Comparative Analysis on Multiclass Brain Tumor Classification Using Deep Learning Architectures

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Abstract— Abnormal growth of cells inside the skull of humans, referred to as brain tumors is time that grows within the brain or surrounds the tissue. Their presence in the brain always affects human health, though they might be benign (noncancerous) or malignant (cancerous). According to data recently provided by the WHO, brain tumors account for around 2% of all cancer diagnoses, making them a serious public health problem. Brain tumor patients frequently have a variety of symptoms, such as headaches, seizures, cognitive decline, and neurological deficiencies. In this research, we have proposed a CNN model that can classify four tumor classes i.e. glioma, meningioma, pituitary, and no tumor. The images in the dataset are grayscale, and in the preprocessing step, the dimensions of the images have been changed. Parameters like batch size, epoch, optimizer, etc., are selected properly in different approaches, and finally, the data with VGG-19, Xception, and CNN architecture is from scratch. We have found accuracies (in percent) of 97.40 (VGG19), 99.24 (Xception), and 99.00 (proposed CNN model).

Keywords— Brain tumor, Glioma, Meningioma, Pituitary, Convolutional Neural Network (CNN), Xception.

I. INTRODUCTION

The human brain (shown in Fig. 1) is an epicenter of the human body. It is dependable in executing all activities through many associations and a tremendous number of neurons. Medical images play a vital role here. Medical pictures regarding surgical arrangements are bare because they could be a significant data source for numerous illnesses. It can moreover be utilized for inquiring about and preparing purposes. The image generated by tomography of computation is essential for the initial identification along with the determination of tumors. A tumor is an unusual and rapid cell division in any organ of the human body. On the off chance that these irregular cells show up within the cells of the brain concerning the Axon, cell body, and Dendron, it is considered as a brain tumor. Considering and comparing with other noncancerous cells, brain tumor is a deadly disease. Essential and auxiliary are prime subclasses of this type of tumor, and metastatic is the most horrifying tumor caused by irregular cells' shift to the brain [1]. Most brain tumors have an unknown specific source. However, some risk factors, such as radiation of ionized particle exposure, a previous history of having brain tumors of a member of the family, some genetic disorders, and sporadically some environmental exposures, might raise the possibility of causing tumors in the brain [2]

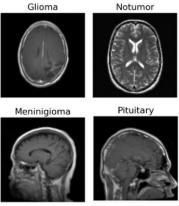


Fig. 1. Sample image

The kind of brain tumor, where it's located, and the individual's general condition all influence the treatment option [3]. A team of medical experts, such as radiation therapists, oncologists, and neurosurgeons, are frequently consulted when creating treatment plans [4]. The circumstances surrounding the class of malignancy, its stage, the patient's gender, age, and their general state of health, the outlook regarding brain tumors might vary greatly [5]. While certain tumors in brain are amenable to successful management or treatment, others may provide greater challenges [6]. Early identification and rapid treatment can improve the likelihood of survival for patients suffering from brain tumors [7]. In the following five years, 771,110 individuals with CNS (central nervous system) malignant tumors will be documented worldwide.

Recurrent brain tumors form 1.7% of all cancers and have a worldwide incidence of 3.9 per 100,000 person-years for all neurological tumors [8]. Age, gender, color, and geography affect this occurrence differently; Northern Europe has the highest prevalence, followed by Australia, the US, and Canada [9].

Synthetic neurons or many layers of interconnected nodes are used in deep learning (DL) to analyze and learn from input in an approach similar to the human cerebral cortex. It is dubbed "deep" learning because deep artificial neural networks have several layers and can automatically learn and extract features from unprocessed data. DL helps classify brain tumors for the following reasons [10].

Brain tumors can be classified into primary and secondary types, even though recognized within the brain and stem from other body regions [11]. The driving force behind this

research is the labor-intensive and skill-dependent preparation of tumor determination using medical imaging. Experts like radiologists carefully look at images from CT scans, MRI scans, and positron outflow tomography checks, shaping the premise for ensuing treatment proposals. This burdening preparation regularly ranges a few hours, underscoring the requirement for automation to assist the discovery solution. [12]

