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**Multiome Individual Assignment – Week 5**

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

Because it gives the most direct access into the state of the cell compared to the other available technologies, with clear quantification of expression of the immediate product of gene expression. It also shows gradual expression changes across populations. Perhaps proteomics would be a more direct reflection, but it remains limited due the technological complexity involved.

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?**

No, since the cell remains a part of a more complex system. Cells are influenced by extracellular signal, their spatial locations, and their local niche composition. Fortunately, new technologies are rapidle developing to reveal these missing pieces of information to provide a fuller picture of the cell and the underlying biological processes.

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

Many mechanisms underlying diseases and biological processes have been elusive due the complexity of their molecular causes. Single-cell multiomics allows the capture of a significant subset of these molecular components, providing a more holistic and resolved view of the cell and its function in the context of disease and physiology. This in turn has allowed us to rapidly relate phenomological observations and phenotypes to specific gene sets and chromatin regions, enhancing our current day understanding of these systems. Further improvements would add more pieces to the puzzle, allowing more effective localization of relevant factors for further investigation.