Characterizing Cellular Communication Networks in Glioblastoma Through Integrative Single-Cell Analysis

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Glioblastoma multiforme (GBM) is among the most pervasive and lethal forms of brain cancer, characterized by extensive heterogeneity, rapid progression, and poor clinical outcomes[1,2]. Despite advances in treatment, long-term survival remains rare, highlighting the need for new approaches to better understand the biological mechanisms that drive disease progression[3].
The tumor microenvironment is increasingly recognized as a key regulator of tumor behavior, influencing processes such as growth, adaptation, and therapeutic response. However, many of the cellular and molecular interactions that shape these complex ecosystems remain poorly understood[4].

To address this challenge, we will analyze publicly available single-cell datasets using computational approaches to characterize cellular states and interactions within GBM. By integrating diverse datasets and systematically exploring patterns of cellular communication, we aim to identify biological processes associated with disease progression and generate hypotheses for future experimental investigation. These studies will provide a foundation for understanding the complex cellular networks that contribute to GBM biology and may inform the development of new therapeutic strategies.

References

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