G.L.O.W.: A Novel Hybrid Neural Network Approach for Glioblastoma Localization Using Carcinogenic Oxidative Stress Biomarkers

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Oxidative stress is a precursor to numerous cancers, including the Grade IV glioblastoma, affecting >300,000 people annually. However, the identification of oxidative stress markers remains incomplete. Effective treatment requires both localizing minuscule tumors and predicting their growth to determine the optimal stage for removal. Our wet lab results showed a 311% increase in glyceraldehyde-3-dehydrogenase (GAPDH) expression, a glycolysis enzyme fueling tumors, and an oxidative stress marker, after radiation. This highlights the connection to cancer through high Optical Density suggesting rapid cell proliferation, indicating potential carcinogenesis. With this association, utilizing a neural network approach allows us to get insights more rapidly. We developed the “Glioblastoma Localization and Optimization Workbench (G.L.O.W)” a novel neural conduit that integrates deep-learning and histone modification factors via ChIP-seq genomics and QUEST MRI, an MRI designed to visualize oxidative redox, to model cancer through a spatial/temporal approach. G.L.O.W. deciphers the spatial distribution of carcinogenic biomarkers (e.g., glycolysis enzymes for energy production) and their genetic precursors to predict the precise location of the tumor. Our model is 98% accurate for localization and carcinogenesis identification for growths scaled upwards from 13 micrometers. G.L.O.W. predicted tumor growth over 50 weeks using longitudinal data, achieving F1 scores from 0.75 to 0.91, surpassing all other clinical diagnostics. Our model also achieved mutation identification of critical tumor-related genes including causative factors for targeted therapies. G.L.O.W. enables us to locate minuscule tumors for early diagnosis while being cost-effective and time-efficient.