Brain tumors are characterized by unregulated and irregular cell multiplication inside the brain, leading to deadly results if they are not instantly recognized. The dangerous nature of certain tumors requires their early discovery to anticipate farreaching intrusion inside the brain. [13] Several studies have been proposed, and diverse automated frameworks have been created for identifying and classifying brain tumors utilizing MR pictures. In this research, we have taken datasets combined of Figshare, Sartaj, and Br35H. Difficulties have been faced while researching to trade off with image dimension. If the dimension is so big, the calculation while creating the model will be increased and if the image is too small, it won't be a robust model. Besides, to find a proper combination of layers that will increase the accuracy. The key contributions of this research are as follows:

- i. Development of an innovative Xception-based DL model incorporating extensive architecture reconfiguration, and fine-tuning for effective brain tumor classification.
- ii. Integration of extensive layers to the architecture reconfiguration, aimed at enhancing model generalizability and robustness, while mitigating overfitting issues commonly encountered in deep learning models.
- ii. Integration of additional layers into the reconfiguration architecture, tailored to capture intricate features relevant to brain tumors, thereby enhancing the performance of the deep learning model on tumor classification.

II. LITERATURE REVIEW

Our 1 goal is to improve the location of brain tumors by applying two division strategies: edge-based segmentation and region-based division. This section offers a selection of state-of-the-art DL-based brain tumor categorization methods. Brain tumors can be classified using a variety of methods based on exchange learning and DL calculations. The three categories of state-of-the-art procedures are machine learning, hybrid learning, and profound learning. summarizes many approaches to brain tumor classification. Arunkumar et al. [14] recommended an automotive procedure for segmenting and identifying brain tumors utilizing counterfeit neural systems (ANN). The demonstration accomplished a precision of 94.07%, a sensitivity of 90.09%, and a specificity of 96.78%.

In their analysis, Gopal S. Tandel et al. [15] classify tumors over numerous classes utilizing Fake Insights standards utilizing CNN (Convolutional Neural Arrange) on MRI Images. Their exploration found that fetch learning-based AI utilizing CNN appears to be 12.12% raised over ML. Coinciding with this analysis, DL (Profound Learning) is much better in terms of execution than ML (Machine Learning).

Malathi and Sinthia [16] utilized convolutional neural organize (CNN) innovation for brain tumor segmentation. They connected the TensorFlow bundle to execute complex scientific operations on high-quality glioma data obtained from the BRATS 2015 dataset. In her research, Priyanka Pareek [17] gives a detailed study counting points of interest,

almost all steps included in brain tumor segmentation and classification.

Taher et al. proposed a CNN model that can classify tumor images 99.46% accurately. Besides, they also implemented some pre-trained models i.e. VGG-19, Resnet-50, Xception. [18]. They also performed segmentation with an attention mechanism where their model achieved 90% accuracy. Hussen et al. proposed a hybrid machine-learning model that reached 99.17% accuracy with a region-based random forest [19].

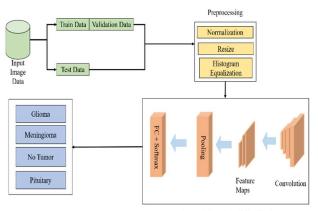
In order to classify meningiomas, gliomas, and pituitary tumors—three different forms of brain tumors—Belaaid et al. [20] presented a DL methodology that used the pre-trained VGG-16 CNNs. The research employed gray-level cooccurrence matrix (GLCM) feature pictures along with the original photos as CNN inputs. On the T1-weighted CEMRI dataset, the method of using both the original and energy pictures as inputs performed much better than current classifiers, with an average accuracy of 96.5%. The research made significant contributions to the integration of CNN and GLCM features to improve accuracy, the modification of the VGG-16 model for training, and the mining of GLCM feature data from the source images. CNNBCN, a novel CNN architecture for the images of tumor inside the brain categorization in the domain of medical sonology and imaging, was created by Huang et al. [21]. With a classification accuracy of 95.49%, our model outperformed several other models in the environment. It also demonstrated a less test loss when compared to popular architectures like MobileNet, ResNet, and DenseNet. Their research demonstrated CNNBCN's benefits for improving medical imaging evaluation methods. They improved the accuracy of the CNNBCN model by 0.5% to 0.75% by incorporating different activation functions, demonstrating the model's efficacy and its potential to equal or even outperform manually constructed models with less intervention.

