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Abstract— **Brain tumor can cause the creation of most aggressive cancer, with a much shorter life expectancy in most advanced stages, unless identified and treated accordingly. In earlier, radiologists have to manually identify the tumors from MRI images or other imaging types. That is both time consuming and threatening to the misclassification that could affect the recovery plan of a patient. Technological innovations and machine learning assist radiologists to detect tumors without invasive procedures. One of the machine learning algorithms that has been shown to be effective at image segmentation and classification is the convolutional neural network (CNN). In this proposed work, a novel CNN architecture was used on a publicly available figshare dataset to identify three brain tumor types. The proposed CNN architecture outperformed most state-of-the-art approaches, achieving a classification accuracy of 96.90 %. Precision, recall, and F1-score are some of the other evaluation metrics used in the study. In addition, the paper includes an in-depth analysis of misclassifications.**

Keywords— *Brain Tumor, CNN, Classification, MRI*

I. INTRODUCTION

Cancer is the second major cause of death worldwide, as per the World Health Organization. Cancer must be detected and treated as soon as possible, but this is not always possible. Unlike cancer, a tumor may be benign, pre-cancerous, or malignant. Benign tumors do not spread to other organs or tissues and can be surgically removed, whereas malignant tumors do spread to other organs [1].

Glioma, meningioma, and pituitary tumors are examples of primary brain tumors. Glioma tumors originate in tissues other than nerve cells and blood vessels. Meningiomas arise from the membranes that cover and surround the brain and central nervous system, whereas pituitary tumors are lumps inside the skull. The main difference between these three tumor types is that meningiomas are usually benign, while gliomas are almost always malignant. Pituitary tumors can cause medical problems even though this type of tumors are benign [2]. The effective identification of these three types of tumors is crucial in the clinical diagnosis and eventual patient evaluation process.

CT scans and EEGs are among the techniques used to diagnose a brain tumor, but magnetic resource imaging (MRI) is the most effective and widely used. MRI uses powerful and efficient magnetic fields and radio waves to construct internal images of the body's organs. In this work we used contrast enhanced MRI images.

The following segment provides a quick overview of related works. Section III summarizes the paper's main points and introduces the datasets used, preprocessing steps, model architecture and parameter tuning. Results using the proposed architecture, also comparison with other methods discussed in section IV. Furthermore, Section V summarizes key findings of the work.

II. PREVIOUS WORKS

Developments of new machine learning algorithm have had a huge impact on the health care area, serving as a vital support method for a wide range of healthcare services, including imaging, detection. MRI image processing for segmentation and detection using machine learning algorithms provide a new way to help radiologist with their work. A number of proposed algorithms for extracting features and brain tumors classification have been proposed in recent research.

