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An Efficient Scientific Programming Technique for MRI Classification using Deep Residual Networks



Abstract: - Classifying brain tumors is crucial for both diagnosing and treating patients with these diseases. Imaging techniques of many kinds are used to detect brain cancers. In contrast, MRI is frequently used because to its superior picture quality and the fact that it does not require ionizing radiation. Recently, the subfield of machine learning known as deep learning has shown especially promising results in the areas of classification and segmentation. To identify the various tumor types seen in the brain, we trained a deep residual network using imaging datasets. There will be a tremendous amount of information generated from the MRI images. It is the radiologist's job to look at these images. Meningiomas, pituitary tumours, and gliomas are the three most prevalent forms of brain tumours. Because of the complexity of brain tumors, a physical inspection might lead to mistakes. Classification methods that use machine learning to automate the process have shown to be superior to human curation every time. Therefore, we developed a CNN-based deep residual network-based detection and classification system.

Keywords: Brain Tumor Classification, Convolutional Networks, Image Recognition, Artificial Neural Network

I. INTRODUCTION

The term "brain tumor" refers to any growth or mass of abnormal cells in the brain. There are many kinds of brain tumors. Some brain tumors are cancerous, while others are not (malignant). Tumors of the brain may originate anywhere in the human body and spread to the brain, although most often they begin in the brain (metastatic). Three common brain tumor types are a) Meningioma: For more than 30 percent of all primary brain tumors, meningioma reigns supreme. The meninges are the three layers of tissue that surround and protect the brain directly beneath the skull, and they are the site of genesis for meningiomas. b) Pituitary Adenoma: The most common pituitary tumor is an adenoma, which develops from gland tissue. Adenomas of the pituitary gland are slow-growing tumors that originate in that gland. Adenomas account for around 10% of primary brain tumor diagnoses. Issues with eyesight and the endocrine system are possible side effects. c) Craniopharyngioma: These benign growths may take the form of either solid tumors or cysts and develop in the area close to the pituitary gland.

An increase in CSF fluid pressure may lead to elevated intracranial pressure. What you see there is cerebrospinal fluid, which protects your brain and spinal cord. One possible cause of elevated ICP is a rise in the pressure inside the brain. A mass (such as a tumor), bleeding into or fluid surrounding the brain, or swelling inside the brain may all lead to this condition. Brain injury following a cardiac arrest. Types of imaging techniques are the following a) **X-rays:** One of the most accessible forms of diagnostic imaging is the X-ray (also known as a radiograph). Even if further, more extensive testing is necessary, an x-ray will generally be the first test conducted. B) **Computed Tomography (CT):** A computed tomography (CT) scan is a kind of imaging that uses a combination of x-rays and computers to create an enhanced cross-sectional picture of your body. C) **Magnetic Resonance Imaging (MRI):** Magnetic resonance imaging (MRI) is a diagnostic imaging technique that, like ultrasound, produces cross-sectional images of the body. D) **Biopsy:** A tissue or cell sample is taken from the patient and analysed in a lab via a process known as a biopsy. MRI segmentation is critical in brain tumour treatment because it allows for precise surgical planning while minimising injury to healthy tissue. It optimises radiation and chemotherapy delivery for improved outcomes by tailoring personalised therapies. It also helps track therapy progress and ensures treatments are successful. MRI segmentation, in essence, improves total brain tumour management by enhancing patient care and results.

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What we call "machine learning" is the field of study that demonstrates how machines may learn to do tasks normally performed by humans without any human input. To select features, RELIEF is often used. RELIEF prioritizes features based on their degree of dissimilarity to those of the nearest neighbor pair. This method made great strides when used to learning feature weights in kernel spaces. This method is often used as a separate data processing step from creating a classifier. We have learned a subspace-parameterized Taylor series kernel expansion for SVM-based classification that makes noise-pixels less crucial. When users are guided through the categorization of their data files by your data classification software, this is known as automated classification.

Deep learning is an additional subgroup of machine learning, the operation of which has the highest possible connection with the way the human brain operates. The structure of artificial neural networks is identical to that of neuronal networks in the human brain. A configuration of numerous layers of nonlinear processing identities is used by DL algorithms throughout the feature extraction procedure. As we go further into the network, the output of each layer will eventually become the input of the layer that follows it, which will help with the abstraction of data. The Convolutional Neural Network, often known as CNN, is a sort of deep learning (DL) technology that is frequently used to evaluate visual pictures even though it requires very little pre-processing of the data. It is designed to cope with data that is presented in several different arrays, and it is modelled after natural processes that take place in the human brain. Convolutional Layer, Pooling Layer, and Fully Connected Layer are the individual components that make up a convolutional neural network. Most of the feature detection work done by CNNs is done in the network's central convolutional layer. Two-dimensional convolution layers (often abbreviated as conv2D) are widely used in practice. In a convolutional 2D layer, a filter or kernel has both a height and a width. The fully connected layer (FC) has a simplified input structure in which all inputs are coupled to all output neurons. These are used to optimize class scores and are often placed at the network's output layer, connecting the network's hidden layers.

