Brain Tumor Detection and Segmentation Using Convolutional Networks Madan Baduwal

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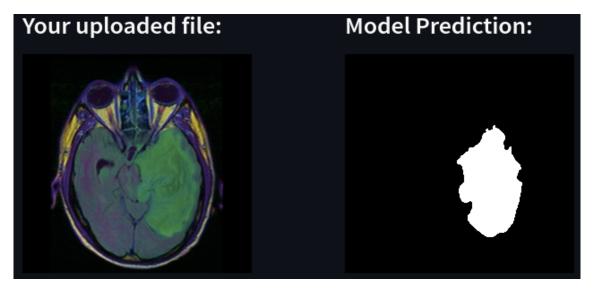


Figure 1: Brain tumor detection and segmentation

Github: https://github.com/madanbaduwal/brain-tumor-segmentation | Video

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1 abstract

In the contemporary landscape, brain tumors have emerged as a prominent cause of global mortality. These tumors manifest through abnormal growth of brain cells, profoundly impacting neighboring cells. This growth can encompass both cancerous and non-cancerous cell types, with symptoms varying based on factors such as location, size, and type. Detecting and precisely classifying brain tumors at their onset poses a formidable challenge due to their intricate and diverse structures, aimed at mitigating the potential loss of life. To address this challenge, this study proposes an enhanced model leveraging Convolutional Neural Networks (CNN) fused with ResNet50 and U-Net architectures. This model operates on the TCGA-LGG and TCIA datasets, publicly available repositories comprising data from 120 patients. The devised CNN, along with the fine-tuned ResNet50 model, is employed for the detection and classification of tumor or non-tumor images. Additionally, the integration of the U-Net model facilitates accurate segmentation of tumor regions. Evaluation of model performance is conducted using metrics including accuracy, Intersection over Union (IoU), Dice Similarity Coefficient (DSC), and Similarity Index (SI). Results from the fine-tuned ResNet50 model showcase impressive metrics: IoU: 0.91, DSC: 0.95, SI: 0.95. Notably, the U-Net model in conjunction with ResNet50 surpasses all other models, exhibiting superior performance in correctly classifying and segmenting tumor regions.

2 Introduction

The human brain is composed of numerous nerve tissues and highly intricate bodily organs. These tissues play a pivotal role in governing fundamental bodily processes, encompassing sensory perception, muscle development, and movement. Each neuron possesses a diverse range of functions and undergoes a process of development. Nevertheless, certain cells may ultimately lose their functionality, deviate from normal growth patterns, and exhibit deformities. Brain tumors are characterized by the abnormal proliferation of cells within the brain or central nervous system. They can manifest as either benign (non-cancerous) or malignant (cancerous) growths and have the potential to arise in any region of the brain or spinal cord. The etiology of brain tumors can be attributed to genetic mutations, exposure to radiation, and disorders of the immune system.

Furthermore, humanity has made significant strides in knowledge and biomedical research over the years. Nevertheless, the malignant proliferation of nerve cells leading to brain tumors remains a source of dismay. The growth rate of tumors varies among individuals, contingent upon factors such as the tumor's location and its rate of expansion.

Brain tumors (BT) represent a substantial contributor to mortality and exhibit the poorest survival rates compared to other cancer types. Identifying and categorizing brain tumors at their onset presents a challenging endeavor, given their irregular shapes, varied textures, diverse locations, and indistinct borders. Precise examination of the tumor's morphology in its early stages enables physicians to make informed decisions regarding the most appropriate treatment options, ultimately aiming to preserve the patient's life.

Brain tumors present themselves in diverse forms, commonly classified as either cancerous or non-cancerous varieties. A benign (non-cancerous) tumor typically grows slowly and remains localized within the brain, without affecting surrounding bodily cells. Its early detection facilitates timely intervention. Conversely, malignant (cancerous) tumors are further categorized into primary and secondary tumors. A primary tumor originates within the brain, whereas a secondary or metastatic tumor initiates elsewhere in the body before spreading to the brain. Among the most frequently diagnosed brain tumor types are meningioma, glioma, and pituitary cancer. Meningioma derives its name from the three protective membranes encompassing the brain and spinal cord, where it tends to develop. Glioma arises from glial cells, which support nerve cell function; however, if glioma progresses aggressively and infiltrates healthy nerve cells, the prognosis for inpatient survival is limited to a maximum of two years. Positioned at the back of the nose lies the pituitary gland, whose abnormal proliferation impacts various brain glands and numerous physiological processes.