Tahir et al. [3] investigated various preprocessing approaches in order to improve the classification results of statistical models. To test their model, they used an SVM classifier. The highest accuracy recorded is 86%. Cheng et al. [4] used three feature extraction methods on the augmented tumor area. Bag of words, gray level covariance matrix, and intensity histogram were the feature extraction methods used. Their best-reported accuracy is 91.28%. Another statistical approach, Ismael and Abdel-Qader [5] used discrete wavelet transform (DWT) to extract the statistical features from MR images. They also used Gabor filter as feature extractor. Finally these statistical features were fed to a fully connected neural network. Their neural network classifier has 270 inputs and 90 neurons in hidden layer, three neurons in output layer. They achieved 91.90% accuracy using their approach. Afshari et al. [6] fed the MR images into a default Capsule Net architecture, and achieve 86.56% accuracy on segmented tumor region and 72.13% on
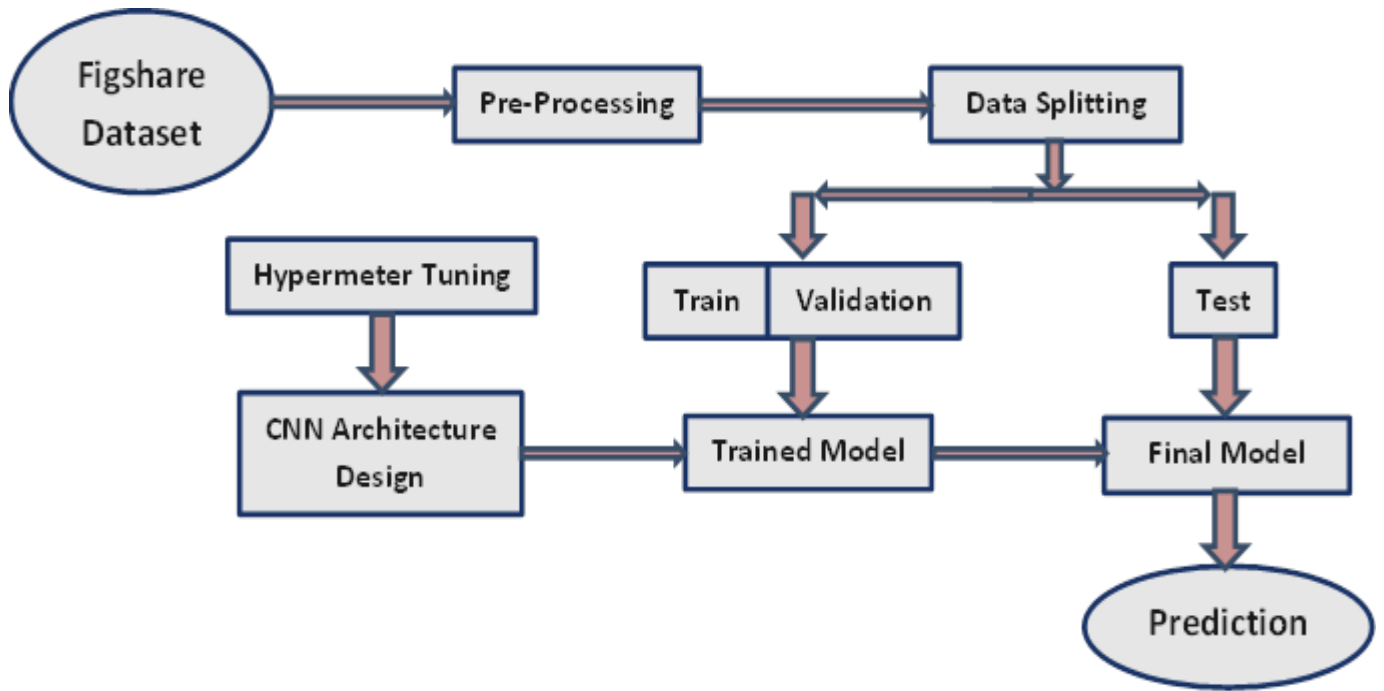
Fig. 1. Summary of Proposed Methodology

raw MRI images. They proposed another work on CapsNet [7], where they fed the Capsule Net with tumor position as well as MRI images. They reached an accuracy of 90.89%.

Another work on Capsule Net was examined by Phaye et al.[8]. They examined different Capsule Network architectures and concluded that, diverse Capsule Net reached best accuracy of 95.30%.

To automate the classification process without segmenting the tumor region, several methods have been proposed. Abiwinanda et al. [9] examined seven different Convolutional Neural Network architectures. Find that, second architecture give best performance with accuracy of 98.51% on training and 84.19% on validation. Architecture two consists of two convolutional layers, 32 filters each and 3×3 filter size, a 64 neuron dense layer. Paul et al.[10] Used three different classifier in their work. CNN, neural network and Random forest were the classifier used to classify brain images. They achieved 90.26% highest accuracy using CNN. Their proposed CNN had two 64 filter convolutional layer with filter 5×5, a Max-Pooling layer, two fully connected layer and a softmax classification layer. Each fully connected layer has 800 neurons and softmax layer have three neurons. Milica et al. [11] presents a new CNN architecture for brain tumor classification. The performance of the network was evaluated using four standard cross-validation approaches and the improvement was tested by using an augmented image database. The best reported accuracy was 96.56%.

Prior to classification, earlier approaches depended on manually delineated tumor regions. They were unable to be completely automated as a result of this. Also the automated algorithms based on CNN and its variants were unable to significantly improve results. To increase the automatic algorithm performance, a classification system is proposed that is both accurate and automated. The method was proposed to identify the three different types of brain tumors

(glioma, meningioma and pituitary tumor). A novel CNN architecture used to classify brain MRI images. The proposed framework is then subjected to a detailed investigation. When tested on the figshare dataset, the suggested approach achieve the best classification performance of all the related works.