After a significant amount of time had passed, the use of a model known as deep convolutional neural network for the categorization of photographs (ImageNet LSVRC-2010) became more widespread (AlexNet). When compared to the other network models available at the time, AlexNet performs very well and has an error rate of 16.4%. After then, its accomplishments served as a catalyst for a series of subsequent breakthroughs for CNNs in deep learning. In 2015, The ZF Net model was unveiled, and when employed on the Image Net dataset, the error was decreased to 11.7 percent. It has better performance than Alex Net in terms of hyperparameters. Later, a new model was introduced, which is known as VGG Net model, which decreased the error to 7.3 percent. VGG models made further increase in the accuracy. Visual Geometry Group is a popular large Convolutional Neural Network (CNN) (VGG) architecture. To be more specific, the "deep" in VGG-16 and VGG-19 refers to the 16 and 19 convolutional layers. The discipline of object identification is making rapid strides thanks to models built on the VGG architecture. ResNet50 and Inception have better accuracy but require more computation. The major benefit of CNNs is that that are extremely good in feature selection which makes them much better than any conventional ML algorithms. CNN models can be made more robust and highly accurate by increasing the input dataset. Convolutional filters serve as extracting the important features in CNN architecture, and when we go deeper, we extract more and more complicated features, and the network's complexity increases.

From the very beginning of the 2000s forward, researchers have been trying to find a solution to solve the issue of brain tumors via the use of computational algorithms to lessen the burden on humans and improve patient care. In their publication, C. C. Leung et al. [1] suggested a unique method to identify borders of brain tumors, including the small edges, with the use of General Fuzzy Operator (GFO), with the goal of minimizing the errors introduced by the previously utilized regional-based approaches. Near the end of the same decade, in 2007, J. J. Corso et al. [2] introduced a novel approach for detecting and segmenting brain tumors and edoema in multichannel magnetic resonance volumes. S. Bauer et al. [3] offered another research that employed multiscale modelling for image analysis of brain tumors and found promising results for atlas-based tumor segmentation and growth prediction. In addition, the Markov-Random-Filled Lesion development model and atlas registration presented by S. Bauer, L. Nolte, and M. Reyes [4] provide yet another approach to brain tumor segmentation. However, over time we can see that Deep Learning models provide a faster and convenient method over diagnosis of medical illnesses and ever since the decade after 2010. The Perturbation Based and backpropagation-based methods provides the faster and convenient method over diagnosis of medical illnesses. The output of an AI model may be easily examined by means of perturbation to determine the impact of altering the input characteristics whereas backpropagation-based techniques use a single forward and backward transit across the network to determine who is responsible for each of the input characteristics. There implementation started in other useful domains of medical background like knee cartilage

segmentation for evaluation of osteoarthritis [5], liver segmentation and detection of lesions using CNN (Convolutional Neural Networks) [6], mass detection in digital breast tomosynthesis using CNN [7] [8] [9] [10] to name a few.

The rest of the paper is organised as follows: Section 2 comprises a review of the literature, the third section describes the methodology and strategies used in this research, Section 4 contains the results of the research and following comments, and the fifth section is a brief summary.

II. LITERATURE REVIEW

Serial no.	Title of the paper	Dataset used	Methodology used	Limitation of the study
1.	Segmenting Brain Tumors from MRI Using Cascaded Multi-modal V-Nets [24]	BraTS dataset is used. Additional datasets also used.	Utilizes four levels of encoding and decoding paths. Two sides of V-net are used for shrinking size and finding image division.	Low results for testing set due to large population size. Also, for higher threshold values, small clusters will be discarded
2.	Brain Tumor Classification Using Convolutional Neural Network [25]	Works on brain tumor dataset of 3064 T-1 weighted freely available MRI images	Trained a CNN to recognize and classify three common brain tumor types: Glioma, Meningioma, and Pituitary.	The trained CNN architecture could achieve an accuracy of 84.19% due to overfitting of data.
3.	GLCM Textural Features for Brain Tumor Classification [26]	Uses four unique brain tumor MR images. Samples obtained from Whole Brain Atlas	Makes use of GLCM to characterize texture of images in MATLAB. Uses two-layer feed forward network for classification	An error of 2.5% is encountered for images of class III and IV while class I and II images are correctly classified.
4.	Brain tumor classification based on long echo proton MRS signals [27]	Makes use of about 200 stratified random samples	Performs comparative analysis of classification methods like LDA, SVM, LS- SVM with linear kernel vs LS- SVM with radial bias function.	Automated binary classifiers couldn't classify glioblastomas vs metastases. LDA and kernel-based methods performed equally for long echo H MRS data.
5.	Application of Edge Detection for Brain Tumor Detection [28]	Multiple datasets are used	Noise removal on acquired MR images using linear, non-linear filters followed by enhancement. Converts grey to binary. Lastly edge detection based on morphological operators.	Accuracy at each step is highly dependent on the results obtained in previous steps.

