

W5 MULTIOME

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

Because it provides a direct snapshot of gene expression in cells at a given moment. This is crucial because it offers real-time insights into which genes are being transcribed and potentially translated into proteins. Additionally understanding mRNA levels provides insights into the cellular processes that are active under specific conditions or in disease states.

2. 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?

Single-cell analyses may miss the broader tissue or systemic context. Cell-to-cell interactions, tissue architecture, and extracellular signals can be crucial for understanding complex biological processes. While single-cell techniques are expanding to cover more types of omics data simultaneously fully integrating these data types at single-cell resolution to get a complete biological picture is still a challenge.

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

By understanding the cellular heterogeneity of tissues, especially in diseases, single-cell multiomics can identify novel biomarkers, therapeutic targets, and mechanisms of disease progression or drug resistance. Also understanding how individual cells differentiate and contribute to the development of complex organisms can be significantly advanced by single-cell multiomics.