World Academy of Science, Engineering and Technology
International Journal of Environmental and Ecological Engineering
Vol:15, No:07, 2021

Single Cell Rna Sequencing Operating from Benchside to Bedside: An Interesting Entry into Translational Genomics

Authors : Leo Nnamdi Ozurumba-Dwight

Abstract : Single-cell genomic analytical systems have proved to be a platform to isolate bulk cells into selected single cells for genomic, proteomic, and related metabolomic studies. This is enabling systematic investigations of the level of heterogeneity in a diverse and wide pool of cell populations. Single cell technologies, embracing techniques such as high parameter flow cytometry, single-cell sequencing, and high-resolution images are playing vital roles in these investigations on messenger ribonucleic acid (mRNA) molecules and related gene expressions in tracking the nature and course of disease conditions. This entails targeted molecular investigations on unit cells that help us understand cell behavoiur and expressions, which can be examined for their health implications on the health state of patients. One of the vital good sides of single-cell RNA sequencing (scRNA seq) is its probing capacity to detect deranged or abnormal cell populations present within homogenously perceived pooled cells, which would have evaded cursory screening on the pooled cell populations of biological samples obtained as part of diagnostic procedures. Despite conduction of just single-cell transcriptome analysis, scRNAseq now permits comparison of the transcriptome of the individual cells, which can be evaluated for gene expressional patterns that depict areas of heterogeneity with pharmaceutical drug discovery and clinical treatment applications. It is vital to strictly work through the tools of investigations from wet lab to bioinformatics and computational tooled analyses. In the precise steps for scRNAseq, it is critical to do thorough and effective isolation of viable single cells from the tissues of interest using dependable techniques (such as FACS) before proceeding to lysis, as this enhances the appropriate picking of quality mRNA molecules for subsequent sequencing (such as by the use of Polymerase Chain Reaction machine). Interestingly, scRNAseq can be deployed to analyze various types of biological samples such as embryos, nervous systems, tumour cells, stem cells, lymphocytes, and haematopoietic cells. In haematopoietic cells, it can be used to stratify acute myeloid leukemia patterns in patients, sorting them out into cohorts that enable re-modeling of treatment regimens based on stratified presentations. In immunotherapy, it can furnish specialist clinician-immunologist with tools to re-model treatment for each patient, an attribute of precision medicine. Finally, the good predictive attribute of scRNAseq can help reduce the cost of treatment for patients, thus attracting more patients who would have otherwise been discouraged from seeking quality clinical consultation help due to perceived high cost. This is a positive paradigm shift for patients' attitudes primed towards seeking treatment.

Keywords : immunotherapy, transcriptome, re-modeling, mRNA, scRNA-seq
Conference Title : ICEGB 2021 : International Conference on Environmental Genomics and Bioinformatics
Conference Location : Zurich, Switzerland
Conference Dates : July 29-30, 2021