6.	Automated Brain Tumor Detection and Identification Using Image Processing and Probabilistic Neural Network Techniques [29]	Uses 64 grayscale MRI database	Uses modified PNN model based on LVQ focused on ROI segmentation. Further extract, select and classify features.	The execution and processing time can be further reduced in the future.
7.	DeepMedic for Brain Tumor Segmentation [30]	Uses BRATS 2015 dataset	Makes use of DeepMedic 3D CNN model with addition of residual networks. It comprises of eleven layers.	Gives high performance for the impact of residual networks but with low precision.
8.	Brain tumor segmentation based on a hybrid clustering technique [34]	Uses DICOM, Brain Web data set and BRATS Multimodal dataset	Uses a combination of K-means clustering and Fuzzy C-means for segmentation of outliers in abnormal MR images	Provides good results for bandwidth lower than 0.2 and threshold of 5. Mean shift is not accurate in all cases.
9.	A deep learning model integrating FCNNs and CRFs for brain tumor segmentation [35]	Uses Multimodal BRATS 2013,2015 and 2016.	Combines FCNN and CRF. Train DL model with 2D image patches for different views of brain.	Suits well for Segmentation model with Flair, T1c, and T2 scans.
10.	3D MRI brain tumor segmentation using autoencoder regularization [36]	Multimodal BRATS 2018 3D MRI dataset (285 cases)	Based on CNN encoder-decoder architecture with addition of auto-encoder branch. Uses VAE for clustering.	Training of model is time consuming. Takes about 2 days for training 300 epochs.

As discussed above that Deep Learning models gained their thrust upon the research realm in medical domain to solve real-life problems [11] [12], it was clear that they can be used for detection of brain tumor. Many researches have been carried out since the advent of DL models and each has given a more efficient, quicker and better result.

In the study provided by D.M. Joshi, N. K. Rana and V. M. Mishra [13], they developed a real-time computer application that accepted MRI images of brain and detected tumor blocks or lesions to classify the type of tumor using Artificial Neural Networks (ANN). Electroencephalograms (EEGs) are rapidly gaining popularity as a reliable method of gauging brain activity, with enormous promise for the analysis and treatment of neurological and psychological disorders. To begin, the EEG signal is subjected to adaptive filtering to get rid of any artefacts. The next step involves using spectral estimation to draw out common characteristics of the EEG data. In another study by Murugesan and R. Sukanesh [14], a novel method of detecting brain tumors in EEG (Electroencephalograms) signals via ANN was proposed and it achieved an accuracy of 94.47% for the normal reports and 98.76% for the abnormal reports. Another study proposed by H. N. Abdallah and M. A. Habtr [15] suggested a method of brain tumor extraction that implied methods of edge detection, feature extraction and ANN modes for classification of tumors into normal, benign and malignant categories which achieved an astonishing accuracy of 96.96% with a specificity of 95.83%. Research by V. Chen and S. Ruan [16] present a graph cut application that segments regions of MRI images to determine brain tumor and also portrayed a visual 3d surface rendering of the segmented tumor to help the radiologist diagnose better. G. Mirajkar and B. Barbadekar [17] in their paper proposed an automatic brain tumor segmentation method that utilized UDWT (Undecimated Wavelet Transform) and Gabor Wavelets for

capturing tumor characteristics which then pass their results to k-means clustering that finally produces the final segmented output.

Virupakshappa and B. Amarapur [18] went even farther by proposing a fully automated method for identifying brain tumors using an ANN classifier that used both clustering and multiple feature extraction through Gabor wavelets. When segmenting enhanced MR images into clusters based on intensities, M. Kadkhodaei et al. [19] proposed a novel approach for automated segmentation and classification of brain tumor pictures using 3D super-voxels. T. Chithambaram and K. Perumal [20] suggested a hybrid of the mathematical algorithms Support Vector Machine (SVM) and Artificial Neural Network (ANN) in their study, with GA-SVM classifying tumours and GA-ANN computing confirmation accuracy. Using the same dataset, N. -E. -J. Moutoshi and K. Tara found that CNN outperformed ANN and SVM for categorising normal and tumor-affected brain pictures. R. Vinoth and C. Venkatesh [22] conducted their own investigation using CNN and SVM.

The spatial grey level dependency matrices (SGLDs) of pictures were used in research by H. E. M. Abdalla and M. Y. Esmail [23] for feature extraction, and supervised ANN learning was used for image categorization into tumor and non-tumor, with an accuracy of 99%. Segmentation and classification of Brain tumors have been performed in the articles using conventional techniques and algorithms developed at the time. In this study, the most recent Residual Network is employed for brain tumour segmentation, and the particulars of the research and its findings, that may aid in the medical detection of brain tumours using MRI images, will be discussed in the following portions of the paper.

The field of detecting brain tumors has seen a lot of advancements recently. [37] With this study, we'll be focusing on the input channel for T2 magnetic resonance images. The segmentation process consists of three steps: (1) identifying abnormal brain regions; (2) assessing the extent of edoema and how it relates to the tumor; and (3) imposing geometric restrictions. [38] Another valuable addition uses a deep learning and convolutional neural network (CNN) based method (DeepLabv3+). The picture is divided into tiny pieces using this method. The tumor is identified using 18 different models. Subsections may be found in a wide variety of orders. Bit packing is then used to combine the outputs. The final Dice coefficient for the whole tumor is 0.8755.

