Computational Pipeline for Spatial Transcriptomics Analysis of Glioblastoma

Translational Science Benefits Model

IMPACT PROFILE

Glioblastoma is one of the deadliest brain cancers, with most patients surviving less than 15 months. This project built a tool to study these tumors in detail. This helps researchers understand why the cancer is so hard to treat and brings us closer to better and more targeted therapies.

The Challenge

Glioblastoma is one of the most aggressive and deadly brain cancers, with a median survival of **only 15 months**, affecting 3 people per every 100,000 per year (roughly 13,000 new cases diagnosed a year. Tumor cell differences create challenges for treatment and recovery. For instance, different types of cells operating in different parts of the brain may lead to treatment evasion where one type of cell is killed while other cells remain alive and able to spread. This lack of uniformity results in failure of treatment. Currently, we lack the tools to map this complexity and identify the right targets in the right places.

The Approach

This project builds a step-by-step analysis tool to study glioblastoma brain tumors. The team used coding and computation techniques to develop ana analysis tool that identifies aggressive cell populations within glioblastomas. We used this technique to understand differences in glioblastoma tumors, which help us:

- Shows which genes are turned on or off in different parts of the tumor.
- Identifies the different types of cells present and how they work together.
- Helps researchers find possible treatment targets based on where cells are located in the tumor.

The Impact

The Computational Pipeline for Spatial Transcriptomics Analysis of Glioblastoma project resulted in **clinical, economic, community, and policy** benefits.

This pipeline gives researchers a faster, more detailed way to study brain tumors. It shows how tumor cells are different across brain regions, helping scientists find better drug targets. By making this type of analysis easier to use, it can speed up the path from lab research to new treatments for patients who have very few options.

RESEARCH HIGHLIGHTS

The Computational Pipeline for Spatial Transcriptomics Analysis of Glioblastoma project resulted in:

- Studied 12 patient samples across 3 regions of the brain, giving a full picture of how glioblastoma tumors vary.
- Analyzed over 2.7 million cells and 6,175 genes using a reliable, reusable pipeline that can handle a large amount of data.
- Cut analysis time by over 90% - from days down to just a few hours.

Key Benefits



Helps researchers understand the biology of one of the most aggressive brain cancers.



Advances in research into a cancer that affects ~10,000 Americans diagnosed each year, including adults of all ages.



Reduces time and cost of tumor analysis by automating a previously manual, labor-intensive process.



Helps identify tumor regions most likely to resist treatment, guiding more targeted therapy decisions.



Guide future research into new drugs and treatment targets for glioblastoma.

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Find out more:

BRaIN Lab: https://dlmp.uw.edu/research-labs/brainlab

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