Brain Cancer Detection using Machine Learning

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Abstract—In the health care sector, Brain tumor evaluation and treatment is one of the significant challenges. Magnetic resonance imaging acts as a front-line diagnostic tool for brain tumors in the absence of ionizing radiation. Manual segmentation of brain tumor prolong from 2D Magnetic resonance imaging volumes is a tedious assessment and all process depends upon the operator's experiences. Deep-learning has proved to be the dominant mechanism for image analysis and is now over a great extent used to segment 2D images. During the segmentation process, an intense class imbalance is probable to occur labels, thus arising in suboptimal performance. In order to overcome this issue, the Dice loss function has been used. In this study, we propose a fully automatic method for brain tumor segmentation, which is developed using U-Net based deep convolutional net- works. Our method was evaluated on Multimodal Brain Tumor Image Segmentation (BRATS 2015) datasets, which contain 220 high-grade brain tumors and 54 low-grade tumor cases. We also propose to use the class re-balancing properties of the Generalized Dice overlap, a known metric for segmentation assessment, as a robust and accurate deep-learning loss function for unbalanced tasks.

Index Terms—Python, Tensorflow, CUDA, Cloud computing, Machine Learning, Deep learning, MRI.

1. INTRODUCTION

Brain tumors are one of the most dreadful diseases. These are hard to detect and treat. Minor inaccuracy can lead to severe consequences. Brain tumors can differ from where they start, grow, spread and the parts they affect. Brain tumors are named according to the types of cells they start from or according to the location in the brain. In most of the cases, the main cancer which is found are primary central nervous system lymphomas and gliomas. Gliomas contain many subtypes of the primary brain tumor which are likely to spread. These ranges from slower-growing "low-grade" tumor to heterogeneous, highly infiltrative malignant tumors. Since we have many advanced methods in imaging, radiotherapy, chemotherapy and surgical procedure still there some cases of malignant brain tumors like high-grade glioblastoma and metastasis that are still considered untreatable. An opinion Identify applicable funding agency here. If none, delete this. based on medical experience depicts results for patients with low-grade gliomas(LGG) with an overall survival rate of about 57 percent.

Studies have shown that the MRI i.e. Magnetic Resonance Imaging scans of the brain tumors can be used for detection , diagnosis and treatment strategies. Multimodal MRI protocols are used to detect brain tumor cellularity, vascularity and also the blood-brain barrier integrity. This is because they provide different contrast images that provide crucial complementary information produced by multimodal MRI protocols. MRI images include different types of images i.e. T1- weighted, T2-weighted(including Fluid- Attenuated Inversion Recovery i.e. FLAIR) and gadolinium-enhanced T1-weighted imaging sequences. These images give promising results in diagnosis. A critical step for MRI images is "Image Segmentation". An image that is segmented can eliminate confounding struc- tures from other brain tissues and so provides more accurate information and inform the subsequent diagnosis. In existing procedure is still based on manual delineation by operators. It is a very labor-intensive task, which involves slice by slice procedure and results are greatly dependent on operators and their subjective decision making. So for a multimodal and longitudinal clinical trial, a fully automatic, objective and reproducible segmentation method is highly in demand There are still several open challenges despite recent semi-automatic and fully automatic algorithms for brain tumor segmentation, mainly due to the high variation of brain tumors in size, shape, regularity, location and their heterogeneous ap- pearance (e.g., contrast uptake, image uniformity and texture). Supervised CNN has attracted lots of interests compared to conventional supervised machine learning methods, these deep learning-based methods are not dependent on hand-crafted features, but automatically learn a hierarchy of

increasingly complex features directly from data. An attribute of deep CNN is constructed, it is stacking several convolutional layers, which involve convolving a signal or an image with kernels to form a hierarchy of features that are more robust and adaptive for the discriminative models.IN recent development in deep learning-based methods, there are still some challenges: (1) tumor segmentation is an abnormal detection problem, it is more challenging and complex than other pattern recognition based tasks; (2) In most methods provided satisfied seg- mentation for HGG cases, general performance of the LGG segmentation is still low; (3) compared to complete tumor segmentation, the outline or border of core tumor regions and enhanced infiltrative regions is still underperformed; (4) a more high performance and memory-efficient development is still in demand because existing CNN based methods require excess amount of computing resources.

In this study, we developed a novel 2D fully convoluted segmentation network that is based on the U-Net architecture. In order to increase segmentation efficiency, a comprehensive data augmentation technique has been used in this work. We have also applied the Soft Dice based loss function which has a unique advantage that is accommodating to unbalanced samples, which is very important for brain tumor segmentation because some sub-tumoral regions may only count for a small portion of the whole tumoral volume. Compared with other manual methods, our fully automatic method has obtained promising results.

