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Detection of Brain Tumor Using Deep Convolutional Network

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Abstract

Introduction: More than 28,000 people are diagnosed with brain tumor every year in India, out of which 80% are cancerous and more than 24,000 people die due to delayed treatment of tumor and cancer identification. This work is focused on "Brain Tumor Detection Using Deep Convolutional Neural Network" and it proposes a method for accurately detecting brain tumours with deep Convolutional Neural Networks (CNNs), eliminating the need of a radiologist to confirm the presence and identifying the type of tumor, thereby putting more focus on immediate treatment and cancer identification using biopsy and reducing the duration of the tumor detection process. This work highlights the importance of early and accurate detection of tumors in brain, as it plays critical role in the successful treatment and management of a brain cancer. It is mentioned that traditional methods for brain tumor detection, such as manual segmentation and feature extraction are time-consuming and subject to human error. Hence, deep learning-based approach using 23 layers CNN architecture and transfer learning based VGG16 architecture has been proposed, which have shown remarkable success in a various image recognition tasks.

Methodology: The methodology used in the research, involves several steps. First step involves collection of brain MRI (Magnetic Resonance Imaging) data from a publicly available dataset- Harvard Medical Dataset and Figshare. The data by resizing the images to a consistent resolution and normalizing the pixel values. Then, the dataset is split into training, and testing sets, in the ratio of 7:3 fora training and evaluating the proposed CNN models. Ab CNN architecture is designed, which consists of multiple convolutional and pooling layers followed by a fully connected layer. Rectified Linear Unit (ReLU) activation functions are used to introduce non-linearity and batch normalization to improve the training stability. Dropout regularization is employed to prevent overfitting, which is a common issue in deep learning models.

Discussion: CNN models are trained using the training set and optimized using Stochastic Gradient Descent (SGD) with a categorical cross-entropy loss function. Experimentations with different hyper parameters, such as learning rate and batch size, were carried out to find the optimal settings for the models. Data augmentation techniques were performed, such as rotation, flipping, and scaling, to increase the diversity of training data and improve the model's generalization ability. Once the training was completed, the CNN model was evaluated on the testing sets. Various performance metrics were reported, such as accuracy, precision, recall, and F1-score, true positive rate and true negative rate to assess the effectiveness of the models in detecting brain tumors accurately. The results were compared with existing methods in the literature and it was observed that the proposed CNN models outperform all of them in terms of accuracy and other performance measures.

Conclusion: Furthermore, additional experiments are carried out to analyze the robustness of the CNN models against different types of brain tumors, such as benign and malignant tumors, as well as different tumor sizes. Ablation studies are performed to investigate the impact of different components of the CNN architecture on the model's performance. In addition, Different kernel sizes, which refer to the width height of the filter mask here, are integrated with the model to extract the complex features from the MRI images to make the model more robust and adaptive. The radiologist uses different experimental procedures for diagnosing brain tumors, including biopsy, Cerebrospinal Fluid (CSF) analysis, and X-ray analysis. The biopsy process introduces many risks including inflammation and severe bleeding. It also has just 49.1% accuracy.

CSF Analysis, similar to biopsy, it introduces many risks including bleeding from the incision site to the bloodstream and perhaps an allergic reaction after the treatment. Similarly, using X-rays on the skull can lead to an increase in the risk of cancer due to the radiation. The results of the research show that the proposed CNN-based approach achieves high accuracy in detecting brain tumors, with promising performance metrics across different types and sizes of tumors. The implications of the findings, includes the potential clinical applications of the approach in real-world scenarios fora assisting radiologists in accurate brain tumor diagnosis. The limitation of the study, is that only a single dataset is used for testing, however testing should have been performed on a diverse dataset of real clinical images.

Keywords: Brain tumor • Magnetic Reasoning Imaging (MRI) • Computer aided diagnostic techniques • Data processing and augmentation • Convolutional Neural Network (CNN) • Confusion matrix

Introduction

Brain tumours

One of the most fatal diseases, brain tumours are brought on by the sudden, uncontrolled growth of brain tissue inside the skull. Brain tumours can be extremely little ore quite enormous in size. Since they produce symptoms that you can immediately identify, some brain tumours are discovered while they are quite little. Other brain tumours grow considerably before they are discovered. The brain has several regions that are more and less active. If a brain tumour develops in a less active area of the brain, symptoms may not appear straight away. Before the tumour is found, its size may increase significantly. The sort of brain tumour one has, as well as its size and location, all affect your treatment choices. Radiation therapy and surgery are frequent forms of treatment. Strong magnets are used in MRI, also known as magnetic resonance imaging, to produce images of the interior of the body [1].