III. METHODS

In this work, we develop Convolutional Neural Network (CNN) architecture and evaluate its performance on a publicly available figshare dataset.
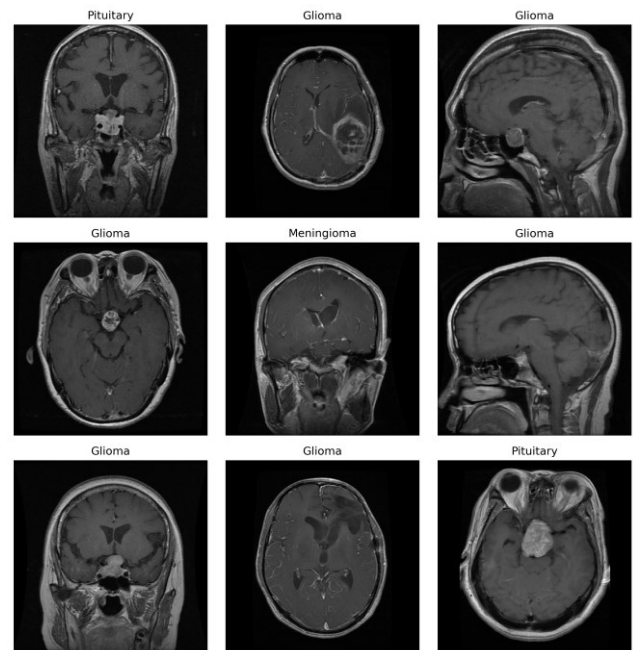

Fig. 2. Sample Images of Figshare dataset.

In the proposed method, the MR images is first preprocessed using rescale to fasten the evaluation process and reduced to pixel size. Then MR images are segmented into three separate segments; training set which is used to train a deep convolutional neural and validation set used to evaluated the model training performance whether the model is a good fit to the data. Finally the tests set were used to evaluate the trained model performance. Fig. 1 summarizes the entire method.

A. Dataset

The image dataset consists of 708 meningioma tumor images, 1426 glioma tumor images and 930 pituitary tumor images. A total of 3064 contrast enhanced T1 weighted magnetic resonance images from figshare [12] dataset. The dataset was first collected from year 2005 to 2010 in Tianjin Medical University, China. This work used the last released version of fighsare dataset in 2017 which was first made public in 2015. In Fig. 2 three types of brain tumor from figshare dataset is shown.

B. Preprocessing

Although traditional approaches require preprocessing techniques such as segmentation, Paul et al. [10] demonstrated that using deep neural networks for MR images produces the best outcomes with only normalization as preprocessing. By using the concept from Paul this work used Min-Max normalization to normalize figshare dataset and finally resized the images into 224 × 224 pixels. The dataset is then segmented into training, validation, and testing three separate segments. The training data is then used to learn the model, while the validation data is used to evaluate the model and tune the parameters. The test data is used to evaluate our model in the end. Table I showed the segmented image number for each datasets.

TABLE I.   SEGMENTED DATASET IMAGE NUMBER

Data Segments	Brain Tumor Classes		
	Glioma	*Meningioma*	*Pituitary*
Training	913	453	595
Testing	245	142	186
Validation	229	113	149

C. Proposed Convolutional Neural Network Architecture

This section explains the proposed CNN's structure and learning system for brain tumor classification. The main goal is to improve brain tumor classification accuracy. The input shape of the proposed CNN architecture is 224 × 224 × 3. Initially, a single 16-filter convolutional layer (Conv) with a filter size of 3 × 3 is used.

Then, a 32 filter convolutional layer with a filter size of 3 × 3 is added. On top of the second Conv layer a max-pooling (MaxPool) layer with 2 × 2 filter size was used to extract the image's maximum information. Then there is a 32 filter Conv layer, followed by a 2 × 2 filter size MaxPool layer. A dropout layer (Drop) of 50% dropout probability was added on top of MaxPool layer.

