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BACKGROUND:

Surveillance of High-Grade Gliomas (HGGs) remains a major challenge in clinical neurooncology. Histopathological validation is not an option during the course of disease and imaging surveillance suffers from ambiguous features of both disease progression and treatment related changes. This study aimed to differentiate between Pseudoprogression (PsP) and Progressive Disease (PD) using an artificial intelligence (support vector machine - SVM) classification algorithm.

METHODS:

Two groups of patients with histologically proven HGGs were analysed, a group with a single time point DSC perfusion MRI (45 patients) and a group with multiple time point DSC perfusion MRI (19 patients). Both groups included conventional MRI studies prior and after each perfusion MRI. This study design aimed to replicate decision making in clinical practice including multiple previous studies for each patient. SVM training was performed with all available MRI studies for each group and classification was based on different feature datasets from a single or multiple (subtracted features) time points. Classification accuracy comparisons were performed by calculating prediction error rates for different feature datasets and different time point analyses.

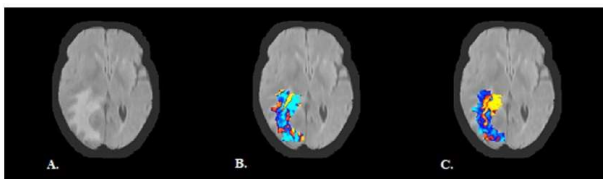


Figure 1. Example of common 3D space following coregistration of axial FLAIR, pre and post contrast T1 for multiple time points. Colour maps are based on differences in signal intensity calculated by voxel by voxel subtractions between different time points.

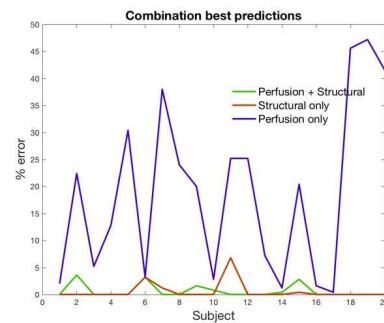


Figure 2. Graphical illustration of the mean prediction error of SVM classification per subject, using the time points offering the best predictions for each case. Combined features and structural features appear to be the best discriminators in most cases, with combined features generally resulting in lower mean classification errors. Perfusion features alone, are consistently outperformed by the other feature categories. These differences were statistically significant (P<0.05).

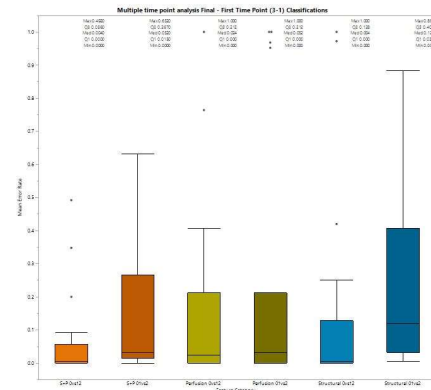


Figure 3. Box plots illustrating the error rate of the SVM classification for the multiple perfusion time point group using subtracted features between the final (3) and initial (1) time points. The best prediction rate was observed when a combination of perfusion and structural features was employed.

RESULTS:

Our results indicate that the addition of multiple time point perfusion MRI combined with structural (conventional with gadolinium-enhanced sequences) MRI features results in optimal classification performance (median error rate: 0.016, lowest value dispersion). Subtracted feature datasets improved classification performance, more prominently when the final and first perfusion studies were included in the analysis. On the contrary, in the single time point group analysis, structural feature-based classification performed best (median error rate: 0.012) (Figures 1-3).

CONCLUSION:

Validation of our results with a larger patient cohort may have significant clinical importance in optimising imaging surveillance and clinical decision making for patients with HGG.

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