Research Plan

a.) **Rationale**

Previous studies have shown that age and the extent of resection as significant predictors of survival. However, the prediction models aren't accurate enough to be used clinically. GBM survival prediction will aid in customizing treatment to minimize risk. Difference drugs can be chosen based on this information to give patients the best chance at survival. Certain surgeries will be recommended if they are in the high survival category as they have more time for different options. If the patient were in the low survival group, more chemotherapy will be used.

b.) **Hypothesis**

Texture of necrosis, T1 weighted non enhancing, and T1 weighted enhancing tumor may be used as biomarkers to predict progression in GBM.

Research Questions

Our aim is to answer the following questions:

1. Is necrosis, T1 weighted non enhancing, and T1 weighted enhancing tumor texture correlated with poor prognosis?
2. Can such feature separate high and low survival groups?

Expected Outcomes

Analysis of features from the histologic sub-regions of necrosis, non-enhancing, and enhancing tumor will show that these features are strong predictors of overall survival and progression free survival in patients with glioblastoma

c.) Procedure

MRI Data of 212 Patients Gathered

From The Cancer Imaging Archive (TCIA), a service which de-identifies and hosts a large archive of medical images of cancer accessible for public download, We will request access to data from the TCGA-GBM collection, which contains various MRI imaging data of post-operational and preoperational glioblastoma patients. The data consists of FLAIR, T1-weighted, T1-weighted contrast enhanced, and T2-weighted MRI scans. Only T1-weighted images will be used. They consist of segmentations of various heterogeneous histologic sub-regions, namely the necrosis, non-enhancing, and enhancing tumor.

Segmentation Masks Drawn

We will use LifeX imaging software, a software for radiomic feature calculation in multimodality imaging that accelerates advances in the characterization of tumor heterogeneity, to analyze the segmentation masks on the images.

Radiomics

LifeX imaging software creates a textural readout from the 3D imaging analysis that provides data on GLCM texture, which measures patterns in combinations of gray levels that occur in an image. Various first order shape features such as sphericity of tumor will also be measured with the software.

Feature Extraction and Survival Group Prediction

These features will be tested in combination with each other. Two combined feature groups will be created, one associated with a low overall survival and one associated with high overall survival. The same will be done using PFS values. Kaplan–Meier estimate survival curves, log-rank tests, and ROC analysis may be used to compare the two groups. All statistical analysis will be completed using textural readouts from LifeX imaging software and R code software.

Risk and Safety

1. Human Participants Research: N/A
2. Vertebrate Animal Research: N/A
3. Potentially Hazardous Biological Agents Research: N/A
4. Potentially Hazardous Chemicals: N/A

Data Analysis

P values less than .05 will be considered statistically significant. A log-rank test will be used to find the difference between the necrosis of the low overall survival(OS) feature group and high OS feature group. The difference in the following features will also be tested between high and low OS groups: non-enhancing tumor and enhancing tumor feature groups, and necrosis. ROC analysis will be used to test these features for prediction capability.

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