The authors of a recent research [41] used Probabilistic Neural Networks to advance a novel approach to brain tumor categorization. Extraction of picture characteristics and PNN were used for categorization. When compared to other neural networks, PNN classifier produces faster and more accurate results. K-means clustering, a color-based segmentation algorithm, has been studied [42] for its potential to track tumors in MR images. The goal is to use K-means and histogram clustering techniques to transform the black and white photos into a color scheme, from which the location of the brain tumor may be extracted. This technique is a novel approach to determining the lesion's extent and location. Another study [43] takes a DNN-based method to designing a tumor segmentation architecture. The architecture employs a multi-layered approach to categorization, with a total of seven levels. CNN, ReLU, and SoftMax are all rolled into one layer here. DNN labels the images based on the center pixels obtained on subdivision of the original image. This model has been tested on an extensive range of data ranging from BRATS 2012- 2015, ISLES 2015 and 2017

III. METHODOLOGY

A. Paper Selection

Scopus and Web of Science indexed articles published between 2013 and 2021 are surveyed for our investigation. Algorithm 1 depicts the procedure that was followed to choose the appropriate literature. Table 2 also details the criteria for which papers are accepted and rejected.

TABLE 1: Inclusion and exclusion criteria for paper selection

IC	EC
IC1: Paper must be peer reviewed.	EC1: Duplicate studies in different databases
IC2: Journals on which papers published must be either scopus or web of science indexed	EC2: MSc and PhD papers
	EC3: Case study papers

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procedure TOPIC (Brain Tumor Classification)
  SearchDatabases ← IEEEXplore, GoogleScholar, ScienceDirect
  SearchYear ← 201-2021.
  i ← 1
  N ← 5
  Initialize counter
  N is the Number of search databases
  for i ≤ N do
    keyword ← braintumorclassification, image recognition, convolutionalnetworks, machinelearning
    if SearchLink ∈ SearchDatabases and Year ∈ SearchYear then
      Search (Brain-Tumor Classification AND Image-Recognition AND machinelearning)
    end if
  end for