A CNN-SVM-based method was put up by Sejuti et al. [22] in an effort to increase the precision of cerebral tumor categorization. In the beginning a 19-layer CNN with sequential normalization and ReLU activation functions was built. This CNN was subsequently utilized to the T1-weighted CE-MRI dataset, which consisted of 3,064 pictures from three different tumor types. Softmax's first classification produced a high training accuracy of 96.74%, which was then increased to 97.1% by using a multiple classes support vector machine (SVM) that made use of CNN-extracted features. This method stood out for requiring very little input data preparation. Subsequent studies could investigate different classifiers and preprocessing techniques and compare their efficacy with the Support Vector Machine (SVM). Swati et al. discussed the difficulty of using limited datasets in DL for medical imaging, namely in brain tumor classification [23]. In their work, a pretrained deep CNN model was employed, and a block-wise transfer learning-based fine-tuning technique was presented. Using five-fold cross-validation, they evaluated their method on a T1-weighted CE-MRI benchmark dataset and obtained an excellent average accuracy of 94.82%. This generic method eliminated the requirement for minimal preprocessing and hand-crafted features. Their comparison analysis demonstrated the method's superiority over conventional deep learning models when applied to the CEMRI dataset, demonstrating the applicability of natural image processing knowledge to medical brain magnetic resonance imaging.

TABLE I. COMPARISON OF PREVIOUS WORKS

Author	Method	Accuracy	Dataset
Dey et	ANFIS	94.51%	ISLES and
al.[24]	classifier		BraTs
Amin et	SVM	97.01%	Harvard,
al.[25]			Rider, a
			local
			dataset
Kumar et	Hyb-DCNN-	97.28%,	BraTs
al.[26]	ResNet 152	94.31%,	
	TL	95.48%	
Aziz et	ResNet50,	87.8%,	BraTs
al.[27]	Densenet201	84.6%	
Our	CNN	99.24%	Figshare,
proposed			SURTAJ
Model			Dataset,
			BR35H[28]

III. METHODOLOGY



Feature Extraction and Classification

Fig. 2. Overview of the framework

A. Overview of the framework

Initially, the images have been resized to 168 by 168. Then the dataset is split into the sub-dateset for training, testing, and for the validation purpose. After that, the data is trained with a CNN model. Finally, we have found a model to perform the task of classification and the overview is presented in Fig. 2.

B. Dataset Description

This dataset amalgamates three distinct datasets: Figshare, Br35H, and the SARTAJ dataset [28]. It comprises a total number of 7023 computed tomographical images of the brain of human, into four types of images: meningioma, glioma, no tumor, and pituitary. The images belonging to the "no tumor" class tare collected from the Br35H dataset. Notably, there appears to be an issue with the categorization of glioma class images within the SARTAJ dataset. This observation surfaced through examining results from various sources and the outcomes of diverse models I trained. Consequently, I opted to discard the images within this category from the SARTAJ dataset and instead utilized images resourced from the Figshare repository. The division of the data for the training set is portrayed in Fig. 3

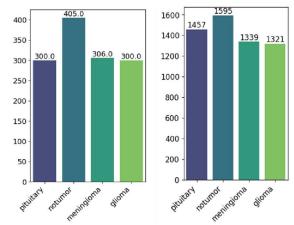


Fig. 3. Distribution of the dataset - train image count (on the left) and test image count (on the right)

C. C. Preprocessing

Image dimension: Understanding the correct method of resizing images is crucial due to their varied sizes. When enlarging an image, its pixels are adjusted, potentially leading to the removal of redundant pixels to decrease its size. However, enlarging may cause pixelation or blurriness. Thus, downsizing is preferable as smaller images load faster. Therefore, all images are standardized to 168 by 168 pixels and converted to grayscale to ensure consistency and efficient loading.

D. D. Feature Extraction and Classification

For classification, the Softmax activation function is used in the output layer that produces the probability distribution of the four classes based on the extracted features of the previous step.

Scratch model: A CNN (Convolutional Neural Network) model can perform well on a brain MRI image dataset consisting of 7023 images split into train, test, and validation sets. CNNs are adept at automatically learning hierarchical features from images, making them suitable for tasks like tumor detection or disease classification. With appropriate architecture design and training, a CNN model can effectively extract relevant features from brain MRI images and achieve robust performance across classification, segmentation, or detection tasks.

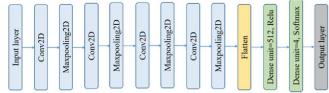


Fig. 4. CNN model architecture

The neural network architecture comprises a series of convolutional (Conv2D) layers followed by max-pooling layers (MaxPooling2D), repeated multiple times. These layers are pivotal for feature extraction, where Conv2D applies filters to the input data to detect patterns, while MaxPooling2D downsamples the feature maps, retaining important information and reducing computational complexity. Subsequently, the flattened layer reshapes the output from the convolutional layers into a one-dimensional vector. This vector is then fed into a fully connected Dense layer with 512 neurons activated by the Rectified Linear Unit (ReLU) function, facilitating complex pattern recognition. Finally, another Dense layer with four neurons and a softmax

activation function outputs the probabilities of the input F. B. Model Performance Analysis belonging to each of the four classes.

