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Brain Tumour Image Segmentation Using Deep Learning

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Abstract –

Automated segmentation of brain tumour from multimodal MR images is pivotal for the analysis and monitoring of disease progression. As gliomas are malignant and heterogeneous, efficient and accurate segmentation techniques are used for the successful delineation of tumours into intra-tumoral classes. Extensively used for biomedical image segmentation, Convolutional Neural Networks have significantly improved the state-of-the-art accuracy on the task of brain tumour segmentation. In this paper, we propose an ensemble of two segmentation networks: a 3D CNN and a U-Net, in a significant yet straightforward combinative technique that results in better and accurate predictions.

Key Words: Deep Learning, BraTS, Medical imaging, Segmentation, U-Net, CNN.

1.INTRODUCTION

Accurate segmentation of tumours through medical images is of particular importance as it provides information essential for analysis and diagnosis of cancer as well as for mapping out treatment options and monitoring the progression of the disease. Brain tumours are one of the fatal cancers worldwide and are categorised, depending upon their origin, into primary and secondary tumour types. The most common histological form of primary brain cancer is the glioma, which originates from the brain glial cells and attributes towards 80% of all malignant brain tumours. Magnetic Resonance Imaging (MRI) is a preferred technique widely employed by radiologists for the evaluation and assessment of brain tumours. It provides several complimentary 3D MRI modalities acquired based on the degree of excitation and repetition times, i.e. T1-weighted, post-contrast T1-weighted (T1ce), T2-weighted and Fluid-Attenuated Inversion Recovery (FLAIR).
In this work, we utilise multiple 3D CNN models for brain tumour segmentation from multimodal MRI scans and ensemble their probability maps for more stable predictions. The networks are trained separately, with hyperparameters optimised for each the training dataset acquired from the Brain Tumour Segmentation (BraTS) dataset.

2. Body of Paper

Numerous research studies highlight the importance of machine learning (ML) to facilitate and improve the efficiency of human practices. From combining ML with ubiquitous computing to employing it for foreign object detection , many techniques have emerged to automate otherwise challenging tasks. Pervasive as gliomas have become, it is imperative that they are monitored carefully and operated on, depending on the prognosis. Many ML algorithms can accurately segment the cancer regions and assist the neuroradiologists in disease monitoring and planning. The data used for these techniques must illuminate the variable characteristics of the gliomas, from the tumour infiltrative growth patterns to their heterogeneity, to attain considerable accuracy during segmentation. A study demonstrates the use of multimodal MRI data in a tissue type mapping protocol that serves to identify the grade as well as acquire spatial information of the tumour. Multi-sequence MRI data is also provided by the BraTS challenge, containing both HGG and LGG scans of multi-institute patients, to facilitate users for devising successful glioma delineation techniques.

Supervised learning techniques with discriminative classifiers have been used for accurate delineation of gliomas, of which the most successful are random forests (RF) and support vector machines (SVM). Numerous research studies highlight the importance of machine learning (ML) to facilitate and improve the efficiency of human practices. From combining ML with ubiquitous computing to employing it for foreign object detection , many techniques have emerged to automate otherwise challenging tasks. Pervasive as gliomas have become, it is imperative that they are monitored carefully and operated on, depending on the prognosis. Many ML algorithms can accurately segment the cancer regions and assist the neuroradiologists in disease monitoring and planning.

The data used for these techniques must illuminate the variable characteristics of the gliomas, from the tumor infiltrative growth patterns to their heterogeneity, to attain considerable accuracy during segmentation. A study demonstrates the use of multimodal MRI data in a tissue type mapping protocol that serves to identify the grade as well as acquire spatial information of the tumor . Multi-sequence MRI data is also