  if NumberofPapers ≥ 0 then
    Refine Papers
    ApplyInclusionCriteria ← IC1, IC2
    ApplyExclusionCriteria ← EC1, EC2, EC3
  end if
end procedure

```

B. Dataset

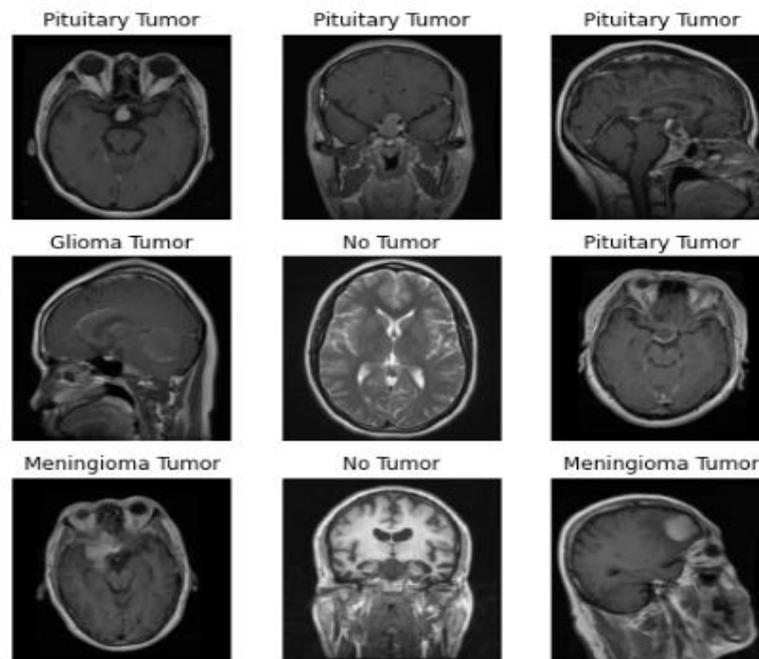


Figure 1. Sneek Peek at the Dataset

The dataset on which we did our work consists of there are three forms of brain tumors. MRI images: I) Glioma Tumor, II) Meningioma Tumor, III) Pituitary Tumor, and the dataset also consists of MRI scans of the brain in normal condition. The dataset was first split into two folders: Train and Test. The train folder consists of 826 image files of Glioma tumor, 822 image files of Meningioma tumor, 827 image files of pituitary tumor and 395 image files of Normal Brain. Similarly, the test folder consists of 100 images of Glioma Tumor, 115 image files of Meningioma tumor, 74 image files of pituitary tumor and 105 image files of brain with no tumor. In total the dataset consists of 3264 image files [42][43][44].

C. Data Manipulation

Firstly, the image dataset was loaded to the machine using the Kaggle API call and then the respective labels were provided to the image datasets. ‘0’ for ‘Glioma Tumor’, ‘1’ for ‘Meningioma Tumor’, ‘2’ for ‘No Tumor’ and lastly ‘3’ for ‘Pituitary Tumor’. After that, the pictures were converted to grayscale and scaled to (256, 256) pixels in

order to shorten the training time. Then, we used Random Horizontal turn with a probability of flipping the photo by 50%. This was done to include some bias in the dataset, to make sure that our design does not overfit the dataset. Lastly, all the pictures are stabilized as well as transformed to tensors for faster tensor calculation. Each pixel in a picture is converted into a tensor along with its location in the image during the tensorization process. We may use this data for model training and other purposes once we have transformed these tensors. Image manipulation options include mirroring, scaling, cropping, and rotation [45][46][47].

D. Model Architecture

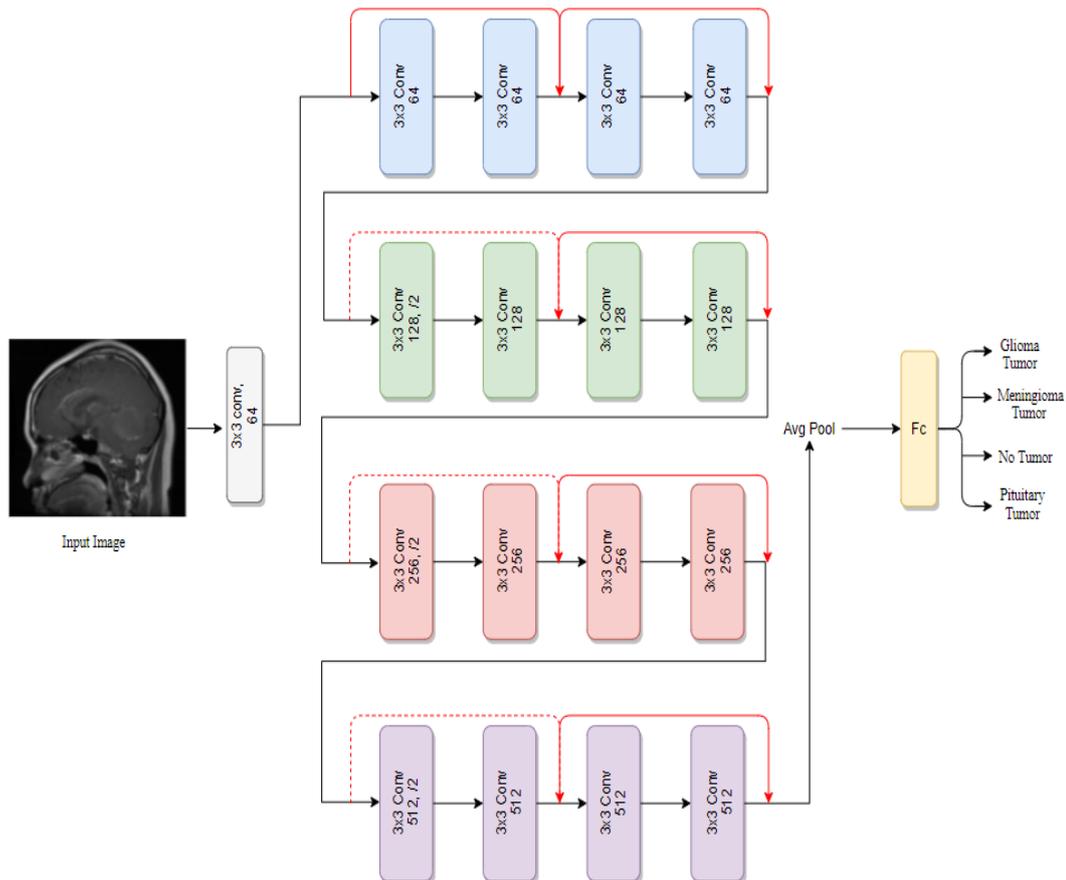


Figure 2. Proposed Network Architecture

As a first step in writing our article, we developed a ResNet model. Instead of learning from unreferenced functions, Residual Networks (ResNets) learn residual functions by referencing the inputs to each layer. Instead, than assuming that each of the many stacked layers exactly matches a desired underlying mapping, residual nets enable these layers to be tailored to a residual mapping. With the assistance of the objective mapping method, one can identify their business, performance, and learning objectives, as well as map those goals out. The act of labelling data is called data labelling. For a machine learning model to understand what sorts of predictions it should make, that model must have those kinds of predictions labelled inside its training data (or data annotation). This is a key phase in the process of making data suitable for supervised machine learning, which is a procedure that uses machine learning. Residue blocks are stacked atop one another to form these structures. While these networks are useful for solving a variety of issues, their effectiveness quickly declines as their depth grows, creating a degradation problem. In the worst case, a shallow network can stand in for a much deeper design's early stages while the remaining layers serve as an identity function. However, in the best case, the additional layers of a much deeper network better match the mapping than their shallower counterparts, leading to a significant reduction in error.

ResNet's designs range widely; some examples are ResNet18, ResNet34, ResNet50, and many more. The numbers indicate layers, even if the layout remains the same. The 18-layer ResNet model was employed in this study. At the heart of these networks is a convolutional layer with a 7x7 filter, followed by 16 convolutional layers with a 3x3

filter size, and then, after some average pooling and dense-layer-and-activation-function processing, the network's output is fed into a SoftMax activation function.

- Model's Forward Propagation

$$a^l := g(W^{l-1,l}.a^{l-1} + b^l + W^{l-2,l}.a^{l-2}) \quad \dots (1)$$

