RNA. The obtained gene expression provides clues of cellular traits and their dynamics in presentations. These can be studied in relation to function and responses. RNAseq is a practical concept in Genomics as it enables detection and quantitative analysis of mRNA molecules. Single cell and spatial transcriptomics both present varying avenues for expositions in genomic characteristics of single cells and pooled cells in disease conditions such as cancer, auto-immune diseases, hematopoietic based diseases, among others, from investigated biological tissue samples. Single cell transcriptomics helps conduct a direct assessment of each building unit of tissues (the cell) during diagnosis and molecular gene expressional studies. A typical technique to achieve this is through the use of a single-cell RNA sequencer (scRNAseq), which helps in conducting high throughput genomic expressional studies. However, this technique generates expressional gene data for several cells which lack presentations on the cells' positional coordinates within the tissue. As science is developmental, the use of complimentary pre-established tissue reference maps using molecular and bioinformatics techniques has innovatively sprung-forth and is now used to resolve this set back to produce both levels of data in one shot of scRNAseq analysis. This is an emerging conceptual approach in methodology for integrative and progressively dependable transcriptomics analysis. This can support in-situ fashioned analysis for better understanding of tissue functional organization, unveil new biomarkers for early-stage detection of diseases, biomarkers for therapeutic targets in drug development, and exposit nature of cell-to-cell interactions. Also, these are vital genomic signatures and characterizations of clinical applications. Over the past decades, RNAseq has generated a wide array of information that is igniting bespoke breakthroughs and innovations in Biomedicine. On the other side, spatial transcriptomics is tissue level based and utilized to study biological specimens having heterogeneous features. It exposits the gross identity of investigated mammalian tissues, which can then be used to study cell differentiation, track cell line trajectory patterns and behavior, and regulatory homeostasis in disease states. Also, it requires referenced positional analysis to make up of genomic signatures that will be sassed from the single cells in the tissue sample. Given these two presented approaches to RNA transcriptomics study in varying quantities of cell lines, with avenues for appropriate resolutions, both approaches have made the study of gene expression from mRNA molecules interesting, progressive, developmental, and helping to tackle health challenges head-on.
Keywords : transcriptomics, RNA sequencing, single cell, spatial, gene expression.
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