provided by the BraTS challenge, containing both HGG and LGG scans of multi-institute patients, to facilitate users for devising successful glioma delineation techniques. The dataset used here is BraTS2020 Dataset (training + validation)). It contains MRI Images from 355 patients, with each patient dataset containing 5 images in NIfTI files (. nii.gz) format that is commonly used in medical imaging format to store brain imaging data obtained using MRI and describe different MRI settings. All BraTS multimodal scans are available as NIfTI files (. nii.gz) and describe a) native (T1) and b) post-contrast T1-weighted (T1ce), c) T2-weighted (T2), and d) T2 Fluid Attenuated Inversion Recovery (T2-FLAIR) volumes, and were acquired with different clinical protocols and various scanners from 19 institutions, are the data contributors. Along with this mask is present in the dataset its annotations are label 0 (Unlabeled), label 1 (Necrotic and non-enhancing tumor core), label 2 (Peritumoral edema), label 3 (missing that is no pixel have label 3) and label 4 (GD - enhancing tumor). All the imaging datasets have been segmented manually and were approved by experienced neuro-radiologists. Along with this, the manual annotations in the dataset were approved as well.

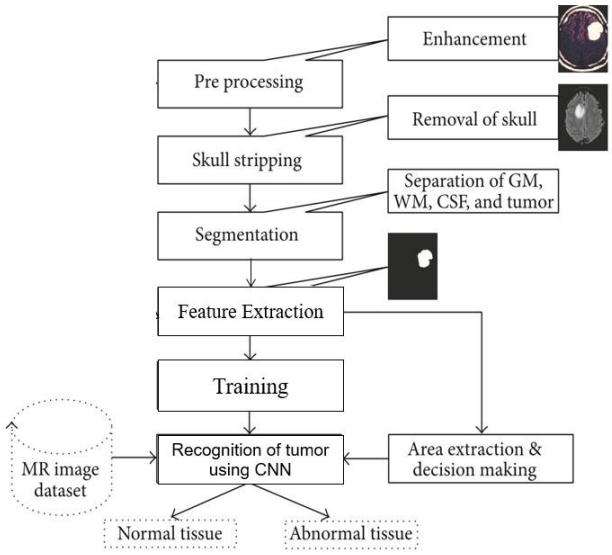

Fig-1: System Architecture

We have used Unet convolutional neural network architecture , for its implementation we can import the model from keras unet 0.1.2, this is a package with multiple U-Net implementations in Keras , in place of importing pre-existing model we have created it from scratch using keras that is useful utility tool helpful in the field of image segmentation along with this Tensorflow which is a foundation library used for building Deep Learning models. Here U-Net algorithm is used for fast and precise segmentation of images. The network has a u-shaped architecture because it has a contracting path and an expansive path. The architecture consists of two parts - encoder and decoder. The encoder is made up of two 3x3 convolutions that are applied repeatedly. After each conv, there is a ReLU and batch normalization. The spatial dimensions are then reduced using a 2x2 max pooling operation. We double the number of feature channels while halving the spatial dimensions at each downsampling step. For the decoder, every step in the expansive path starts with an upsampling of the feature map and then a 2x2 transpose convolution, which reduces the number of feature channels in half .Ensembling is often adapted for the task of brain tumour segmentation and has the advantage of improving both results and performance. We propose lightweight ensemble consisting of as few as two networks, each selectively trained on the training set. The outputs of these networks are segmentation map that differs in terms of segmented tumour sub-regions. The segmentation maps are then combined to get the final prediction. The model of our ensemble is a 3D CNN and 3D U-Net variant which is different from the classical U-Net architecture

3. CONCLUSION

Here we present results from an ensemble of 2 networks, variants of a U-Net and a CNN, both selectively trained on the BraTS 2019 training set (n = 335) and tested on the provided BraTS 2019 validation set (n = 125). We then intelligently combine the segmentation maps from these models to give a final prediction for tumour tissue type instead of simple averaging. The dice scores achieved by the ensemble (proposed) are 0.750 for enhancing tumour, 0.906 for the whole tumour, and 0.846 for tumour core. The segmentation maps are generated from both models separately, and then the final merged output is shown. The dice score for the patient was 0.930, 0.949 and 0.927 for enhancing tumour, whole tumour, and tumour core, respectively.

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