$$\Delta a^l := g(Z^l + W^{l-2,l}.a^{l-2}) \quad \dots (2)$$

here,

a^l = activations of neurons in layer l

g = activation function for layer l

$W^{l-1,l}$ = weight matrix for neurons between layer $l - 1$ and l

$W^{l-2,l}$ = weight matrix for neurons between layer $l - 2$ and l

$$Z^l = W^{l-1,l}.a^{l-1} + b^l$$

- Model's Back Propagation

$$\Delta\omega^{l-1,l} := -\eta \frac{\delta E^l}{\delta\omega^{l-1,l}} \quad \dots (3)$$

$$\Delta\omega^{l-1,l} = -\eta\alpha^{l-1}.\delta^l \quad \dots (4)$$

$$\omega^{l-2,l} := -\eta \frac{\delta E^l}{\delta\omega^{l-2,l}} \quad \dots (5)$$

$$\Delta\omega^{l-2,l} = -\eta\alpha^{l-2}.\delta^l \quad \dots (6)$$

here,

η = learning rate ($\eta < 0$)

a^l = neuron activations in layer l

δ^l = neuron error signal at layer l

$\Delta\omega^{(l-1,l)}$ = change in weight matrix between neurons between layer $l - 1$ and l

$\Delta\omega^{(l-2,l)}$ = change in weight matrix between neurons between layer $l - 2$ and l

E. Model Optimizer and LR scheduler

In the current paper, we have utilized AdamW optimizer which is stochastic optimization method which is a modified implementation of weight decay in Adam. In general execution of Adam optimizer, the weight degeneration is unconditionally bound to the knowing rate which means if we are enhancing the discovering price, we would additionally need to locate a new weight degeneration for each and every of the discovering rate that we are going to attempt. In AdamW optimizer decoupling of weight degeneration takes place that implies the weight decay as well as learning rate can be enhanced independently, i.e., they do not affect the other. This causes enhanced simplification efficiency.

$$w_t = w_{t-1} - \eta \frac{m_t}{\sqrt{v_t + \epsilon}} \quad \dots (7)$$

$$w_{t+1} = (1 - \lambda)w_t - \eta \nabla f_t(w_t) \quad \dots (8)$$

$$w_t = w_{t-1} - \eta \left(\frac{m_t}{\sqrt{v_t} + \epsilon} + \lambda w_{t-1} \right) \quad \dots (9)$$

$$\dots (10)$$

here,

w_t = weight decay at time 't'

η = learning rate or step size at time t

m_t = aggregate of gradients at time t (bias corrected)

v_t = sum of square of past gradients (bias corrected)

ϵ = small positive constant to avoid 'division by 0' error when $v_t=0$

In addition, we utilised Lambda's Learning Rate Scheduling, which is used to manage the rate of learning during training by raising or reducing the learning rate based to a predetermined timeframe. In Pytorch's Lamba lr scheduler, every parameter's learning rate was adjusted by multiplying the starting training rate with an individual function at the beginning of each epoch. This makes it simple to change the function that is needed to correspond with the model's output.

$$lr_{epoch} = lr_{initial} * \text{Lambda}(epoch) \quad \dots (11)$$

IV. RESULT AND EVALUATION

A. Evaluation Metric

Some of the measures we utilised to gauge the success of our model are detailed below:

- Precision:

Precision is a performance metric that is utilised to information obtained from an isolated source [26]. It is a ratio of the number of precisely predicted positive observations to the total number of projected positive values observed. Thus, precision indicates how accurate our model is when employing projected values (i.e., positives), as well as how many of those are true positives.

$$\text{Precision} = \frac{\text{True Positive}}{\text{Total Predicted Positives}} \quad \dots (12)$$

Here, the sum of the true positives and the false positives is the overall number of positives projected. In the event of a tumor, this is crucial information. All tumor cells must be removed during brain surgery to prevent the cancer from returning. Here, accuracy is thus much improved.

- Recall:

Recall is another performance statistic that is used for the data that is retrieved. It is additionally referred to as sensitivity and is defined as a percentage of correct projected positive numbers compared to total actual positive values [27]. As a result, recall calculates the overall amount of actual positives captured by the model[44].

$$\text{Recall} = \frac{\text{True Positive}}{\text{Total Actual Positives}} \quad \dots (13)$$