Accurate segmentation of brain tumors following a cancer diagnosis is imperative for treatment planning and outcome assessment. Despite the laborious, time-consuming, and intricate nature of manual segmentation, recent research has focused extensively on automatic and semi-automatic methods for this purpose. These methods rely on either generative or discriminative models as their foundation. Discriminative models leverage image features to classify normal and malignant tissues, while generative models necessitate information from probabilistic images for brain tumor segmentation. Classification techniques, including support vector mechanism (SVM) and random

forest, are utilized in discriminative models, primarily focusing on visual features such as histograms, image textures, and structure tensor eigenvalues.

Deep learning techniques are increasingly utilized for tasks such as object detection, classification, and feature extraction. Convolutional neural networks (CNNs) are particularly recognized for their effectiveness in semantic image segmentation, consistently producing reliable results. Among these, CNNs, the most advanced mechanism, have the ability to learn representations of data and make predictions based on available information. They achieve tasks such as image categorization and feature extraction through self-learning, extracting both low and high-level information. While CNN-based approaches typically require substantial training datasets, they excel in making accurate predictions and drawing meaningful conclusions. However, applying CNNs to clinical research topics like brain tumor segmentation presents challenges due to constraints in available datasets.

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Deep learning provides a transfer learning strategy to address challenges associated with implementing CNNs on small datasets. This approach is based on two main hypotheses: (1) fine-tuning the ConvONet and (2) freezing the ConvONet layers. Transfer learning techniques utilize both large and small datasets, referred to as the base and training datasets, respectively. Initially, the CNN is trained on a large dataset, serving as a pre-trained network. Subsequently, the output from this training is employed as input and adapted to a smaller dataset, a process known as fine-tuning.

The study utilizes a dataset comprising two-dimensional, wide-slice-gap CE-MRI images collected from multiple hospitals across China spanning the years 2005 to 2020. This dataset encompasses four tumor classifications: glioma, meningioma, pituitary, and no tumor. Glioma, originating from the glial cells surrounding neurons in the brain, can manifest as either benign or malignant and can emerge in any region of the brain or spinal cord. Meanwhile, meningioma arises from the meninges, the protective tissue layers covering the brain and spinal cord. While meningiomas typically exhibit slow growth and are often benign, they can occasionally display aggressive or malignant behavior. The pituitary tumor type develops within the pituitary tissues, a small gland situated at the brain's base and a crucial component of the endocrine system responsible for regulating various hormones in the body. The transfer learning approach involves transferring the weights from pre-trained networks established on extensive datasets.

This research introduces a CNN model incorporating fine-tuned ResNet50 and U-Net architectures for brain tumor (BT) classification and MRI detection. The CNN model, featuring fine-tuned ResNet50 and U-Net architecture, is deployed to identify and classify patients affected by tumors. By applying this model to the TCGA-LGG and TCIA datasets, computer-aided systems leveraging this innovative integration could assist radiologists in discerning tumor stages.

The primary contribution of this study lies in the development of a CNN model featuring fine-tuned ResNet50 and U-Net for brain tumor (BT) classification and detection in MRIs. By integrating these two distinct architectures, the model harnesses their respective strengths to achieve high accuracy in both classification and detection tasks.

In this study, the fine-tuned ResNet50 architecture serves the purpose of brain tumor detection, aiming to identify the presence of tumors in MRI scans. Conversely, the U-Net architecture is employed for brain tumor segmentation, focusing on precisely delineating the tumor from the surrounding healthy tissue.

By leveraging a combination of these architectures, the model achieves remarkable accuracy, precision, recall, and F1 scores in both tasks. This comprehensive approach not only enhances the speed and accuracy of brain tumor diagnosis but also contributes to improved patient outcomes. The subsequent sections of the manuscript are structured as follows: related work, which delves into relevant literature in the field; methodology, outlining the overall approach utilized; results, detailing the outcomes obtained from all applied models; and conclusion, which summarizes the findings and outlines potential future directions.