Then two Conv layer with 64 filters, 128 filters was added. On top of these Conv layers, a MaxPool of 2 × 2 filter and a dropout layer with a 30%, 50% dropout probability were added respectively. Each convolutional layer uses the Rectified Linear Unit (ReLU) activation function. Finally, a dense layer with 128 neurons is applied, as well as a softmax output layer with three neurons. These three neurons on softmax layer then measure the probability of each tumor type. The layout of our proposed CNN architecture is shown in Fig 3.
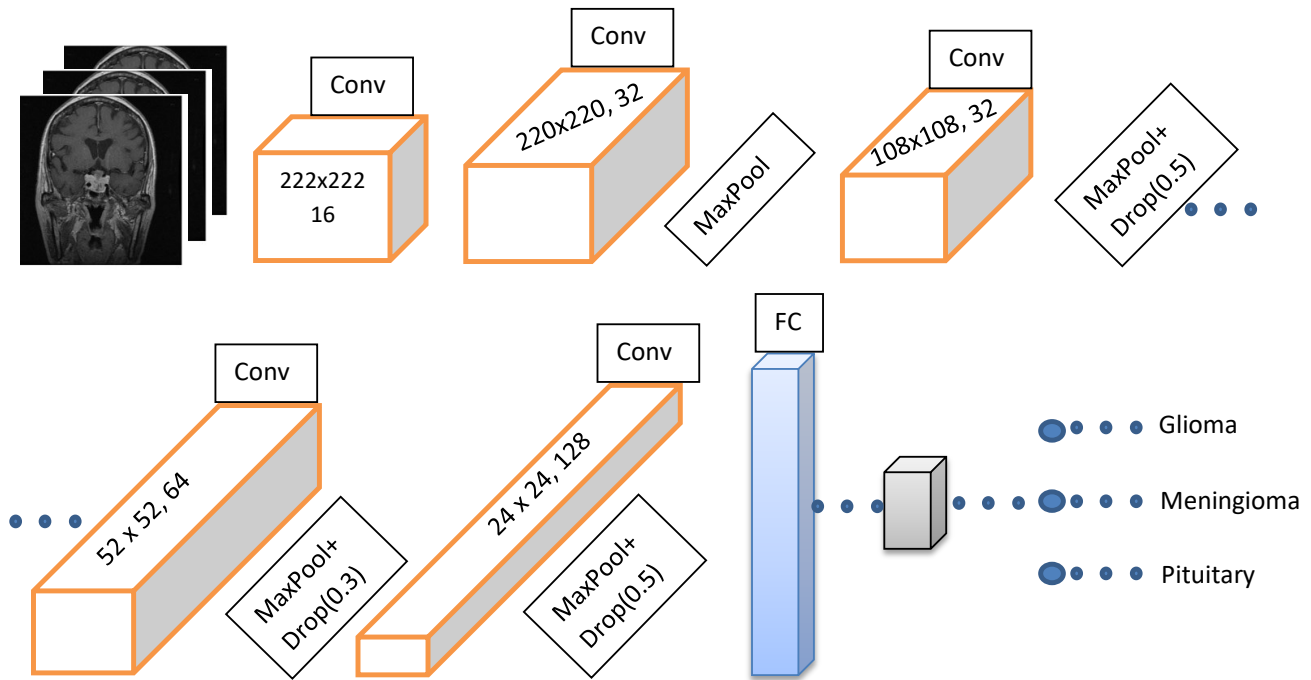