Different types of brain tumors

It might be benign or cancerous. While benign tumors typically grow slowly, malignant tumors can quickly enlarge and spread throughout the surrounding brain tissue. Benign tumours, however, can also be harmful because their growth may affect the surrounding brain tissues. 30% of tumours

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are malignant, and 70% are benign. Meningioma, glioma and pituitary tumors, which are the most prevalent ones, are among the more than 120 different types of brain tumours that have so far been found and identified. Meningioma tumours are perhaps the most common primary brain tumours that affect the meninges and the brain and spinal cord among these three.

In contrast, glioma tumours develop from glial cells known as astrocytes. The most noticeable glioma tumour is an astrocytoma, a low-risk tumour with slow growth. However, one of a the most dangerous brain tumours is high-risk glioma. Another type of a tumour is pituitary, which results from the overgrowth of a brain cells in the pituitary gland of the brain. As a result of a brain tumor's potentially fatal nature, early diagnosis is crucial [2].

Brain and other Central Nervous System (CNS) tumors are among the most fatal cancers and account for substantial morbidity and mortality in the United States. Population-based data from the Central Brain Tumor Registry of the United States (a combined data set of the National Program of Cancer Registries [NPCR] and Surveillance, Epidemiology and End Results [SEER] registries), NPCR, National Vital Statistics System and SEER program were analyzed to assess the contemporary burden of malignant and non-malignant brain and other CNS tumors (hereafter brain) by histology, anatomic site, age, sex and race/ethnicity. Malignant brain tumor incidence rates declined by 0.8% annually from 2008 to 2017 for all ages combined but increased 0.5% to 0.7% per year among children and adolescents.

Malignant brain tumor incidence is highest in males and non-Hispanic White individuals, whereas the rates for non-malignant tumors are highest in females and non-Hispanic Black individuals. Five-year relative survival for all malignant brain tumors combined increased between 2015 to 2022 from 23% to 36%, with larger gain among younger age groups. Less improvement among older age groups largely reflects a higher burden of glioblastoma, for which there have been few major advances in prevention, early detection, and treatment the past 4 decades. Specifically, 5-year glioblastoma survival only increased from 4% to 7% during the same time period. In addition, important survival disparities by race/ethnicity remain for childhood tumors, with the largest Black-White disparities for diffuse astrocytoma (75% vs 86% for patients diagnosed during 2009- 2015) and embryonal tumors (59% *vs.* 67%). Increased resources for the collection and reporting of timely consistent data are critical fore advancing research to elucidate the causes of sex, age, and racial/ethnic differences in brain tumor occurrence, especially for rarer subtypes and among understudied populations [3].

Malignant and non-malignant brain and other Central Nervous System (CNS) tumors comprise a diverse constellation of over 100 histologically distinct subtypes with varying descriptive epidemiology, clinical characteristics, treatments, and outcomes. Although primary malignant brain and other CNS tumors are rare in the United States, they account for a disproportionate burden of cancer mortality because of their high fatality rate; only one-third of individuals survive at least 5 years after diagnosis. The classification and reporting of these tumors have rapidly changed in recent years in parallel with expanding molecular understanding and advances in detection and diagnosis, although much of the etiology remains unknown. This article provides an overview of primary malignant and non-malignant brain and other CNS tumor incidence, mortality, and survival rates and trends in the United States, as well as differences in occurrence by major histologic subtype, anatomic site, geography, race/ethnicity and sex.

Contemporary incidence, survival and mortality

Pilocytic astrocytoma is clinically considered non-malignant but is included in the malignant category according to historical convention for cancer reporting. Data source: Central Brain Tumor Registry of the United States data provided by the Centers for Disease Control and Prevention's National Program of Cancer Registries and the National Cancer Institute's Surveillance.

