

INTRACRANIAL TUMOUR BIFURCATION USING Convent IN MRI IMAGE JUNCTURE

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Abstract— Among brain tumors, gliomas are the most common and aggressive, leading to a very short life expectancy in their highest grade. Thus, treatment planning is a key stage to improve the quality of life of oncological patients.

Magnetic Resonance Imaging (MRI) is a widely used imaging technique to assess these tumors, but the large amount of data produced by MRI prevents manual segmentation in a reasonable time, limiting the use of precise quantitative measurements in the clinical practice. So, automatic and reliable segmentation methods are required; however, the large spatial and structural variability among brain tumors make automatic segmentation a challenging problem.

We investigated the use of intensity normalization as a pre-processing step, which though not common in CNN (Convolutional Neural Network) achieves remarkable performance in image processing and computer vision.

Keywords—RESNET, SFCM, ROI, CRF, GRAPHICS PROCESSING UNIT, TIFF,CNN

I. INTRODUCTION

Brain tumor is one of the most rigorous diseases in the medical science. An effective and efficient analysis is always a key concern for the radiologist in the premature phase of tumor growth. Tumor biopsy being challenging for brain tumor patients, non-invasive imaging techniques like Magnetic Resonance Imaging (MRI) have been extensively employed in diagnosing brain tumors. Therefore, development of systems for the detection and prediction of the grade of tumors based on MRI data has become necessary. Brain tumor occurs when abnormal cells from within the brain. Causes of brain tumor are unknown. In brain tumor, gliomas are the most common leading to a short life time. Quantitative analysis of brain tumors is critical for clinical decision making. While manual segmentation is tedious, time consuming and subjective, this task is at the same time very challenging to solve for automatic segmentation methods. In this paper we present our most recent effort on developing a robust segmentation algorithm in the form of a convolutional neural network. We use a dice loss function to cope with class imbalances and use extensive data augmentation to successfully prevent overfitting. Our method beats the current state of the art on BraTS 2015, is one of the leading methods on the BraTS 2017 validation set (dice scores of 0.896, 0.797 and 0.732 for whole tumor, tumor core and enhancing tumor, respectively) and achieves very good Dice scores on the test set (0.858 for whole, 0.775 for core and 0.647 for enhancing tumor). We furthermore take part in the survival prediction subchallenge by training an ensemble of a random forest regressor and multilayer perceptron's on shape features describing the tumor subregions.

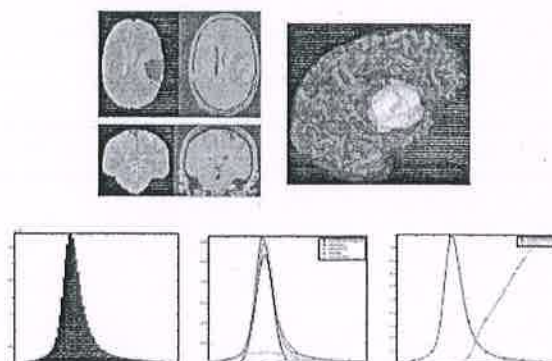


Fig : A T1 pre- and post-contrast difference histogram.