3 Related Work

In their study, Deng et al. [5] implemented Convolutional Neural Networks (CNNs) using the extensive ImageNet dataset, achieving top performance in visual recognition tests. Everingham et al. [6] similarly demonstrated the effectiveness of CNNs, obtaining optimal results in image classification and detection tasks. Meanwhile, research conducted by Mustafa et al. [7] utilized the Figshare dataset [4] and applied an adaptive spatial division algorithm to enhance tumor area identification. This involved segmenting the tumor region before further division into subsections, extracting features such as intensity histograms, grey-level co-occurrence matrix values, and employing a bag of words (BoW) technique. Their approach yielded accuracy rates of 87.54%, 89.72%, and 91.28%. Mustafa et al. [7] further classified meningioma, glioma, and pituitary tumors with a remarkable 91% accuracy, utilizing statistical characteristics retrieved from MRI scans via a 2D Gabor filter. Additionally, Shakeel et al. [12] proposed fractional and multi-fractional dimension techniques for essential feature extraction. They suggested a classification approach, enhancing brain tumor detection performance through machine learning algorithms and backpropagation.

Setio et al. [11] employed multiple streams of 2D CNNs to extract patches from specific regions of interest within candidate nodules. By aggregating the data from these streams, the approach facilitated the identification of lung nodules. Consequently, the proposed architecture for pulmonary nodule detection was founded on multiview convolutional networks. In a similar vein, another study [3] utilized MATLAB and the ImageJ library to discriminate between benign and malignant tissues in MRI images. For brain tumor identification in this investigation, nearly ten features were extracted from the MRIs. Anil Singh Pirhar [9] proposed a CNN-based methodology involving intensity normalization during preprocessing, CNN architecture for classification, and tumor classification during post-processing.

Sultan et al. [13] employed two publicly available datasets and two deep-learning models to classify tumors into meningioma, glioma, and pituitary tumors. One model also categorized gliomas into Grade II, III, or IV. The first model achieved an accuracy of 96.13%, while the second model attained an accuracy of 98.7% using a 16-layer CNN. Ismael et al. [8] conducted experiments with a relatively small CE-MRI dataset to determine the prevalence of meningioma, gliomas, and pituitary tumors, achieving accuracy rates of 45%, 15%, and 15%, respectively. Abdalla et al. [1] utilized the MRI dataset from the complete brain atlas website for their experiment. They preprocessed the dataset before segmentation and developed a method using statistical feature extraction and an artificial neural network (ANN) model for computer-aided tumor detection. The suggested approach demonstrated accuracy and sensitivity of 99% and 97.9%, respectively.

Gliomas are a prevalent type of brain tumor, categorized into high and low grades based on their severity, with corresponding benign and cancerous classifications. In a study by the author [15], a CNN-based technique was proposed to differentiate between low- and high-grade tumors, employing an effective SVM classifier to distinguish between benign and malignant tumors using collected parameters and results. Similarly, Rehman et al. [10] utilized CNN architecture and transfer learning to classify brain tumors. They leveraged ImageNet as the base dataset and Figshare as the target dataset for transfer learning, applying three deep CNN architectures (AlexNet, GoogLeNet, and VGGNet) to MRI scans from the target dataset to identify tumor types. Discriminative visual and pattern characteristics were extracted from MRIs using transfer learning, fine-tuning, and freeze techniques. Swati et al. [14] proposed a blockwise fine-tuning method for brain tumor image classification, training their model on a standard dataset of T1-weighted contrast-enhanced magnetic resonance images. Through comparisons with conventional machine learning and deep learning CNN-based approaches using a five-fold cross-validation technique, they achieved an accuracy of 94.82%.

Kaoutar et al. [2] conducted a study aiming to predict the duration of glioblastoma brain tumors by employing feature learning and deep learning techniques with MRI images sourced from the ImageNet dataset. They utilized a deep CNN that was pre-trained on the dataset, leveraging transfer learning to adapt the pre-trained models to new tasks. This approach is particularly useful as the complexity of models increases with training on massive datasets. By pre-training the CNN on a large dataset and subsequently predicting survival time using the pre-trained features, they achieved a predicted success rate of 81.8% for the flare sequence.

4 Methodology

This section delineates the proposed method and architecture. Specifically, it introduces a convolutional neural network (CNN) model incorporating fine-tuned ResNet50 and U-Net. The operational details of the methodology, delineated on a model-by-model basis, are provided below.

