Brain tumour segmentation on contrast enhanced T1w MRI using local texture and Random Forests

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Aims and objectives

Brain tumour segmentation of medical images is a very challenging task due to the large variety in tumour shape, position, appearance and scanning parameters. In recent years, a lot of research has been conducted on automated methods for brain tumour segmentation. In particular, the Brain Tumour Segmentation Challenge (BraTS [1]) has provided us with state-of-the-art algorithms with excellent performance. Nevertheless, most of these techniques use information from multiple MRI-sequences. In many institutions however, a large number of patients only receive a post-contrast T1-weighted (T1ce) MRI before surgery. There is thus also a need for a method able to delineate the different tumour tissues based only on this single scanning procedure. Several authors have proposed methods to delineate brain tumours on T1ce scans ([2-4]), but restrict themselves to segmenting only the tumour core. However, for applications such as radiomics or radiotherapy planning, information from different tumour tissues can show a large added value.

Therefore, the goal of this study was to design a segmentation algorithm able to delineate multiple brain tumour compartments on post-contrast T1-weighted MRI based on local texture and (ab#)normality features combined with a random forests (RF) classifier.

Methods and materials

134 features are calculated for every voxel of the T1 contrast-enhanced MRI scan. Thirty local texture features are calculated on the Grey Level Co-occurrence Matrix (GLCM), the Grey-Level Run-Length Matrix (GLRLM) and the Grey Level Size-Zone Matrix (GLSZM) in a 3×3×3 voxel neighbourhood of every voxel (see e.g. [5] for more information on these texture features). These 30 features are calculated on 4 different (sub)sampling scales to include distant interactions, resulting in 120 texture features. Additionally, 5 healthy tissue probability maps are calculated using the SPM12 segmentation step (implemented in Matlab R2017b). These contain the probabilities in every voxel to belong to grey matter, white matter, cerebrospinal fluid (CSF), skull or background, assuming a healthy brain intensity distribution. Since this is not the case for the patients considered, we also calculated 9 abnormality features starting from the SPM12 probability maps, including Z-maps in different tissues, outlier probabilities [6] and symmetry features (based on [7]). An illustration of these features is given in figure 1.

Sequential forward selection was used to identify 23 highly predictive features, which were used in a random forest classification algorithm with 200 trees. This model calculates the probabilities for every voxel to belong to 4 tumour classes (necrosis,

edema, non-enhancing and enhancing tissue) or 5 normal classes (background, non-brain tissue, grey matter, white matter, CSF). Afterwards, a dedicated voxel clustering algorithm provides the final tumour segmentation. The workflow is illustrated in figure 2.

We trained the classifier on the BraTS 2013 database [1], consisting of 10 low-grade and 20 high-grade glioma with manual segmentation masks. The validation was performed on the BraTS 2017 database, containing scans of 74 low-grade and 210 high-grade glioma.

Images for this section:

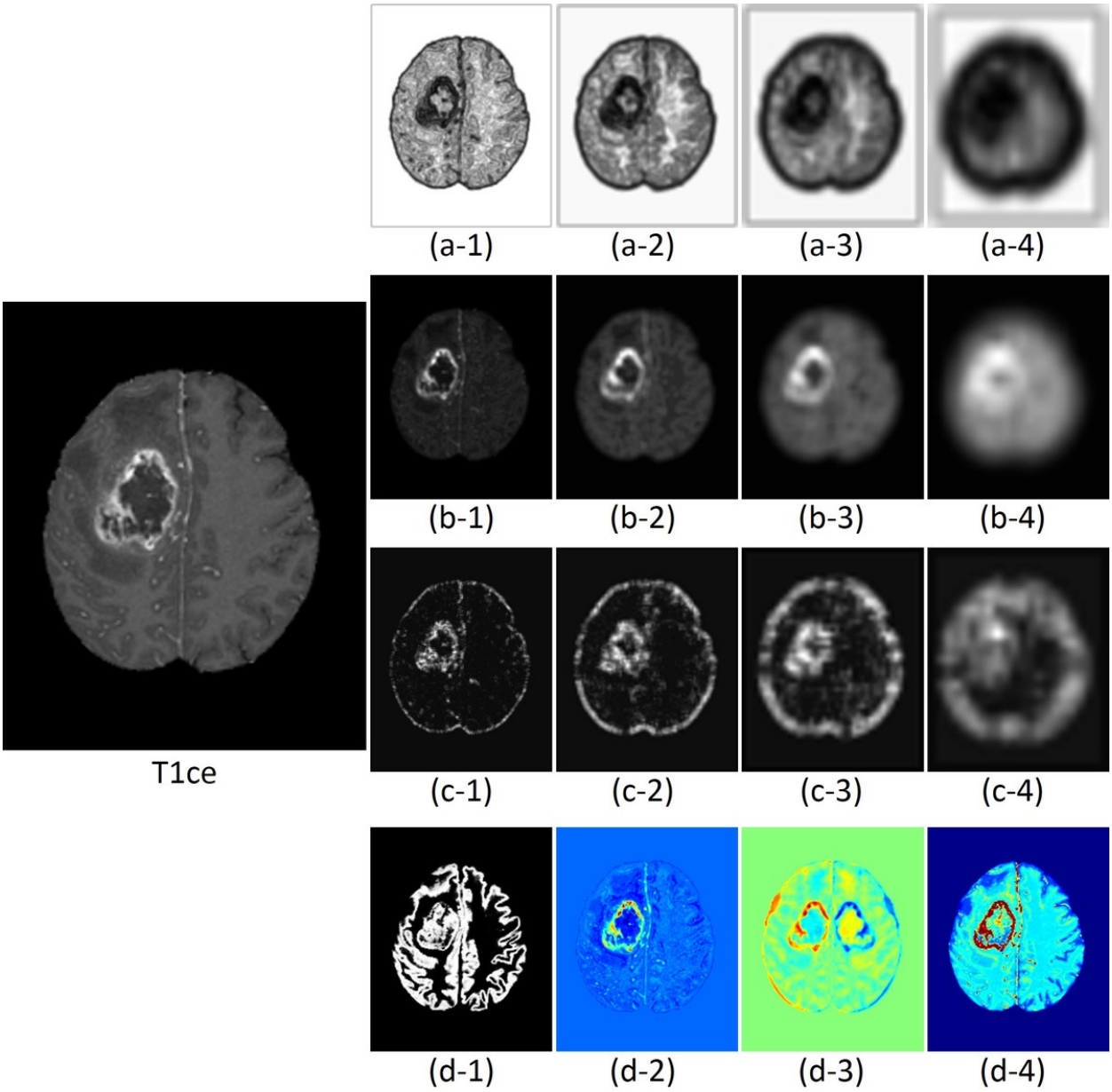

Fig. 1: Example of different features on a T1ce scan of a high-grade glioma patient. Row a: feature "homogeneity" calculated using the local GLCM. Row b: feature "Short Run with High Grey Level Emphasis" calculated using the local GLRLM. Row c: feature "Size-zone non-uniformity" calculated using the local GLSZM. For rows a-c: column 1: no subsampling, column 2: subsampling with factor 2, column 3: subsampling with factor 4, column 4: subsampling with factor 8. Row d: abnormality features: d-1: healthy grey level probability, d-2: Z-map, d-3: symmetry feature, d-4: tumour probability.

