Investigating How to Optimally Combine Multimodal MRI Data to Better Identify Glioblastoma Infiltration.

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Introduction:

Glioblastoma (GBM) is the most common and aggressive primary brain tumour, with an average survival of 6-12 months after diagnosis. GBM cells can progressively infiltrate neighbouring normal brain regions. For surgical resection and radiotherapy planning it is important to be able to identify the outer boundary of this infiltration, however conventional MRI fails to do this. Hence, it is crucial to develop methods that better enable delineation of marginal regions with low tumor cell density. In a previous work, we investigated the ability of individual MRI contrasts (T2, CE-T1, DWI, ADC, DTI, and ASL) to identify the boundary of infiltration. This was quantitatively assessed by using stacks of in-plane histological sections to generate tumour cell density maps, which were then co-registered to the MR images. In this study, we investigate how the information contained in the individual MR contrast images can best be combined, to achieve this we performed a voxel-by-voxel multi regression analysis of the co-registered MRI/histology dataset.

Material and methods: Nine nude CD1 mice were injected intracranially with infiltrative human glioblastoma cells (G7). Multi-modal MRI was acquired, T2w, DE-T1, DTI, multi boli Arterial Spin label (mbASL) [1]. Following MRI, mice were sacrificed and the brains were frozen. Staining for Human Leukocyte Antigen (HLA) allowed determining the cellular burden. Five histological slices were cut in the plane of the MRI slice, registered and stacked to account for MRI slice thickness. A Tumour cell density maps (TCD) was produced and the outer boundary of the tumour manually delineated. A multiple quadratic regression method (equation 1) was used to find the best combination of MR data, ie the coefficients b_i. Finally, these coefficients were used to generate a Quadratic Regression Map (QRM), with which to compare with the actual TCD.

$$y = b \circ +b1\ x1 + b2\ x2 + b3\ x1\ x2 + b4\ x1^2 + b5\ x2^2 \ldots\ldots\ldots\text{(equation 1)}$$

Results: Figure 2 shows two CMR maps created from FA, ADC, mbASL and T2w MR Images. These QRM maps exhibit high linear correlation (r>0.8) the corresponding TCD map generate with histology (HLA).

Fig.1

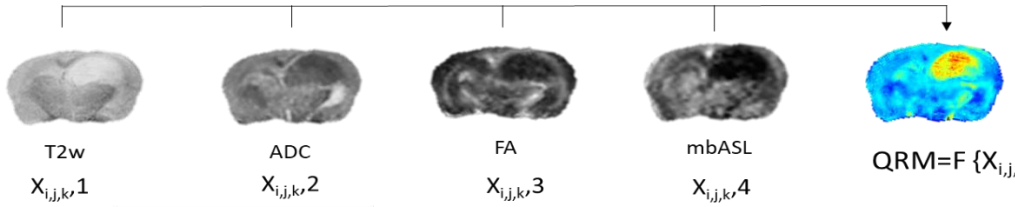
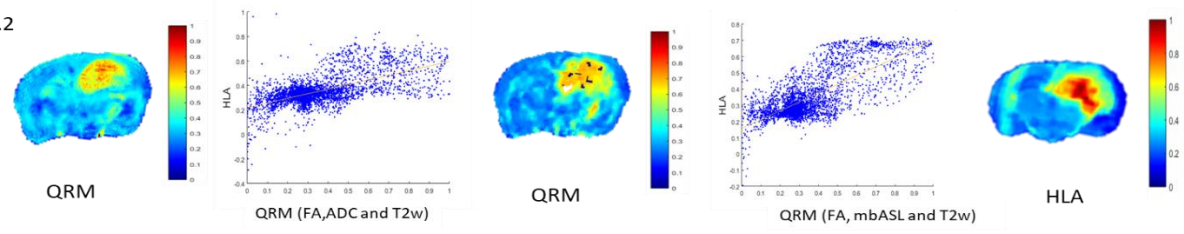


Fig.2



Conclusion: QRM maps were generated using a multiple quadratic regression method and compared to TCD maps generated from stacked in-plane histology (HLA). This approach shows much promise in probing the boundary of tumour cell infiltration in glioblastoma.

References: [1] Vallatos and et al, Magnetic Resonance in Medicine, 2017.