2. LITERATURE SURVEY

Mazzara GP1, Velthuizen RP, Pearlman JL, Greenberg HM and Wagner H proposed To assess the effectiveness of two automated magnetic resonance imaging (MRI) segmentation methods in determining the gross tumor volume (GTV) of brain tumors for use in radiation therapy treatment planning. Intra- and inter-operator variability in outlining was found to be an average of 20percent +/- 15percent and 28percent +/- 12percent, respectively. Lowest intraoperator variability was found for the physician who spent the most time producing the contours. The average accuracy of the kNN segmentation method was 56percent +/- 6percent for all 11 cases, whereas that of the KG method was 52percent +/- 7percent for 7 of the 11 cases when compared with the physician contours. For the areas of the contours where the oncologists were in substantial agreement (i.e., the center of the tumor volume), the accuracy of kNN and KG was 75percent and 72percent, respectively. The automated segmentation methods were found to be least accurate in outlining at the edges of the tumor volume. [1]

Bauer S1, Wiest R, Nolte LP, Reyes M proposed MRI-based medical image analysis for brain tumor studies is gaining attention in recent times due to an increased need for efficient and objective evaluation of large amounts of data. While the pioneering approaches applying automated methods for the analysis of brain tumor images date back almost two decades, the current methods are becoming more mature and coming closer to routine clinical application. This review aims to pro- vide a comprehensive overview by giving a brief introduction to brain tumors and imaging of brain tumors first. Then, we review the state of the art in segmentation, registration and modeling related to tumor-bearing brain images with a focus on gliomas. The objective in the segmentation is outlining the tumor including its sub-compartments and surrounding tissues, while the main challenge in registration and modeling is the handling of morphological changes caused by the tumor. The qualities of different approaches are discussed with a focus on methods that can be applied on standard clinical imaging protocols. Finally, a critical assessment of the current state is performed and future developments and trends are addressed, giving special attention to recent developments in radiological tumor assessment guidelines. The drawback of this proposal was that it doesn't work for dim images and is computationally expensive. [2]

Soltaninejad M, Yang G, Lambrou T, Allinson N, Jones TL, Barrick TR, Howe FA and Ye X proposed a fully automated method for detection and segmentation of the abnormal tissue associated with brain tumour (tumour core and oedema) from Fluid-Attenuated Inversion Recovery (FLAIR) Magnetic Res- onance Imaging (MRI). The proposed method is evaluated on two datasets: (1) Our own clinical dataset: 19 MRI FLAIR im- ages of patients with gliomas of grade II to IV, and (2) BRATS 2012 dataset: 30 FLAIR images with 10 low-grade and 20 high-grade gliomas. The experimental results demonstrate the high detection and segmentation performance of the proposed method using ERT classifier. For our own cohort, the average detection sensitivity, balanced error rate and the Dice overlap measure for the segmented tumour against the ground truth are 89.48 percent, 6 percent and 0.91, respectively, while, for the BRATS dataset, the corresponding evaluation results are 88.09 percent, 6 percent and 0.88, respectively. The draw back of this technique is augmented image required by expert for training and is also unable to detect tumor incase of faded image. [3]

Pinto A, Pereira S, Correia H, Oliveira J, Rasteiro DM and Silva CA proposed Gliomas are among the most common and aggressive brain tumours. Segmentation of these tumours is important for surgery and treatment planning, but also for follow-up evaluations. However, it is a difficult task, given that its size and locations are variable, and the delineation of all tumour tissue is not trivial, even with all the different modalities of the Magnetic Resonance Imaging (MRI). We propose a

discriminative and fully automatic method for the segmentation of gliomas, using appearance- and context-based features to feed an Extremely Randomized Forest (Extra- Trees). Some of these features are computed over a non- linear transformation of the image. The proposed method was evaluated using the publicly available Challenge database from BraTS 2013, having obtained a Dice score of 0.83, 0.78 and 0.73 for the complete tumour, and the core and the enhanced regions, respectively. Our results are competitive, when compared against other results reported using the same database.The vdrawback of this technique is that it is very time taking process and also computationally expensive. [4]

Michal Drozdzal, Eugene Vorontsov, Gabriel Chartrand, Samuel Kadoury and Chris Pal proposed the influence of both long and short skip connections on Fully Convolutional Networks (FCN) for biomedical image segmentation. In stan- dard FCNs, only long skip connections are used to skip features from the contracting path to the expanding path in order to recover spatial information lost during downsampling. We extend FCNs by adding short skip connections, that are similar to the ones introduced in residual networks, in order to build very deep FCNs (of hundreds of layers). A review of the gradient flow confirms that for a very deep FCN it is beneficial to have both long and short skip connections. Finally, we show that a very deep FCN can achieve near-to- state-of-the-art results on the EM dataset without any further post-processing but it requires augmented image required by expert for training. [5]