VGG-19: The VGG-19 pre-trained model, renowned for its simplicity and effectiveness, can perform admirably on brain MRI image datasets. With 7025 images segmented into train, test, and validation sets, VGG-19's deep architecture can effectively capture intricate features, enabling accurate classification or segmentation tasks. Its straightforward design and pre-trained weights make it a solid choice for such data, providing reliable performance in tasks like tumor detection, disease diagnosis, or anatomical segmentation. However, due to its complexity, VGG19 demands more computational resources and training time compared to alternatives.

Xception: The Xception pre-trained model, known for its depth and efficiency, generally performs well on tasks like brain MRI image classification due to its ability to capture intricate features. With 7023 images split into train, test, and validation sets, Xception's sophisticated architecture can effectively learn representations from the data, leading to strong performance in tasks such as segmentation, tumor detection, or disease classification, making it a suitable choice for such datasets. Through this approach, Xception strikes a harmonious equilibrium between precision and efficiency by minimizing parameters and computations. Demonstrating promising results across diverse tasks of computer vision, such as image classification, object detection, and image segmentation, Xception emerges as a favored pre-trained model, frequently employed for transfer learning in various applications of computer vision.

IV. RESULT ANALYSIS

A. A. Evaluation Metrics

An assessment metric is a metric used to evaluate a machine learning model or system's efficacy or performance. It gives a platform for comparing various models or techniques and quantifies the model's performance. The definition of these measures is as follows:

Accuracy: The ratio of cases that were successfully classified to all instances in the dataset.

B.
$$Accuracy = \frac{TN + TP}{TN + TP + FN + FP}$$
 (1)

Recall (Sensitivity): The model's ability to catch positive occurrences is measured by the ratio of true positive predictions to the total number of actual positive examples.

C.
$$Recall = \frac{TP}{TP + FN}$$
 (2)

F1 Score: The harmonic mean of precision and recall, providing a balanced measure of the model's performance.

D.
$$Recall = \frac{2 * \frac{Precision*Recall}{Precision+Recall}}{(3)}$$

Precision: The ratio of accurate positive predictions to the total number of optimistic predictions, indicating the model's ability to correctly identify positive instances.

$$E. \ Precision = \frac{TP}{TP + FP}$$
 (4)

Confusion Matrix: A confusion matrix offers insights into the model's performance and aids in comprehending the many kinds of errors the model makes. When working with unbalanced datasets or when the prices of several error kinds vary, it is especially helpful. TP, FP, TN, and FN refer to true positive, false positive, true negative, and false negative.

Custom CNN Architecture: We have run a total of 50 Epochs to perform training. To evaluate our model, we compiled it with ADAM optimizer, and the accuracy found is 90.00%. The confusion matrix is shown in Fig. 6, and the model loss and accuracy is shown in Fig. 5.

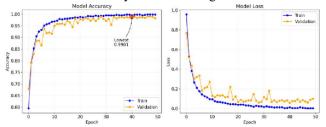


Fig. 5. (a) Model loss) and (b) accuracy graph (custom CNN)

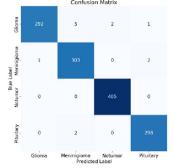


Fig. 6. Confusion matrix of custom CNN model

VGG-19: The overall accuracy for the VGG-19 pretrained model was 97.40% with 20 epochs. A total number of 17 images are misclassified. The confusion matrix is projected in Fig. 8 and model loss and accuracy are shown in Fig., 7.