However, pituitary tumor incidence decreases in females with advancing age and sex differences in older adults are driven primarily by non-malignant meningioma sex differences in lifetime exposure to endogenous hormones have been proposed as a cause for this differential risk, since rates in children are generally similar, but results in published cohort studies have been inconsistent because of obstacles in long-term hormone measurement.

Available diagnostic methods and associated risks

The radiologist uses a variety of cutting-edge techniques, such as biopsy, Cerebrospinal Fluid (CSF) analysis, and X-ray analysis, to diagnose brain tumours. Surgery is used to remove a tiny piece of tissue during the biopsy procedure. The radiologist then decides if there is a tumour present in the tissue or not. But there are numerous risks associated with the biopsy procedure, such as inflammation and severe bleeding.

In addition, its accuracy is only 49.1%. The CSF fluid, which depicts the interior of the brain, is colorless. The liquid is examined by the radiologist to look for brain tumors. Similar to a biopsy, there are a number of risks associated with this procedure, including the possibility of an allergic reaction and bleeding into the bloodstream at the site of the incision. Similar to using X-rays on the skull, doing so exposes the head to radiation, which raises the risk of cancer.

Radiologists are using image modalities more frequently these days because they are more accurate and put patients at significantly lower risk. Medical imaging data can be recorded using a variety of techniques, such as radiography, magnetic resonance imaging (MRI), tomography, and echocardiography. Among them, MRI is the most well-known because it offers radiation-free images with a higher resolution. Radiologists can diagnose brain abnormalities using medical image data obtained through the non-invasive MRI procedure. The Computer- Aided Diagnosis (CAD) method, on the other hand, was created to find brain tumors in their early stages without the need for human intervention. On the basis of MRI images, CAD systems can generate diagnostic reports and provide the radiologist with instructions [4].

Need of convolutional neural networks

Machine Learning (ML) and Deep Learning (DL) applications in the field of medical imaging have significantly improved the CAD process. These methods improve the CAD system's ability to accurately detect brain tumors. The principles of feature extraction, feature selection and classification are the foundation of machine learning techniques. The tumor region is separated from the human skull using a variety of feature extraction techniques, such as thresholding-based, clustering-based, contour-based, and texture-based. These methods extract features from MRI images, choosing only the most significant features through a feature selection process (Figure 1). Achieving high accuracy requires extracting features with significant discriminatory information. However, it is possible to ignore crucial information from the original image by using features extraction [5].

However, DL techniques deal with this problem by incorporating the original image as input. They don't need handcrafted features, in other words, to be classified. Convolutional Neural Network (CNN) is one of the DL models that offer various convolution layers that will automatically extract features from the images. When given a large dataset, which is sometimes difficult to come by a in the field of medical imaging, CNN performed well. The use of transfer learning is one strategy to handle this problem. In transfer learning, a model

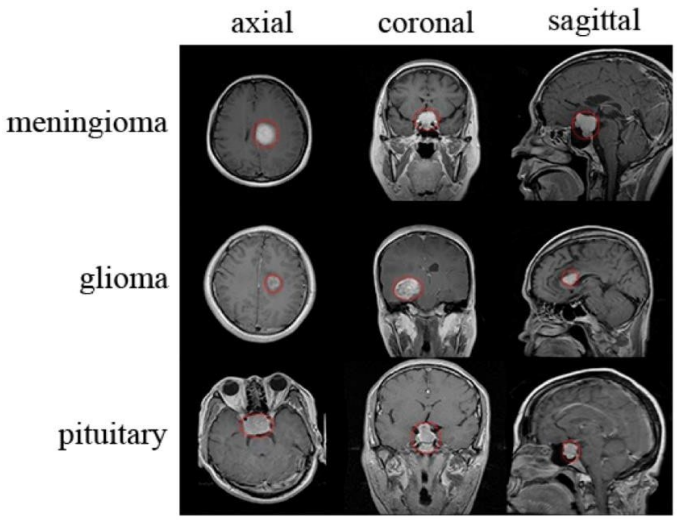

Figure 1. MRI scans of different types of brain tumor.

that has already been trained on a sizable dataset pertaining to a different domain is used to classify data. Such information enables the model to perform well on a limited dataset.