Diederik P. Kingma and Jimmy Ba proposed a system in which they introduce Adam, an algorithm for first-order gradient-based optimization of stochastic objective functions, based on adaptive estimates of lower-order moments. The method is straightforward to implement, is computationally efficient, has little memory requirements, is invariant to diag- onal rescaling of the gradients, and is well suited for problems that are large in terms of data and/or parameters. The method is also appropriate for non-stationary objectives and problems with very noisy and/or sparse gradients. The hyper-parameters have intuitive interpretations and typically require little tuning. Some connections to related algorithms, on which Adam was inspired, are discussed. We also analyze the theoretical convergence properties of the algorithm and provide a regret bound on the convergence rate that is comparable to the best known results under the online convex optimization framework. Empirical results demonstrate that Adam works well in practice and compares favorably to other stochastic optimization methods. Finally, we discuss AdaMax, a variant of Adam based on the infinity norm. The drawback in this technique is it is unable to detect tumor incase of faded image and is extensive time consuming. [6]

3. EXISTING SYSTEM

The (MRI) Magnetic Resonance Imaging plays a crucial role in Brain Tumor Detection. It is a tool that helps in the detection of brain tumors without ionizing radiation. The process is done with the help of doctors and lab operators. Due to manual manipulation, the segmentation of From 2D volumes is a very time-consuming task. The performance is dependent on the lab operators as well as the doctor's experiences. Using MRI, Doctor can make a decision whether it is benign (which id not cancer) or there is the presence of malignant (cancer).

4. LIMITATIONS

One of the limitations of the existing systems is that man- ual segmentation of brain tumor prolong from 2D Magnetic Resonance Imaging volumes is a tedious assignment and the performance highly depends on the operator's experience. This may also cause Human Errors with a lack of experience or neglection which leads to improper decision of Diagnosis. Medical Business Strategies are observed, where advantage is taken of the patients by manipulating their mind and convincing them to undergo treatment. This is strategy will lead to a bad effect on a patient's health.

5. PROPOSE SYSTEM

A reliable fully automatic segmentation approach for brain tumor segmentation is crucial for efficient analysis and evalu-ation of the tumor. We propose a fully automatic method for brain tumor segmentation, which is evolved using U-Net based deep (CN) convolutional networks. Our system will cover the limitations observed in the existing system. It will tackle the illegal medical business strategies as well as it will reduce time obtaining the results.