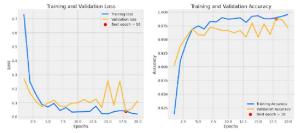


Fig. 7. Model accuracy & loss graph (VGG-19)

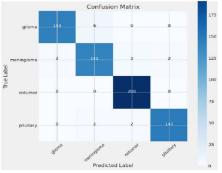


Fig. 8. Confusion matrix of VGG-19

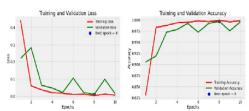


Fig. 9. Model accuracy & loss graph (Xception)

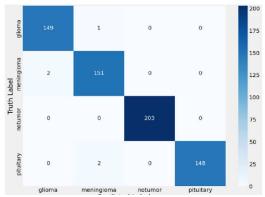


Fig. 10. Confusion matrix of Xception

Xception: The Xception model is designed to be computationally efficient while maintaining strong performance. It achieves this through a novel approach called depthwise separable convolutions. This technique separates the spatial convolution and the Results and Discussions 35 channel-wise convolution, reducing the number of computations required. As a result, the Xception model typically has fewer parameters and is more computationally efficient compared to other CNN architectures with similar performance. In multiclass classification, the model achieved an accuracy of about 99.24% with 10 epochs, F1 score. The figures for model loss and accuracy are shown in Fig. 9 and Fig. 10 shows the confusion matrix. Classification report of Xception is shown in Table 1 and comparison of accuracy is shown in Table II.

TABLE II. CLASSIFICATION REPORT (XCEPTION)

Class Name	Precision	Recall	F1 score	Support
Gliom	0.99	0.99	0.99	150
Meningioma	0.98	0.99	0.98	153
No tumor	1.00	1.00	1.00	203
Pituitary	1.00	0.99	0.99	150
Accuracy			0.99	656
Micro Avg	0.99	0.99	0.99	656
Weighted Avg	0.99	0.99	0.99	656

TABLE III. COMPARISON OF ACCURACY

Model	Accuracy	Dataset
CNN model	99.00%	Figshare, Sartaj, Br35H
VGG-19	97.40%	Figshare, Sartaj, Br35H
Xception	99.24%	Figshare, Sartaj, Br35H

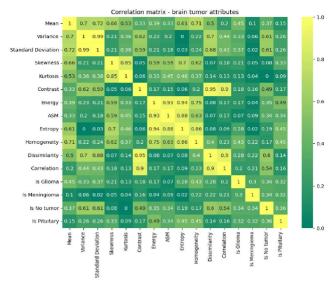


Fig. 11. Correlation matrix

The figure above, fig. 11, shows the correlation matrix. From the figure, we can observe the impact of homogeneity, mean, variance, dissimilarity, entropy, etc., on the four classes of brain tumors (Glioma, Meningioma, Pituitary, no cancer) clearly. From these parameters, we have learned the pattern of the features of the images, and helped us to choose a better CNN architecture to classify properly.

High Correlations Within Tumor Types: Glioma, Meningioma, and Pituitary Tumor: These three tumor types show strong positive correlations with each other. This suggests that they share similar characteristics or are closely related in terms of their attributes.

Negative Correlation with "No Tumor": All Attributes: Most of the attributes (Mean, Variance, Standard Deviation, Skewness, Kurtosis, Contrast, Energy, ASM, Entropy, Homogeneity, Dissimilarity, Correlation) have a negative correlation with "No Tumor." This indicates that these attributes are more likely to be associated with the presence of a tumor rather than its absence.

Relationships between Attributes: Energy and ASM: These two attributes have a strong positive correlation, suggesting that they are closely related.

Entropy and Homogeneity: These two attributes also have a strong positive correlation, suggesting a close relationship. Dissimilarity and "No Tumor": Dissimilarity has a relatively strong negative correlation with "No Tumor," indicating that it might be a useful feature for distinguishing between tumor and non-tumor cases.

Based on the correlations observed, we can infer some potential factors that might contribute to the differentiation between the three tumor types (Glioma, Meningioma, and Pituitary Tumor):

Mean, Variance, and Standard Deviation: These attributes likely relate to the overall intensity or distribution of certain signals or features within the tumor region. Differences in these attributes might help distinguish between tumor types. Skewness and Kurtosis: These attributes measure the shape of the distribution of values. Deviations from a normal distribution might indicate specific characteristics of each tumor type.

Contrast, Energy, ASM, Entropy, Homogeneity, and Dissimilarity: These attributes likely relate to the texture or pattern of the tumor region. Differences in these features might help differentiate between tumor types.

V. CONCLUSION

In this research, we have had a study through a merged dataset of MRI images of the human brain and have tried to find a machine-learning model that can properly predict the type of brain cancer. During the research, we have preprocessed the image data, and trained it through machine learning approaches and finally, we have found the best accuracy in the Xception pre-trained model with 99.24% accuracy. Other pre-trained models also performed well but Xception outnumber the accuracy. Further, more image data should be included and other noise (if available) should be removed to find a further accurate model that will classify brain cancer. In addition, more classes of images also can be included.

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716