11th March 2024

Multiome assignment

1. Why is transcriptomics used as a cornerstone to the different multiome technologies?

Transcriptomics provide one of the most pivotal layers of biological information. The analysis of mRNA molecules allows for a deep understanding of gene expression and gene regulation across various organisms and cell types, both in healthy and disease conditions. By integrating this data in a multiome setting, scientists aim to provide a comprehensive view of biological systems. From a knowledge perspective, transcriptomics serve as a functional bridge between the genome and the proteome, allowing for inferring the snapshot of active cellular processes. Combination of this data with other omics is simply very insightful, allowing for a more complete understanding of a system. From a technical point of view, transcriptomics is one of the most developed and accessible omic technologies. Numerous efforts have been made to advance this technology, resulting in outputs of a high resolution and sensitivity, all achieved in a cost-effective and timely manner.

1. Does focusing on single cells within the context of multiomic data provide a complete picture of biological processes, or are there important aspects that this approach might miss?

The answer to this question depends a lot on the biological question. Single-cell technologies indeed provide a remarkable resolution of biological processes at the cellular level. Nevertheless, there are some aspects that remain challenging and not fully resolved with single-cell technologies. For instance, single-cell multiomics typically require cells to be dissociated from their tissue, losing the spatial information of the original tissue architecture, which can influence down-stream cell-to-cell interaction analyses. Moreover, while single-cell technologies provide a snapshot of cellular states at a given moment, they often do not capture dynamic processes, which are crucial for understanding differentiation pathways and the evolution of cellular phenotypes over time. Finally, the process of cell isolation can alter cellular behavior and introduce bias to the readout.

1. How might the future of multiomic single-cell technology contribute to our understanding of complex biological phenomena?

In general, single-cell technologies enable the characterization of unknown cell types that are undetectable in bulk analyses. However, there are still some cell populations that appear in very low quantities, which cannot be detected with the current single-cell resolution. Advances that increase sensitivity, reduce technical noise, and enable the detection of additional molecular modalities will enrich the data obtained from single cells. Additionally, coupling multiomics with live-cell imaging could provide insights into the dynamics of cellular processes. Whereas, the development of new algorithms and statistical models that can integrate data across time points, molecular modalities, and spatial dimensions will provide a better computational power to achieve a more complete understanding of biological complexity.