Single-cell RNA sequencing

- Kininogen enhances seizure susceptibility in mice possibly through bradykinin-induced modulation of calcium transients in glutamatergic and GABAergic neurons
- Lactate dehydrogenase B A Hypoxia and lactylation relative-gene as potential biomarkers for alcoholic liver disease: Integration of single-cell, bulk RNA-sequencing and experimental validation
- Interrogation of macrophage-related prognostic signatures reveals a potential immune-mediated therapy strategy by histone deacetylase inhibition in glioma
- ITGA5 drives glioblastoma progression through SLK-mediated activation of the PI3K-Akt pathway
- Pro-repair macrophages driven by CGRP rescue white matter integrity following intracerebral hemorrhage
- Zileuton protects against arachidonic acid/5-lipoxygenase/leukotriene axis-mediated neuroinflammation in experimental traumatic brain injury
- Cholinergic neuron-to-glioblastoma synapses in a human iPSC-derived co-culture model
- Common AAV gene therapy vectors show nonselective transduction of ex vivo human brain tissue

scRNA-seq is the most common technique used to measure gene expression at the single-cell level. It allows the profiling of transcriptomes (complete set of RNA transcripts) of individual cells, capturing differences in gene expression across thousands of cells.

This specialized form of RNA sequencing can analyze gene expression at the single-cell level, providing insights into cellular heterogeneity within tissues and organs.

Single-cell RNA sequencing (scRNA-Seq) is a powerful molecular biology technique that allows researchers to profile the gene expression of individual cells within a heterogeneous population. Unlike traditional bulk RNA sequencing, which measures the average gene expression of a mixed cell population, scRNA-Seq provides detailed information about the transcriptome of individual cells. This technology has revolutionized our understanding of cellular heterogeneity, development, disease, and various biological processes. Here are some key points about single-cell RNA sequencing:

Cell Isolation: The first step in scRNA-Seq involves isolating individual cells. This can be achieved through various methods, such as fluorescence-activated cell sorting (FACS), microfluidics, or manually picking individual cells.

Library Preparation: After cell isolation, the RNA from each cell is extracted, and unique molecular identifiers (UMIs) or barcodes are added to each RNA molecule. This step is critical for distinguishing between RNA molecules originating from the same gene but different cells.

Sequencing: The RNA libraries are then sequenced using high-throughput next-generation sequencing (NGS) technologies, such as Illumina platforms, 10x Genomics, or single-molecule sequencing technologies like PacBio and Oxford Nanopore.

Data Analysis: The analysis of scRNA-Seq data is complex and typically involves several steps:

Quality Control: Filtering out low-quality data. Data Normalization: Correcting for technical biases. Clustering: Grouping cells with similar gene expression profiles into clusters. Differential Expression

Analysis: Identifying genes that are differentially expressed between cell clusters. Trajectory Analysis: Inferring cell development or differentiation paths. Applications:

Cell Heterogeneity: scRNA-Seq allows researchers to understand and characterize the heterogeneity within tissues, organs, or cell populations. Developmental Biology: It can be used to study how cells develop and differentiate into specific cell types during embryogenesis or in tissue regeneration. Disease Research: It helps identify disease-associated cell subtypes and understand the cellular basis of diseases like cancer. Immunology: Researchers use scRNA-Seq to dissect immune cell populations and their responses to various stimuli. Neuroscience: It provides insights into the diversity of neuron types in the brain and their development. Stem Cell Biology: scRNA-Seq aids in characterizing pluripotent stem cells and their differentiation into specific lineages. Challenges: scRNA-Seq presents challenges such as high data dimensionality, the need for specialized bioinformatics tools, and potential technical noise.

Overall, single-cell RNA sequencing is a transformative technology that has enabled the exploration of cellular diversity and the identification of rare and novel cell types, ultimately advancing our understanding of biology, disease, and developmental processes.