Fig. 3.   Proposed CNN model architecture

D. Hyperparameter Tuning

To tune the required hyper-parameters for model training this work used Bayesian optimization [13] technique. The aim is to find the hyper-parameters combination, which gives best performance on validation dataset using proposed CNN structure. To find best optimized output batch size is selected from three different batch sizes 32, 64 and 128. Learning rate was selected from 0.01 to 0.000001 and Adam[14], RMSprop [15] optimizers was used. After 50 evaluations on Bayesian optimization using Gaussian Processes, the best accuracy was achieved using a batch size of 32, learning rate of 0.001 with Adam optimizer. This hyper-parameter setting was used for final model training and evaluation purpose. The learning rate and accuracy of two optimizers are shown in Fig. 4.
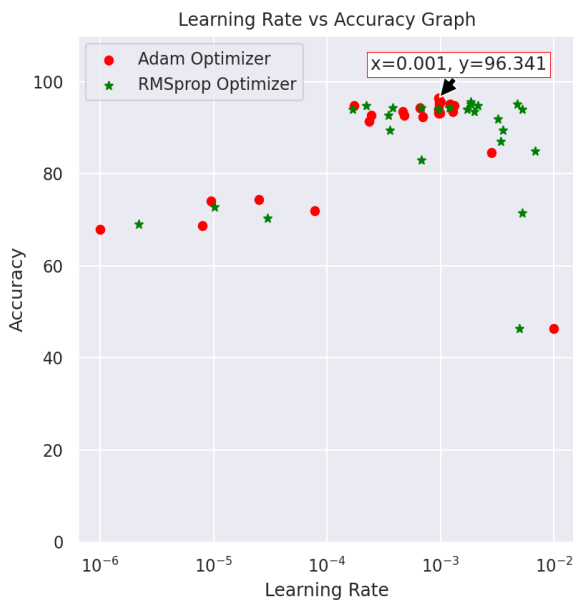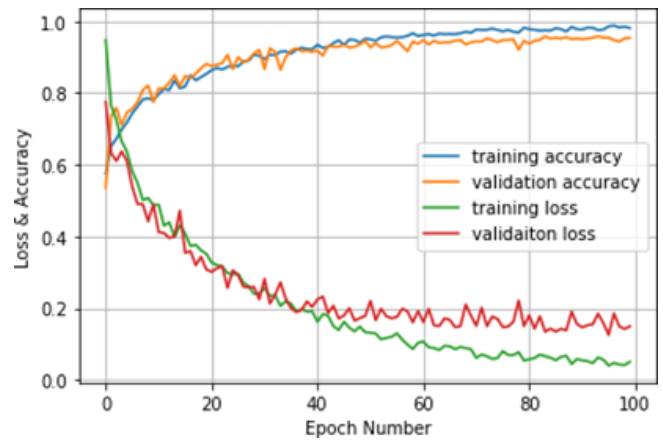

Fig. 5. Training and Validation Loss, Accuracy graph with Number of Epoch

Fig. 6 shows confusion matrices for the proposed CNN architecture. This work has testing set's classification error of 3.1%. From a total of 613 test images, the proposed architecture correctly identified 594 of them.

Fig. 4. Learning rate with accuracies for different optimizer

IV. RESULTS

This work is done using TensorFlow and Keras libraries in python on Google Colaboratory [16].

Based on Fig. 5 the accuracy of the training set and validation set tends to increase for every epoch of training which is a "good fit". Also the training loss and validation loss tends to decreasing on every epoch. Which result in a good generalization of proposed architecture.

Trained CNN model was evaluated on unseen testing data. The proposed model showed 96.90% accuracy on test dataset. Accuracy, Precision, Recall, and F1-Score also calculated for proposed CNN models. The measurement of actual true classifications is called accuracy. Precision determines the number of positive labels we predicted. The number of positive labels we correctly predicted from our data is measured by recall. The weighted mean of Recall and Precision is used to calculate the F1-Score. The performance of proposed CNN Model for different evaluation metrics is shown in Table II.
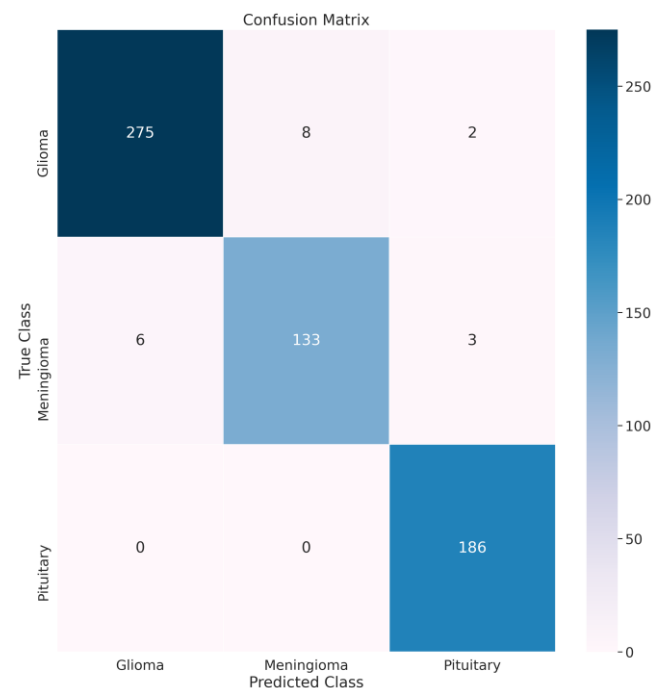