6. SOFTWARE REQUIREMENT SPECIFICATIONS

- Google Cloud Platform

- I5 processor

- 16 GB RAM

- 500 GB SSD

- Tesla k-100
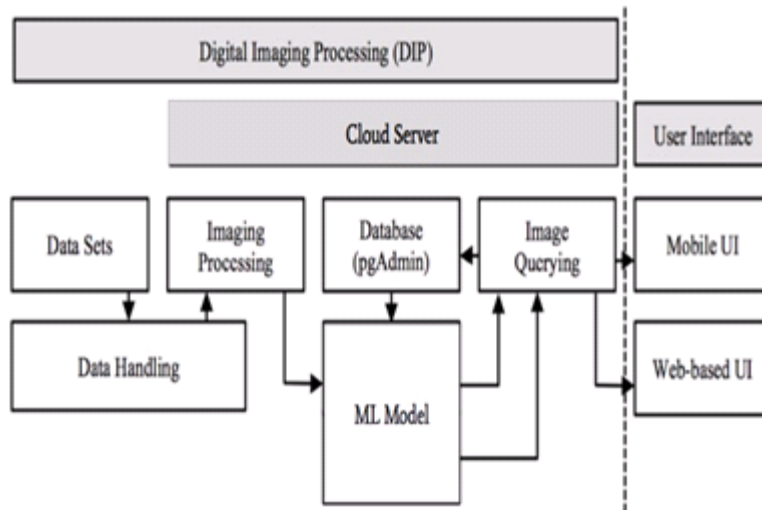
- OS: MAC/Windows/ubuntu

7. SYSTEM ARCHITECTURE

Fig. 1. fig.: Structure of System Architecture

8. ALGORITHM

A. U-net Algorithm

U-Net is a convolutional neural network that was developed for biomedical image segmentation. The network is based on the fully convolutional network and its architecture was modified and extended to work with fewer training images and to yield more precise segmentation. Segmentation of a 512*512 image takes less than a second on a modern GPU. The main idea is to supplement a usual contracting network by successive layers, where pooling operations are replaced by upsampling operators. Hence these layers increase the resolu- tion of the output. The network has to contract and expanding path, which gives U-shaped structure. The contracting path consisting of repeated applications of convolutions followed by ReLu and max-pooling operation. The expansive path combines the feature and spatial information through up-scale convolutions and combining the images with high-resolution features of the contracting path.
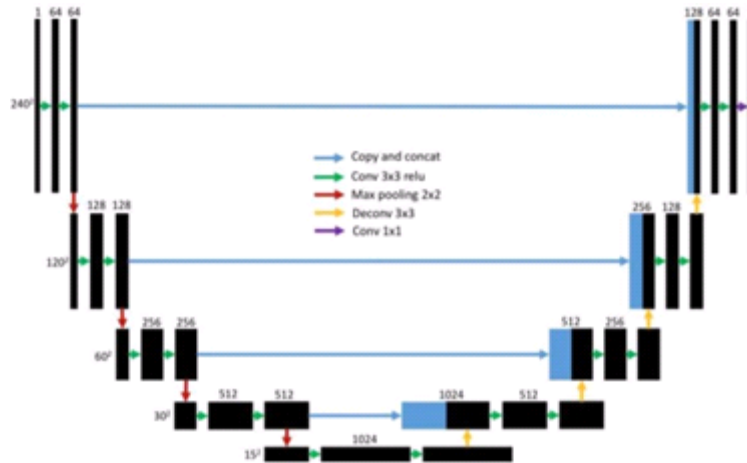
Fig. 1. Our developed U-Net architecture.

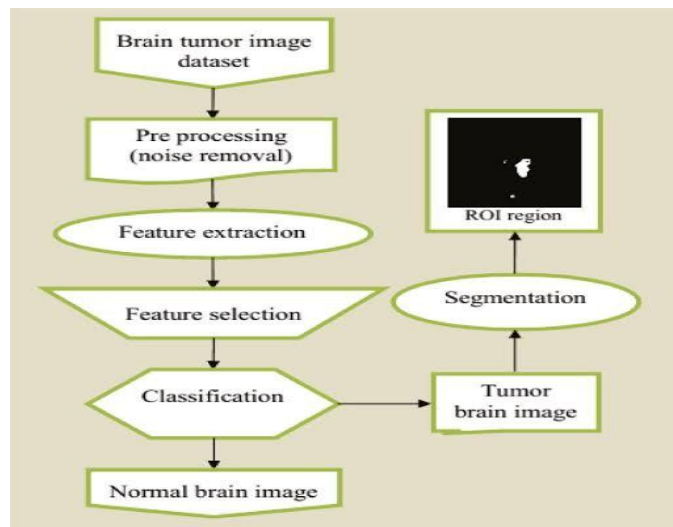Fig. 2. fig.: U-net Algorithm

B. UML Diagram

Fig. 3. UML Diagram
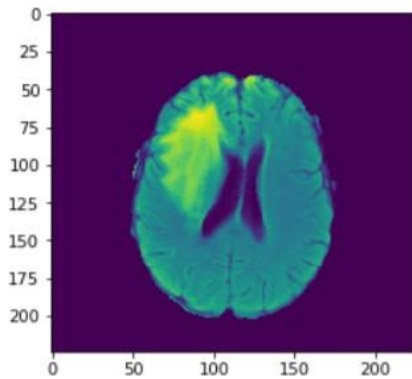
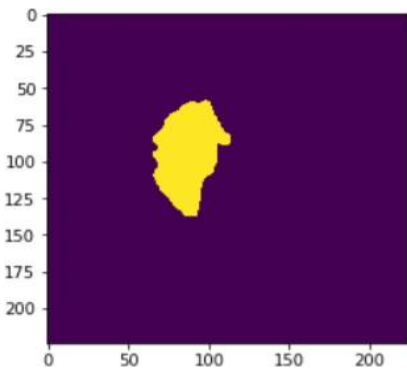*C. Original Image, Predicted Image and Labelled Image*

Fig. 4. Original image

Fig. 5. Predicted image

Fig. 6. Labelled image

9. CONCLUSION

We projected a fully automatic segmentation method approach for Brain Tumor which is crucial for efficient analysis and evaluation of the tumor. We propose a fully automatic method for brain tumor segmentation, which is evolved using U-Net based convolutional networks. The u-net architecture achieves very good performance on very different biomedical segmentation applications. The proposed method m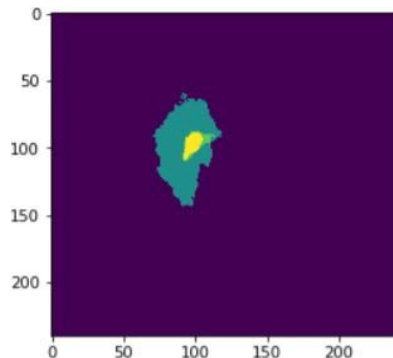akes it possible to generate a brain tumor segmentation model without manual interference, and this potentially enables objective le- sion assessment for clinical tasks such as diagnosis, treatment planning, and patient monitoring. It will also tackle illegal medical business strategies as well as low experience lab operator's work.

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