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Deep learning classifier for MGMT promoter methylation status in glioblastoma cancer

Javier Barranco Garcia, *Switzerland*

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Abstract

Abstract Title: Deep learning classifier for MGMT promoter methylation status in glioblastoma cancer

Authors: Javier Barranco Garcia[1], Daniel Abler[2], Mauricio Reyes[3], Diem Voung[1], Matthias Guckenberger[4], Stephanie Tanadini-Lang[4], Adrien Depeursinge[5]
[1]USZ, Radio Oncology Clinic, Zurich, Switzerland; [2]HES-SO Valais-Wallis, Institute of Information Systems, Sierre, Switzerland; [3]University of Bern, ARTORG Center for Biomedical Research, Bern, Switzerland; [4]USZ, Radio Oncology Clinic , Zurich, Switzerland; [5]HES-SO Valais-Wallis, Institute of Information Systems, Sierre, Switzerland
Hide Affiliations

Purpose or Objective

O^6-methylguanine-DNA-methyltransferase (MGMT) promoter methylation status in glioblastoma cancer is accepted as a promising prognostic and predictive biomarker. We explore the possibility of deep learning algorithms to predict the presence of MGMT status in MRI imaging as a non-invasive method.

Material and Methods

The RSNA and the MICCAI collaboration provided a dataset composed of 582 patients with four MRI modalities included (T1, T1ce, T2, FLAIR). MGMT status was encoded with 0/1. Out of the 582 patients, 306 were methylated and 276 not. The dataset was divided into training/validation (90%) and test (10%). using a random split. Then training and validation are splitted 80/20. The raw images are pre-processed: a) bias correction, b) normalization z-score and c) cropping and resampling to fit the entire brain (across all patients) into 144x144x144 voxels. To build the classifier we used two publicly available pre-trained image classifiers models to initialize the weights (ResNet50 and DenseNet121). Prior to training the networks, the 2D slice with the largest tumor area is selected in the horizontal view. For the largest tumor size, the surrounding bounding box is calculated and each image is cropped from the center of mass of the mask. This ensures that the tumor surrounding tissue is taken into consideration by the model. To combine the information of the different modalities the RGB channels were replaced with 3 modalities. Different techniques of data augmentation were used to prevent overfitting and improve performance. Affine transformations including horizontal and vertical translations and z-rotations were applied to the input images. The model was evaluated first for each modality independently using 5-fold cross validation.

Results

FLAIR obtained the best performance with DenseNet121 architecture with validation and test accuracies (0.7429,0.5953). We evaluate in groups of 3 modalities obtaining the best performance for the combination of (T1, T1ce and FLAIR) with validation and test accuracies of (0.7124, 0.6245) with the others combinations showing lower but close accuracies. Finally, data augmentation was performed during each epoch leading to similar results with the best combination again (T1, T1ce and FLAIR) and accuracies of (0.7035, 0.6355).

Conclusion

Deep learning classifiers shows promising results to predict the MGMT status in glioblastoma cancer. Combination of different modalities and data augmentation techniques improved the accuracy of the model.

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