Abstract:

There is an interest in the field of radiomics and radiogenomics to correlate imaging features with histopathologic features, in attempts to better understand imaging signatures, predict treatment response, and ultimately patient prognosis. Most of the literature draws on data sets that utilize single-location histopathology, failing to account for tumor heterogeneity often observed in higher grade tumors. The purpose of this study was to investigate if multi-location histopathology correlates with prognostic factors with less variance than single-location histopathology. We accessed retrospective data from IVYGap and analyzed biopsy data from 42 patients diagnosed with glioblastoma. Each patient had at least five unique biopsy sections with at least one hematoxylin and eosin (H&E) stained slide. We randomly selected unique biopsies from each patient, and incrementally increased the number of biopsies for multi-location analysis. Eleven H&E features were investigated for correlation to overall survival (OS) and progression free survival (PFS). Statistical tests included Pearson’s correlation, and Bartlett’s test for equal variances. For correlation between PFS and H&E feature perinecrotic zone \( (p=0.036) \) there was significant variation from the number of biopsies. For correlation between OS and H&E features leading edge \( (p=0.026) \), hyperplastic blood vessels in leading edge \( (p=0.011) \), and microvascular proliferation \( (p=0.003) \) there was significant variation from the number of biopsies. Radiomic and radiogenomic findings are frequently grounded by H&E features from a single biopsy site. Our results demonstrate that the correlation between H&E features and prognostic measures vary significantly between single and multi-location biopsy.