Distinguish the Differences Between Populations with Glioblastoma Multiforme and Populations with a Low-Grade Glioma in a Genetic Level: How Does the Copy Number Variations of the Somatic Cells Reveal the Story About a Disease?

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1. **Introduction**

1.1 Abstract

The goal of this project is to find what specific genes distinguish the Glioblastoma cells from the Low-Grade Glioma cells, in genetic levels. By genetic levels, we are specifically referring to the copy number variants (CNVs) that make those two types of cancers distinguishable. Hypothetically, since Glioblastoma Multiforme is lethal and aggressive, people with Glioblastoma Multiforme are expected to have more CNVs in their somatic biospecimen than those with Low-Grade Glioma. The significance to distinguish the Glioblastoma Multiforme against the Low-Grade Glioma lies in the fact that the former cancer develops fast and has a severe symptom. To reduce the work and time needed for the diagnosis of those diseases, we wish to discover if using CNVs would more efficiently distinguish and draw conclusions about the Glioblastoma Multiforme and the Low-Grade Glioma.

The dataset we use comes from the Cancer Genome Atlas (TCGA) program from the National Cancer Institute. TCGA contains a full spectrum of Genome-related data ranging from DNA sequence reads to CNVs files. In this project we will concentrate on using the CNVs to study the differences between Glioblastoma Multiforme (GBM) and the Low-Grade Glioma (LGG).

Adding conclusions/methods

1.2 Background [1][2][3][4][5]

Firstly, Gliomas are a type of tumor in the brain or the spinal cord occurring from glial cells. The glial cells most prone to developing tumors are astrocytes, a specific type of brain cells whose main function is to support neurons and form scar tissue in damaged areas. Glioma that occurs from astrocytes are called astrocytoma. Glioblastomas, or GBM are a subtype of gliomas that exhibit more genetic abnormalities than other astrocytoma and are the most aggressive and fatal of all glial tumors. All other gliomas that are not glioblastomas are referred to as lower-grade non-GBM tumors. The causes of glioblastoma are largely unknown, but research suggests that approximately 5 percent of all glioblastomas are caused by hereditary conditions, with some of the cases being from people with Neurofibromatosis type 1 (NF1), Turcot syndrome and Li-Fraumeni syndrome all being genetic syndromes associated with increased susceptibility to cancer. Because there are multiple syndromes associated with glioblastomas and hereditary causes comprise only a small percentage of the entire affected population, it is difficult to predict whether glioblastomas will occur in an individual or not, and how dangerous they are in those harboring mutations.

Copy Number Variants are the numbers of copies that a gene gets mutated. Such mutations can involve deletions, insertions, duplications or any combination among these three. Cancer cells are typically related to a set of multiple mutated genes, so CNVs are good indicator for some diseases like cancers.

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