OMICs scripts for exome, transcriptome and other data analysis.

OMICs technologies, in particular, have emerged as powerful tools in dissecting the complex molecular networks involved in cancer. The term "omics" encompasses genomics, proteomics, metabolomics, and transcriptomics, each offering a unique lens through which to explore different facets of the disease. Bulk RNA sequencing (transcriptome) analysis has provided fundamental insights into the study of gene expression in exploring the functions related to the process of life development, disease progression, and drug action, etc. However, it represents an average across the myriad of cells within a tissue, merely reflecting the characteristics of cell populations or perhaps predominantly the information of the most numerous cells. To tackle these constraints, Single cell RNA-seq has revolutionized biomedical science by single-cell expression profiling. This technology enables detailed exploration of genetic information at the cellular level across various tissues and diseases, capturing the inherent heterogeneity within samples. Single-cell multi-omics technologies have emerged. They refer to the simultaneous measurement of various types of data in the same cell, allowing for an accurate and detailed depiction of the cellular state. Integrating single-cell transcriptomic sequencing with comprehensive multi-omics data to map their inherent connections represents a critical and inevitable trend toward a more nuanced, multidimensional understanding of life development and the mechanisms underlying diseases.

Various Single cell multi-OMICs technologies like scTCR-seq, scBCR-seq, CITE-seq, scATAC-seq, Spatial transcriptomics were emerged recently which serve specific purpose at single cell level. The holistic view created by single-cell multi-omics technologies is crucial for understanding the complexities of biology, providing insights into cellular diversity, disease mechanisms, and potential therapeutic targets.

As independent researcher I want to focus on neuroendocrine cancers that start in specialized cells in patient neuroendocrine system. Neuroendocrine cells are distributed throughout the body, but the most common places for tumors to develop from them are in the lungs, appendix, small intestine, rectum, prostate and pancreas. A treatment to these types of cancer are based on the type of tumor, its location, whether it produces excess hormones, how aggressive it is and metastasis organs. However, most common ancestor to all these cancers are endocrine cells. Although, rare in incidence, these types of cancers detected in vary late stage, high grade and low overall survival.

Researchers had shown commonalities in gene regulatory networks between different types of neuroendocrine tumors, which indicates conserved biologic pathways that may be exploited therapeutically across tumor types. Question I want to ask is can multi-OMICs single-cell analysis of neuroendocrine tumors improve our understanding of intercellular interactions which contributing to the development, growth, spread, and evolution of tumors? Understanding neuroendocrine tumors at single cell level will provide new insights into the many different cell types that comprise a single tumor, and may ultimately contribute to uncovering common genes/pathways that may lead to improved treatment options which may responsible for drug resistance. This types of analysis helps in charting the cellular diversity within neuroendocrine tumors could advance the understanding and treatment of neuroendocrine tumors through the identification of: cell-of-origin, mechanisms that enable metastasis, causes of drug resistance, pre-selection of right patients for appropriate treatment and the potential for immunotherapies.