**Discover how scRNA-seq is revolutionizing biomedical research: from fascinating discoveries to clinical promises! by FAUREL Alyx and CALLANQUIN Lenaïc, based on Sabrina Bibi-Triki's conference**

Did you know that single cell RNA sequencing (scRNA-seq) technology allows the exploration of cellular heterogeneity with a high precision? This revolutionary method analyzes biological complexity in detail, providing an in-depth view of RNA transcripts in each cell. Now a key tool, scRNA-seq enables the identification, the characterization and the classification of new cell types, with vast and rapidly expanding applications in fields as diverse as immunology, cardiovascular diseases, infectious diseases, and oncology. In Strasbourg, the team led by Prof. Seiamak Bahram (Molecular ImmunoRheumatology) has identified a rare mutation in the *ITPR3* gene responsible for a multisystem disorder and severe immunodeficiency in patients by combining scRNA-seq with other omics technologies. However, its high cost and the complexity of the data still hinder its use in routine diagnostics. Fortunately, advances in automated pipelines and user-friendly interfaces promise to broaden its clinical applications, and the development of new techniques makes it possible to sequence more cells with greater depth at equivalent cost. A persistent limitation is the loss of histological information, but spatial transcriptomics complements this approach by integrating the localization and cellular interactions within tissues, organs, or organisms. Combined with other high-throughput tools, scRNA-seq paves the way for groundbreaking discoveries and therapies.

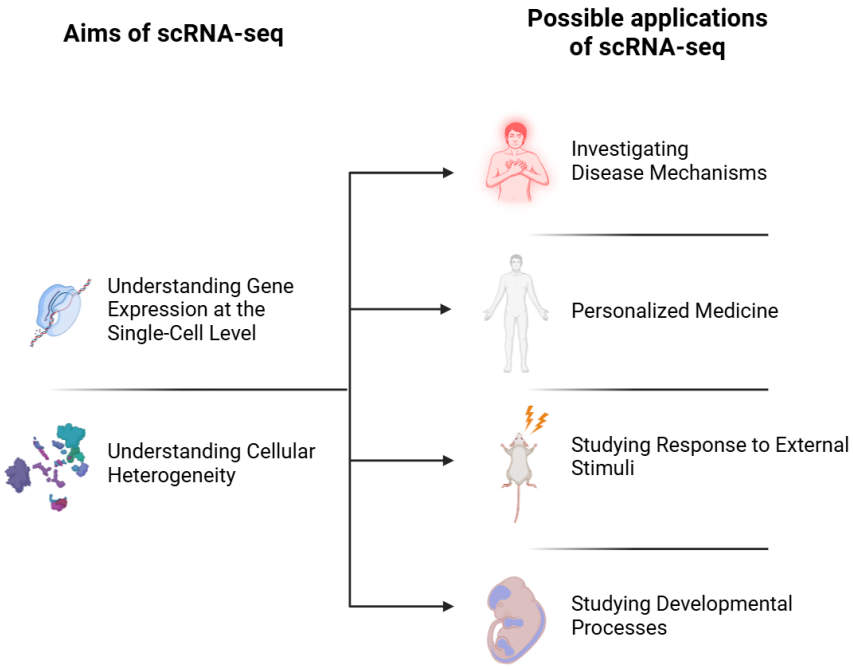


Figure : Possible uses of scRNA sequencing technology (made with Biorender)

References


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