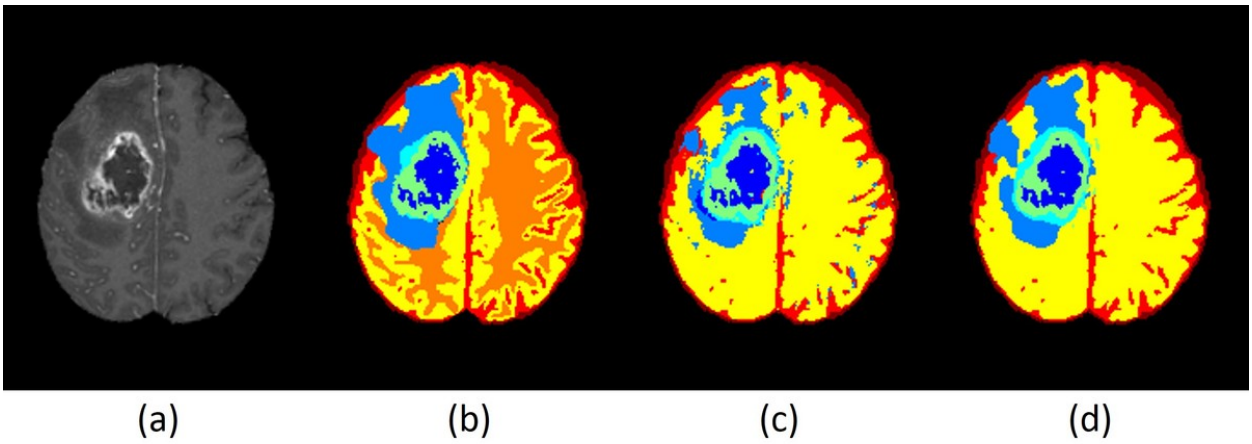

Fig. 2: Example of the segmentation proces. a: T1ce scan of a high-grade glioma, b: ground truth segmentation, c: output of the Random Forests model, d: final segmentation masker after voxel clustering.

Results

The results obtained on the BraTS 2013 training set are illustrated as Dice scores in figure 3. On low-grade glioma, the median Dice scores for segmenting non-enhancing tumour, tumour core and total abnormal region are 44.7%, 52.2% and 59.3% respectively. These tumour types show in general neither necrosis nor enhancing tissue, explaining the very low Dice scores for these tissues. For high-grade glioma, the median Dice scores for necrosis, edema, enhancing tumour, tumour core and total abnormal region are 70.2%, 57.3%, 80.4%, 82.8% and 75.9% respectively.

The ground truth labels of the BraTS 2017 dataset do not contain separate labels for non-enhancing tissue, but these are combined with the necrotic voxels. Our algorithm will however still predict non-enhancing tumour voxels, which is why we have calculated the Dice scores for the combinations non-enhancing tumour + edema and non-enhancing tumour + necrosis. These results are summarised in figure 4. As could be expected, the performance is lower in this independent validation dataset as compared to the training set. On low-grade glioma, the median Dice scores for segmenting non-enhancing tumour + necrosis, tumour core and total abnormal region are 30.4%, 37.3% and 45.8% respectively. For high-grade glioma, the median Dice scores for necrosis, edema, enhancing tumour, tumour core and total abnormal region are 46.6%, 30.9%, 77.4%, 72.2% and 63.7% respectively.

Images for this section:

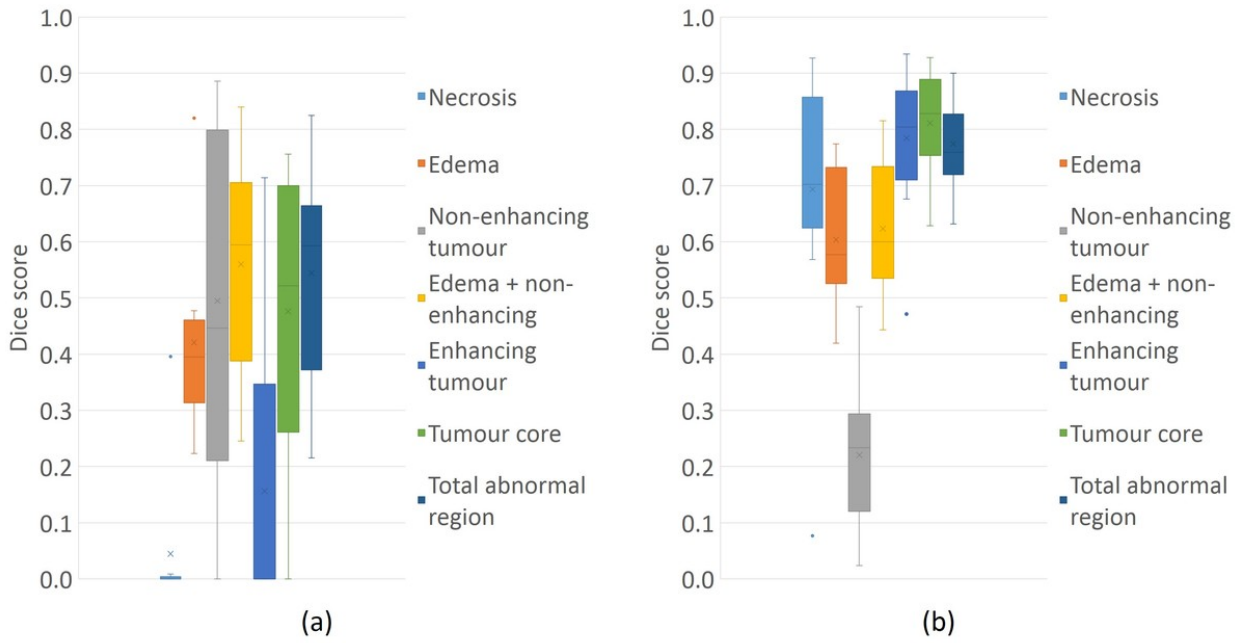

Fig. 3: Dice scores obtained on the BraTS 2013 training set. a: low-grade glioma, b: high-grade glioma.