Here, total real positives include both correct and incorrect results. This becomes relevant when malignant and healthy brain cells coexist in the same area of the brain. Keeping the healthy cells undamaged is essential for proper brain function, thus only the aberrant ones should be removed. In this case, recall improves but accuracy worsens. Relevance is the foundation for both recall and accuracy.

- F1-Score:

It's a metric for determining the test's precision. The F1 score is a weighted average of recall and precision. It is more effective as compared to accuracy [28] as well as functions well even with unequal distribution since it attempts to strike an equilibrium among recall and precision.

$$F1\ Score = 2 \times \frac{(Precision \times Recall)}{(Precision + Recall)} \dots (14)$$

B. Loss Function

Loss functions are basically used to optimize the model during training. Most often, the goal is to minimize the loss. For our paper, we have used Categorical Cross Entropy loss function which is also known as logarithmic loss. Cross Entropy is similar to SoftMax function and is used to evaluate the performance of a classification model specifically for those whose values lies between the range of 0 and 1. It is basically an error detection function. If the predicted probability deviates from the actual value, then the cross-entropy loss increases.

C. Results



Figure 3. Training Confusion Matrix

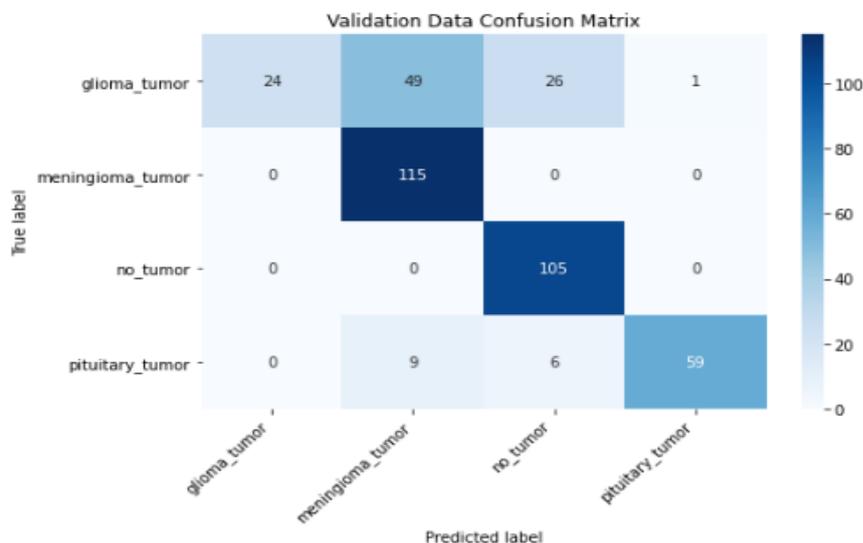


Figure 4. Validation Confusion Matrix

We usually repeat this process many times, assessing and validating the acceptance of the established technique each time by tweaking the model's hyperparameters. There are new results to be obtained every time. The best answer is shown in this paper. Our suggested model's efficacy is shown by the produced confusion matrices for the training and validation datasets.

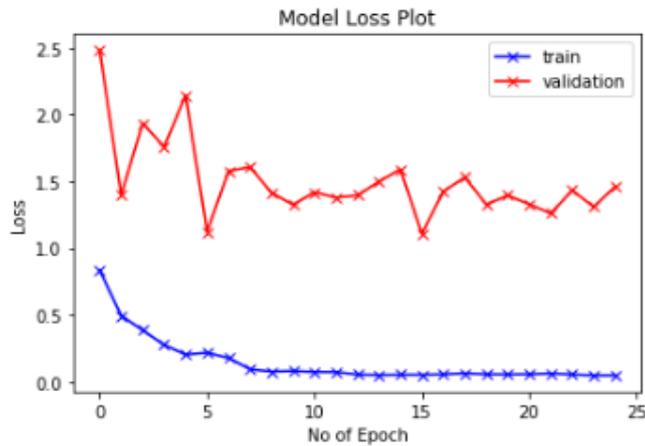


Figure 5. Model Loss Plot

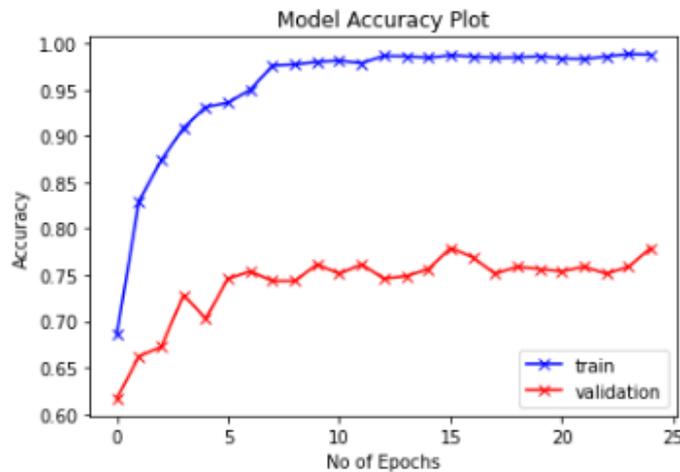


Figure 6. Model Accuracy Plot

When compared to other types of neural networks, Deep Neural Networks are exceptionally resistant to environmental variability and noise. The model is also able to learn complicated data patterns because to the model's multiple hidden layers. In the validation dataset, the above figures show that the model has achieved its highest and lowest levels of accuracy and validation loss after 15 epochs. Since 15 epochs is enough time to train a model, we may terminate the training loop early to save computational resources. Furthermore, the capacity to customise the model's hyperparameters results in a very domain-specific model, which resulted in a 98% accuracy rate on the training dataset and a 78.85% success rate on the validation dataset in the case of brain tumour classification.

Table 2: Training Evaluation Report

	Precision	Recall	F-1 Score	Support
Glioma Tumor	0.99	1	0.99	826
Meningioma Tumor	1	1	1	822
No Tumor	1	1	1	395

Pituitary Tumor	1	1	1	827
Accuracy			1	2870

Table 3: Validation Evaluation Report

	Precision	Recall	F-1 Score	Support
Glioma Tumor	0.24	1	0.38	100
Meningioma Tumor	1	0.7	0.82	115
No Tumor	1	0.8	0.88	105
Pituitary Tumor	0.79	0.98	0.87	74
Accuracy			0.78	394

Table 2 and 3 can be served as the base for the information retrieval for analyzing the performance of our CNN based Deep Neural Network for the task of brain tumor classification. From the table 2, we can see that the precision score for glioma tumor came out to be 0.99 and 1.00 respectively for other tumors in the training dataset whereas the recall came out to be 1.00 for all tumors and the accuracy which we have obtained in the training set is came out to be 1.00.

From the table 3, we can see that the precision score for glioma and pituitary tumor came out to be 0.24 and 0.79 respectively and 1.00 for other tumors in the validation dataset. The recall lies between 0.70 to 1.00 for all the tumors and the validation accuracy came out to be 0.78 which are highly respectable results considering that brain tumors are much more difficult to classify.