Review of available studies

Different researchers have given their contribution in the domain of computer aided diagnosis, especially in the field of brain tumor detection. Some used tradition machine learning techniques like K Nearest Neighbors, Support Vector Machines, Logistic Regression and Boosting algorithms like ADA Boost, XG Boost, while some used advanced deep learning techniques like Convolutional Neural Network to perform their analysis. With the aim to develop the problem statement these researches were studied and gaps were identified. A compilation of the reviewed papers in the concerned domain have been discussed below [6].

Literature survey

Used a machine learning based Back propagation neural network framework which has major practical importance in acknowledging data and in the segmentation of the image of the tumor. The pictures are characterized into 2 classes. While analysis, the machine learning based Back propagation neural network uses 30 example images for the process of tumor classification. Then, the classification is carried out utilizing two methods, Adaboost Classifier and machine learning based Back Propagating Neural Network. Contrasting Adaboost, NN has an extra benefit of recognizing whether the tumor is in beginning phase or in an advanced stage.

Based on the gaps identified, it has been found that no work on brain tumor detection using CNN with the proposed parameterization has been yet carried out. Therefore in the present work, A "Fine-tuned proposed model with the attachment of the transfer learning based VGG16 and 23 layer CNN" architecture is being constructed to be used as a Computer-Aided Diagnosis Model for classifying normal and abnormal brain images, coming into play to increase efficiency and reduce human intervention. After thoroughly reviewing the available studies and researches in the concerning areas related to MRI scanning and brain tumor identification, and developing the problem statement the following objective were worked upon and identified [7].

Methodology

The block diagram suggested in the study for automated binary and multiclass brain tumour identification is displayed in figure 2. The architecture begins with label loading from the dataset and picture extraction. Before dividing the retrieved photos into training and testing set, preprocessing is required. Finally, the used datasets are subjected to our suggested "23-layers CNN" and "Fine-tuned VGG16" work flow. The block descriptions of our suggested techniques are thoroughly described in the sections that follow.

Dataset

Two distinct datasets are used in this investigation. The first one is a publicly accessible CE-MRI Figshar dataset and is referred to as dataset 1 in this paper. Between 2005 and 2010, information was gathered from General Hospital, Tianjin Medical University, and Nanfang Hospital in China. A total of 3064 T1-weighted contrast MRI slices from 233 individuals who were identified as having one of the three types of brain tumors—meningioma, glioma or pituitary—are included in this dataset. The axial, coronal and sagittal perspectives of the MRI scans included in this dataset are all distinct.

The Harvard repository gathered the second dataset, which is referred to as dataset 2 in this paper. There are 152 T1 and T2 weighted contrast MRI slices in the dataset. There are a total of 81 aberrant photos with tumours among them, and 71 slices are tumor-free, normal images. Five distinct tumor forms may be seen in the aberrant brain slices, including gliomas, metastatic adenocarcinomas, bronchogenic carcinomas, meningiomas and sarcomas. Details about these two datasets are included.

Data preprocessing

Many preprocessing approaches were used before sending the photos into the proposed classifiers. For instance, the whole Figshare dataset's MRI pictures are of the in.mat type (specified in Matlab). Thus increase the image's dimension in order to read it. Then, to make the model fit into less space, each image was converted into a NumPy array using Python. To enable the model to train on unordered input, the data was shuffled before dividing the dataset. The dataset was split into three parts after rearranging the data: train and test. 30% of the data is utilised for testing, while the remaining 70% is used for training (Table 1).

The Harvard Medical dataset, however, onlycontains. GIF files for all of the MRI pictures. In the study the MRI pictures were changed to the .JPEG format in order to process the dataset. The original picture was lowered from 256 256 1 to 128 128 3 in order to decrease the dimensionality of the image. According to the pre-trained VGG16 architecture input size, the pixel intensity value was duplicated three times to produce three channels. Despite the fact that dataset 2 only contains 152 pictures, a number of data augmentation strategies were employed to address the overfitting problem, expand the dataset, and strengthen the model.

Development environment

The suggested models are put into practise using Python's Keras and Tensor Flow. The implementation was done using Google Collaborator, which offers 15 GB of free Google Drive space in addition to free online cloud storage.

Performance matrics

Several assessment measures have been employed including accuracy, precision, recall, False-Positive Rate (FPR), True Negative Rate (TNR), and F1-score, to assess the performance of "23-layers CNN" and "Fine-tuned VGG16" architectures and compare our findings with those of other research.