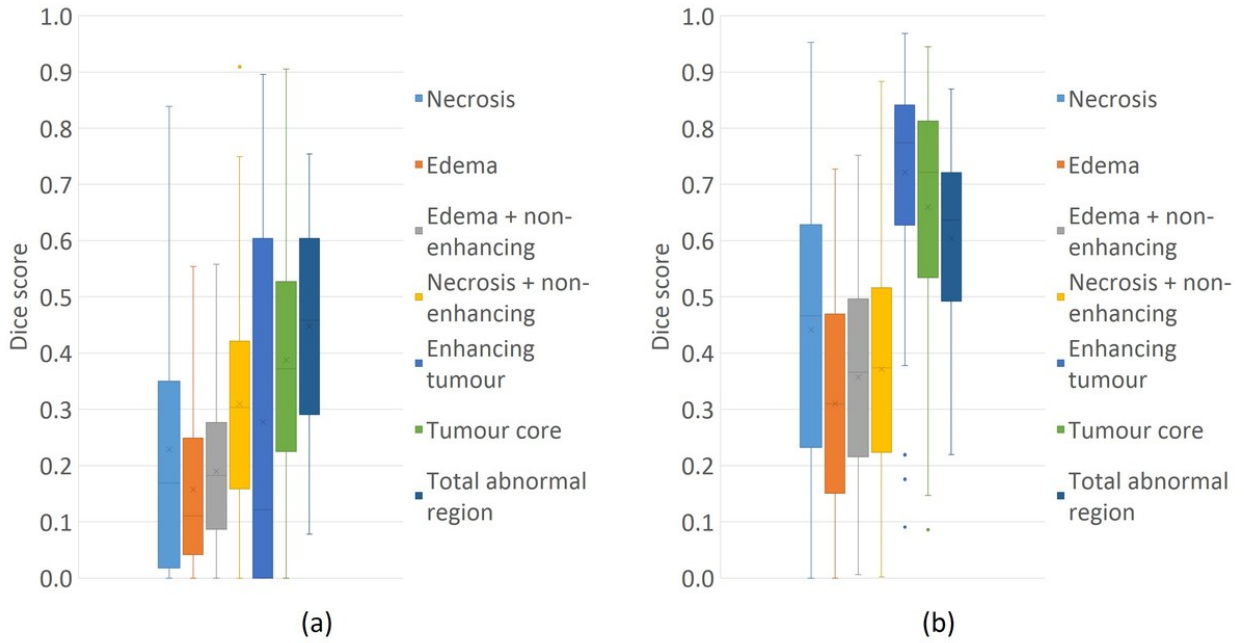

Fig. 4: Dice scores obtained on the BraTS 2017 validation set. a: low-grade glioma, b: high-grade glioma

Conclusion

Our fully automated brain tumour segmentation algorithm is able to delineate enhancing tissue with high accuracy based only on post-contrast T1-weighted MRI, whereas for non-enhancing tumour, necrosis and edema moderate accuracies are obtained. This can be explained by acknowledging that these tumour tissues are only moderately visible on a T1-weighted MRI scan. We assume that performing the same analysis on both T1ce and T2-weighted images (such as Fluid Attenuation Inversion Recovery - FLAIR) might improve the performance. Another drawback of our method is the strong dependency of the (ab#)normality features on the output of the SPM12 segmentation step. This algorithm assumes the intensity distribution of the normal appearing brain. Therefore, for large tumours or tumours causing a large midline shift, this segmentation step might produce unsatisfying results. This is also illustrated in figure 1 (d-1), where there is a slight misalignment between the tissue probability maps and the T1ce scan. This causes the random forest output to severely underestimate the white matter region (figure 2-c). Nevertheless, the tumour region is well delineated in this case.

In general, we obtained good results on T1ce scans only for delineating the contrast enhancing tissue, tumour core and total abnormal region, in particular of high-grade glioma.

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