To evaluate the model's performance keeping in mind the precision and recall trade-off, the F1 score was evaluated which gives the harmonic mean of precision and recall values. F1 score for the proposed model is 1.00 for all the tumors int the training dataset and 0.38, 0.78 for glioma and pituitary tumor and lies between 0.80 to 0.90 for the remaining tumors in the validation dataset.

V. CONCLUSION AND FUTURE WORKS

Researchers have merged cancer simulation and medical imaging tools with the aim of simulating the growth of malignancies. This method for modifying a standard brain atlas for use with MR scans taken of people with tumors. To create an association among a reference atlas and a pathological clinical image, tumour development models must be used in conjunction with registration techniques. As the first stage of our process, we employ an entirely novel multi-scale, multi-physics model to model the growth of the tumour in the atlas, beginning at the level of cells and working our way up to the biomechanical level, where we can account things like cell proliferation and tissue deformations. This model allows us to replicate the tumor's growth from the cellular to the biomechanical levels. Because it is possible to execute computations based on finite elements using a eulerian approach directly on the voxel mesh of an image, it is an option that is ideal for dealing with large-scale deformations. After that, a method known as non-rigid registration is used to provide a close match between the patient's photo and the updated atlas.

Brain tumors are a deadly illness because they consist of a group of aberrant cells clumped together. Any kind of development within the skull is dangerous because of how small it is. The brain tumors may or may not be malignant. Eventually, the pressure within a person's skull will rise to the point where it will damage the brain and make it impossible for them to carry out even the most fundamental of tasks, guaranteeing their untimely demise. There are 4 steps to it. Because damaged cells still superficially resemble normal ones, the first and second phases are exceedingly modest and difficult to identify. Those cells have a distinctly aberrant appearance as the process advances from one stage to the next.

A precise and accurate diagnosis of the brain tumor may still prove challenging. Imaging tests and biopsies are the main tools for diagnosis. The size and location of a tumor may be determined via imaging. CAT/CT scans and MRIs are the most frequently used diagnostic imaging techniques (computed tomography). These tests might not be highly

accurate, but they can detect subtle changes which provides more intel to the doctors/scientists. MRI focuses on high precision method so as to create sharp and better results. Slightest of movements could cause problems and result in a blurred image. MRI uses radio waves, powerful magnets, and sometimes, cannot differentiate between cancer tissue and excessive fluid. CT scan on the other hand uses X-rays to create multiple images. The amount of radiation, a person is exposed to is huge. CAT/CT scans don't produce accurate details like MRI and fail to capture many details, which might be crucial. High precision methods might be inaccurate. Achieving very high accuracy and precision simultaneously is ideal and not possible. Therefore, it would be quite useful in clinical trials to develop this model. As a result, we trained a deep neural network using a convolutional neural network to analyze MRI scans of brain tumors and sort them into four distinct categories. This CNN model first reduces the file size of reconstructed MRI scans of the patient's frontal lobe and determines whether the tumor is a glioma, meningioma, or pituitary. Rather of relying on outdated clinical trials, healthcare organizations will use this robust model instead.

Declarations Conflict of interest

We, the authors of this manuscript have no conflicts of interest to disclose.

Human participants and/or animals

We, the authors ensure that no human or animal participation is involved in this research.

Informed consent

We haven't used human participation or other personal information, informed consent is not required.

Data Availability

The data that support the findings of this study are openly available.

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