Results and Discussion

From the methodology developed for the proposed architecture of CNN models – “23 layer CNN model” and “fine-tuned VGG16 model” which is discussed in the previous section, the results obtained post training the models with the training dataset are discussed below.

Results obtained from 23-layers CNN architecture

The Figshare dataset used a "23 layers CNN" architecture for the prediction purpose. It was observed that 140, 270 and 180 MRI slices were correctly classified for meningioma, glioma, and pituitary tumors, respectively.

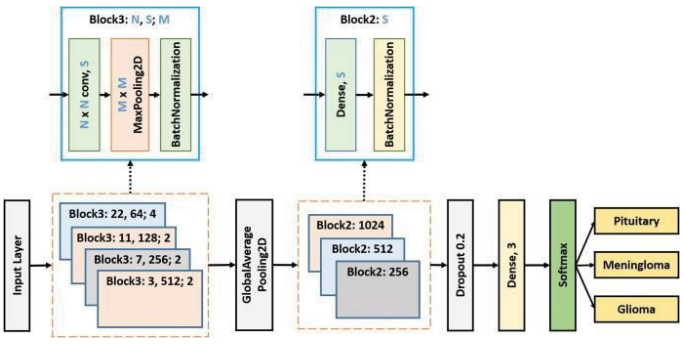

Figure 2. Proposed 23-layers CNN architecture.

Table 1. Data set 1 and 2 according to the category split.

	Category Splits	Train	Test
Data set 1	Meningioma	502	206
	Glioma	1032	394
	Pituitary	674	256
	Total	2208	856
Data set 2	Normal	357	55
	Abnormal	406	65
	Total	763	121

The other performance metrics, such asaccuracy, precision, recall, FPR (false positive rate), TNR (true negative rate) and F1-score. The prediction accuracy of 96.7%, 97.2% and 99.5% was achieved for meningioma, glioma and pituitary tumors, respectively. The overall prediction accuracy achieved on the Figshare dataset was 97.8%.

For the other performance metrics, an average precision of 96.5%, a recall of 96.4% and an F1-score of 96.4%. The False-Positive Rate (FPR) was approximately 0 and the true negative rate was close to 1, which demonstrates that the "23-layers CNN" architecture can achieve excellent efficiency on the Figshare dataset.

Confusion matrix and ROC curve for dataset 1

The ROC curve (receiver operating characteristic curve) here is showing the performance of a classification model at all classification thresholds. This curve plots two parameters: True Positive Rate and False Positive Rate

ROC curve here plots TPR *vs.* FPR at different classification thresholds. Lowering the classification threshold classifies more items as positive, thus increasing both False Positives and True Positives.

Variation of accuracy and loss for dataset 2

Depicts variation of accuracy value during training and testing process, High variation is observed with different iterations and the highest value is preferred. Depicts variation of loss value during training and testing process. low variation is observed with different iterations and the lowest value is preferred.

By achieving better than 90% accuracy, the categorical cross entropy yielded significant results. However, its performance lagged behind that of categorical cross-entropy. In addition, three activation functions were used in this study, with the softmax activation function and the sparse categorical cross-entropy loss function outperforming all other configurations with more than 97% accuracy.

To validate the developed model, a comparison of the accuracy obtained from present research and previous research has been done in the present work. It was observed that through the improvising made in this project report, the accuracy achieved is better than that of researches using the base model without modification. The proposed fine turned VGG-16 model gave 100% accuracy while the proposed CNN architecture gave 97.8% accuracy, which are in accordance to the accuracies achieved by researches with a similar methodology.

Conclusions & Future Scope

Two deep learning models (23-layer CNN and Fine-tuned CNN with VGG16) are introduced for detecting irregularities in the brain and categorising various tumour grades, such as meningioma, glioma and pituitary. The proposed 23-layer CNN architecture is made to handle a considerable quantity of image data, in contrast to the Fine-tuned CNN with VGG16 architecture, which is made to handle a smaller volume of image data. Additionally, to improve the performance of the "Fine-tuned CNN with VGG16" model, a thorough data augmentation approach is used. The computational findings show that both models improve the ability to predict the diagnosis of brain tumours. Based upon the literature survey mainly four major gaps were identified that can be worked upon for further research and implementation,

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