4.1 Dataset Description

The dataset utilized in this study was sourced from TCGA (The Cancer Genome Atlas) and TCIA (The Cancer Imaging Archive). Among the patients identified from TCGA with lower-grade malignant tumors of the nervous system, there were initially 120 individuals who possessed preoperative imaging data, with at least one scan featuring an inversion recovery process with fluid attenuation. However, ten patients were excluded from this dataset due to the requirement for informed consent regarding available genomic constellation information. Consequently, the final dataset comprised 110 patients. A comprehensive list of these patients is available in Online Resource 1. The remaining patients were partitioned into 22 distinct and non-overlapping clusters, each comprising five patients. This segmentation process was carried out to facilitate evaluation using a cross-validation technique. The imaging dataset utilized in our study was obtained from the Imaging Archive, featuring sample images showcased in Figure 1. This dataset comprises images of patients associated with TCGA and is supported by the National Cancer Hospital. Whenever available, we incorporated all treatment modalities; however, in cases where one was unavailable, only FLAIR sequences were utilized. Six patients lacked the pre-contrast sequence, nine were devoid of the post-contrast sequence, while 101 had access to all relevant sequences. Detailed patient information is accessible in Online Resource 1. Among the patients, between 20 to 80 individuals had recorded slice numbers. We exclusively examined bilateral data to ascertain the initial pattern of tumor progression. Moreover, the genomic dataset employed in this study included IDH mutation and DNA methylation measurements. In our research, we considered six previously identified genetic classifications of LGG, recognized to be associated with various aspects of tumor morphology.

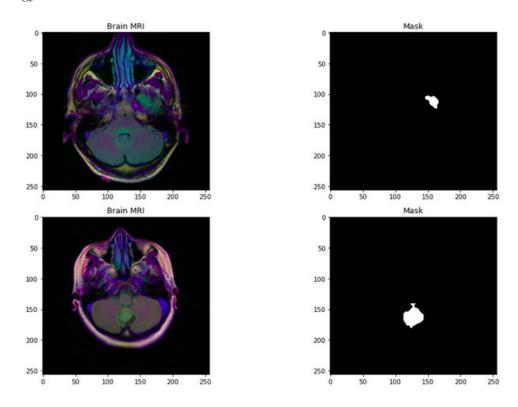


Figure 2: Accuracy

4.2 CNN architecture

Convolutional neural networks (CNNs) represent the cutting-edge technique for identifying brain tumors in medical imagery. When predicting tumors, the CNN model relies solely on MRI scans, neglecting the associated masks. This indicates that the CNN evaluates MRI images alone to discern the presence or characteristics of tumors, disregarding supplementary information from the corresponding masks, which might include segmentation or labeling data pertaining to tumor regions. Typically, the initial layer comprises a Conv layer, utilizing filters to extract features from the images. The output of this layer consists of feature maps, indicating the response of each filter to the input image. Subsequently, a pooling layer, often added as the second layer, reduces the size of the feature map while preserving crucial features, thereby diminishing parameters to mitigate overfitting. The outputs of both layers are then condensed and forwarded to fully connected layers, completing the classification of extracted features. The CNN produces a probability distribution over potential class labels, with a predetermined threshold determining tumor presence. During training, the CNN adjusts the weights of the Conv and fully connected layers to minimize the disparity between predicted and ground truth classes of the training data, typically employing backpropagation and stochastic gradient descent. Once trained, the CNN can detect and classify brain tumors in medical imagery by generating a probability score for tumor presence, categorizing an image as tumor-containing if the score surpasses a set threshold.

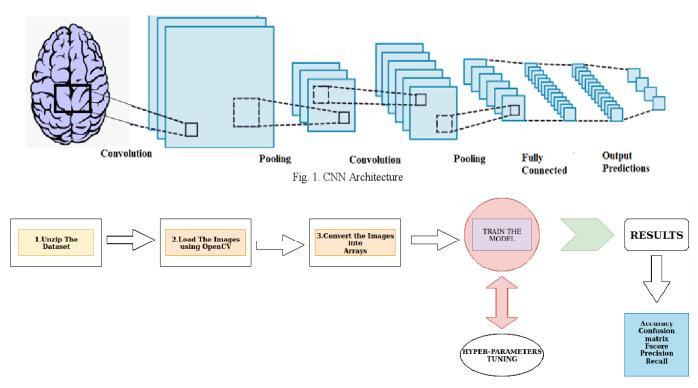


Figure 3: CNN

4.3 ResNet50 Model

Fine-tuning the ResNet50 model with CNN is a conventional approach for detecting and classifying brain tumors (BT) using MRI scans. ResNet50, originally trained on the extensive ImageNet dataset for object recognition assignments, encompasses various layers such as convolutional, pooling, and fully connected layers. This model serves as a feature extractor for the brain tumor detection task, with its lower layers acquiring generic image features pertinent to brain tumor detection. To tailor it for the specific task of brain tumor detection and classification, the final few layers of the ResNet50 model are substituted with a fresh set of fully connected layers.

