Classification of MGMT methylation status of glioblastoma in MRI images with AI

Aim and problem statement: Glioblastomas (GBM) are the most common primary brain tumors. There is an average life expectancy of 4 months without treatment and 15 months with treatment. Newly discovered drugs have led to important developments in cancer treatment, as in every field. GBM may benefit greatly from a drug called temozolomide if the enzyme encoding the MGMT protein is epigenetically silenced by methylation, otherwise expected benefit is limited. Today, the standard method to determine this is to take a piece of the tumor and examine it in the laboratory. However, this is an expensive, difficult, and burdensome procedure that requires the patient to be operated many times over. With artificial intelligence (AI) technologies, it is possible to automatically classify images. My aim in this project was to build a AI model that classifies the MGMT methylation status of GBM in MRI without any invasive procedures.

Method: For this purpose, I used MR images of 577 patients (276 MGMT unmethylated, 301 MGMT methylated), whose MGMT status were determined and shared for public use by the BRATS 2021 competition. Preprocessed, co-registered and bias field corrected T1, T1CE, T2 and FLAIR images along with segmentation masks of necrosis, enhancing tumor and edema regions were used. With a novel mask fusion strategy, the pathological signal in each sequence combined and used to guide to mask out the most relevant regions of images for the classification task. Keeping the 3D context, multiparametric information of all sequences and eliminating non-relevant pixels, a reduced tensor is built and fed into a custom 3D CNN model with 4 down-sampling blocks each comprised with convolution, max pooling and ReLU operations. Global average pooling of last convolutional layer is fed into a full connected layer followed by a sigmoid layer.

Results: Accuracy values of 0.77 were obtained in the model developed using T1CE images, and 0.65 in the model developed with T1W images without contrast. Accuracy values of 0.71 were obtained in the model developed using T2W images, and 0.82 in the model developed using FLAIR images. Jointly trained, cross modality guided model using T1CE, and FLAIR sequences reached 0.88 accuracy and 0.90 ROC-AUC score. A Streamlit application was built and locally deployed for experimental use in a couple of major hospitals.

Conclusion:

The results of this study indicate that with the novel mask fusion strategy and the cross modality guided region of interest input along with keeping 3D context and multiparametric information, state of the art prediction accuracies can be reached which can be translated into clinic as a promising tool to predict MGMT methylation status of GBM with MRI.