Fig. 6. Confusion Matrix of our Proposed CNN Model

Examples of misclassified tumor types from the original dataset with proposed CNN model are shown in Fig. 7. The majority of the misclassifications were found on class meningioma and glioma, as seen from Fig. 7. This is due to the fact that meningioma has fewer examples in the dataset. And no class specific augmentation is applied to reduce the class imbalance problem of the dataset.

Further investigation from Fig. 7 shows misclassification induced for gliomas tumors are examples that were rotated at an angle in the original dataset, also by the images that were vertically flipped. These problem may be solved by applying different vertical and horizontal flipping, random rotation augmentation techniques during training.

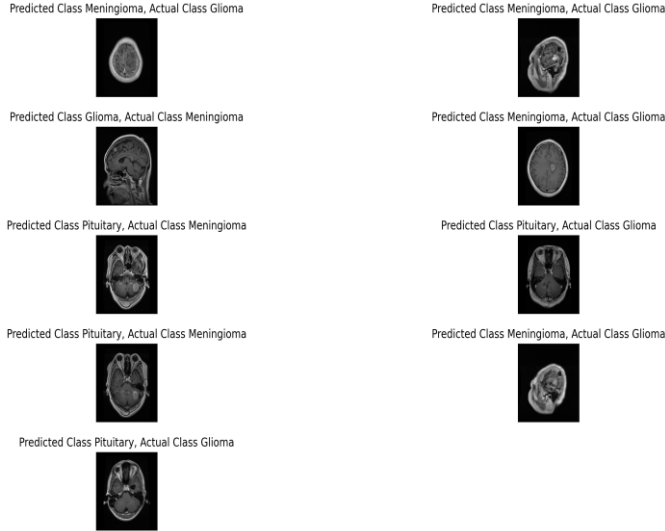|	Accuracy	Precision	Recall	F1-score	Support
Glioma	-	0.98	0.96	0.97	285
Meningioma	-	0.94	0.94	0.94	142
Pituitary	-	0.97	1.00	0.99	186
Total	0.97	0.97	0.97	0.97	613

Fig. 7.   Examples of incorrectly predicted class

Table III shows a comparison of the proposed method with other methods. All of the models mentioned used 60% to 80% of their data for training and 20% for evaluation. For comparison, this work used 70% data on training and 20% for testing. As compared to state-of-the-art approaches, the proposed approach obtained the highest accuracy of 96.90 % on this dataset while having no manual segmentation.

TABLE III.   ACCURACY COMPARISON FOR DIFFERENT METHODS ON FIGSHARE DATASET

Works	Training Data Size	Accuracy
Afshar et al.[6]	-	86.56
Sultan et al. [17]	68%	96.13
Phaye et al.[8]	-	95.03
Pashaei et al.[18]	70%	93.68
Cheng et al.[4]	80%	91.28
Ismael et al. [5]	70%	91.9
Bedza et al. [11]	60%	96.56
Proposed ConvNet	70%	**96.90**

V. CONCLUSION

A deep convolutional neural network is used in this current study to distinguish brain tumors from MR images. CNN architecture was established during the first phase of the work. Rather than manual tuning, the Bayesian Optimization algorithm was used to find hyper-parameters for.

Various assessment methods were used to assess the proposed architecture's efficiency. Proposed work achieved classification accuracies as high as 96.90%, which is better than most of state-of-the-art works on this dataset. Though proposed work gives a high performance on Pituitary type's classification but has a problem with misclassification among glioma and meningioma tumors. Further improvement can be done on this by applying class specific data augmentation and investigating other pre-trained CNN architectures.

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