After incorporating the new fully connected layers, the complete model undergoes fine-tuning on a fresh dataset comprising MRI scans. This process entails updating the weights of all model layers through backpropagation and stochastic gradient descent. The input data comprises brain MRI scans, typically preprocessed to accentuate

the contrast between the tumor and surrounding tissue. The output of the fine-tuned model is a probability distribution across potential class labels, distinguishing between tumor (yes) or non-tumor (no). By setting a threshold on this probability, the ultimate determination regarding the presence or absence of a tumor can be made.

Throughout the training process, the fine-tuned ResNet50 model with CNN acquires the ability to discern discriminative features from brain MRI scans and categorize them as either tumor or healthy. Leveraging the pre-trained ResNet50 model furnishes a sturdy foundation of features for brain tumor detection, while fine-tuning the model on a fresh dataset of MRI scans facilitates its adaptation to the precise task. This methodology has demonstrated notable accuracy in detecting and classifying brain tumors using MRI scans.

4.4 U-Net Model

This model represents a widely employed deep learning technique designed for semantic segmentation assignments, particularly focused on brain tumor segmentation within MRI imagery. It consists of two integral components: a contracting path and an expanding path. The contracting path operates by extracting high-level features from MRI images through the application of convolutional and pooling layers. These pooling layers reduce the spatial dimensions of features while increasing their depth, enabling the network to capture more abstract features. Conversely, the expanding path incorporates convolutional and upsampling layers that progressively augment the spatial dimensions of features while reducing their depth. The U-Net architecture incorporates skip connections, which connect corresponding layers across both paths, enabling the network to retain spatial information that may be lost during downsampling.

The outcome of this model is a probability map illustrating the likelihood of each pixel in the input image belonging to the tumor region. This probability map is derived by applying a softmax function to the network's final layer. During the training phase, the weights of the U-Net architecture are optimized via backpropagation and stochastic gradient descent to minimize the loss function, typically binary cross-entropy. A loss function, also referred to as a cost function or objective function, is a mathematical metric that gauges the disparity between the model's predicted values and the true values of the target variable. It assesses the model's performance by quantifying a penalty or loss based on the deviation between the predicted and actual values.

The primary role of a loss function is to steer the optimization process throughout model training. By computing the loss for every training instance, the model can fine-tune its parameters in a manner that diminishes the overall loss, thereby enhancing the accuracy of predictions.

The loss is computed and network weights are adjusted based on the ground truth segmentation map. Once the U-Net model undergoes training, it becomes capable of segmenting brain tumors in new MRI scans. The trained model receives the input image to generate an output probability map. By applying a threshold to this probability output, a binary segmentation map is obtained, indicating the presence or absence of a tumor in each pixel of the input image. This method has showcased notable accuracy in such tasks and has gained widespread adoption in image analysis.

5 Results

6 References

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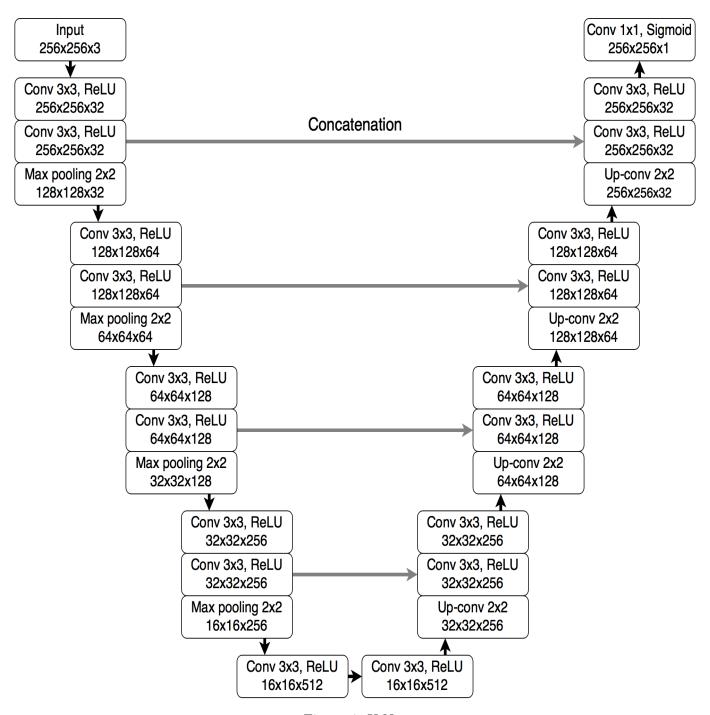


Figure 4: U-Net