MRI Brain Images Mapping for Tumour Detection Using CNN

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Abstract

Brain tumor is a serious life-threatening disease which occurs due to peculiar growth of cells or tissues present in brain. In recent times it is becoming a considerable cause of death of many people. The seriousness of this tumor growing in brain is very huge when compared to all other varieties of cancers and tumors. Hence, to save the affected people detection of the tumor and proper treatment should be done instantaneously without any delay. In this new age of technology, Machine Learning (ML) and Deep Learning (DL) models can be utilized to identify the tumor at early stages more precisely so that proper medication can be given to the affected person which will help in curing them. This paper proposes two different machine learning models to identify the brain tumor by analysing the Magnetic Resonance Image (MRI) scans of the brain. Both unsupervised and supervised learning models were implemented to detect the tumors in brain. Fuzzy C means is used as a part of unsupervised learning model, it is a data clustering algorithm in which entire data set is grouped into predefined number of clusters with every data point belonging to every cluster to a specific degree of membership value. In this approach tumor region is treated as one cluster and healthy brain is another cluster. Moving forward, as a part of supervised learning, transfer learning approach is implemented for classifying whether the given input MRI scan consists of tumor or not. Visual Geometric Group (VGG-19) model was used which is a 19-layer deep pre-trained neural network architecture for better accuracy and results. All the models were developed using python in jupyter notebook.

Keywords: Brain Tumor, Fuzzy C means, Jupyter notebook, MRI, VGG-19

1. Introduction

An accumulation of aberrant brain cells is known as a brain tumour. When normal cells experience alterations to their DNA (mutations), primary brain tumours start to form. The instructions for what a cell should perform are encoded in its DNA. When healthy cells would stop dividing and dying, the mutations instruct the cells to proliferate and multiply quickly. A tumour is created as a result from a mass of aberrant cells. Adults who have primary brain tumours are considerably less likely to get secondary brain tumours, which develop after disease has progressed from one organ to another [1]. Brain tumours can take many distinct forms. Some benign (noncancerous) brain tumours and some malignant (cancerous) brain tumours exist (malignant). Your brain may develop a primary brain tumour if this is the case [2].

1.1 Brain Tumor Causes

Some genes on a cell's chromosomes are thought to become damaged and cease to function correctly when brain tumours develop. These genes often control how quickly a cell divides (if at all), repair genes that correct other genes' flaws, and genes that should trigger the cell to self-destruct if the damage is too great to be repaired. In some circumstances, a person may be born with one or more of these genes partially defective. Environmental factors could then cause more harm. Other times, the damage to the DNA caused by the environment might be the only factor. It is unclear why some persons in a particular "environment" have brain tumours while others don't. When a cell begins to divide quickly and the internal controls that regulate its growth are compromised, the cell may eventually develop into a tumour.

The immune system of the body, which ideally would recognise the aberrant cell and eliminate it, might be another line of defence. It's possible for tumours to create chemicals that prevent the immune system from identifying the abnormal tumour cells, ultimately overcoming all internal and external inhibitors of their growth.

1.2 Types of Tumors

1.2.1Gliomas

These tumours, which include astrocytomas, ependymomas, oligoastrocytomas, and oligodendrogliomas, start in the brain or spinal cord.

1.2.2 Meningiomas

A tumour called a meningioma develops from the membranes that cover your brain and spinal cord (meninges). Meningiomas are typically not malignant.

1.2.3 Acoustic neuromas (schwannomas)

These benign tumours grow on the nerves that transmit hearing and balancing information from the inner ear to the brain.

1.2.4 Pituitary Adenomas

At the base of the brain, in the pituitary gland, these tumours grow. The pituitary hormones are impacted by these tumours, and this has an impact on the entire body.

1.2.5 Medulloblastomas

Although they can happen to anyone at any age, these malignant brain tumours tend to arise in children. A medulloblastoma typically spreads through the spinal fluid and begins in the lower back region of the brain.

1.2.6 Germ cell tumors

Children may get germ cell tumours where the ovaries or testicles may eventually grow. However, germ cell cancers can occasionally spread to other organs, such the brain.

1.2.7 Craniopharyngiomas

These uncommon tumours originate close to the pituitary gland, which secretes hormones that regulate numerous bodily processes. The pituitary gland and other tissues close to the brain may be impacted when the craniopharyngioma gradually expands.

As per the discussion of different types of brain tumours in above, it is essential to propose methods to detect brain tumours in early-stage detection. In this paper, two methods are implemented, and results are tested. Firstly, Fuzzy C means-based clustering algorithm [3] is used to determine whether the given image consists of tumour or not based on the similarity of different data pixels of the segmented image. In the second algorithm, a pre-trained convolution neural network (CNN) [4] model is used to classify the tumour images and predict whether the image is of a healthy brain or an affected brain. The CNN are a special type of deep neural network whose structure is inspired by biology of cat's vision cortex.

2. Literature Survey

There are many methods that have been proposed to solve these challenging problems on image classification, which can be categorized into two types of methods: traditional methods and deep model methods. In this section, we will first give a detailed introduction to the previous work on image classification for brain tumour detection.

2.1 SPECT

A variant of random forests on single photon emission computed tomography (SPECT) [5] image classification to help diagnose Alzheimer's disease (AD). First, they extracted score features using partial least squares from the image datasets to structure the random forests. Using this system as a classifier helped to classify all the images. The specific process is to classify the image to the closest centroid recessively until reaching a leaf of a single tree, which is the classification of the image. The most important characteristic of this algorithm is that it can extend from the previous model, a process referred as to incremental learning, without retraining the images from scratch.

2.2 Fourier Transform

A classifier that is based on a fractional Fourier transform and nonparallel support vector machine to classify magnetic resonance brain images into pathological brain image and healthy brain image categories. Thus, it was a binary classification task. For a given image, the system first used a weighted-type fractional Fourier transform to extract the spectrum features, and then, it utilized principal component analysis to reduce the dimensionality of the spectrum features [6]. Finally, its incorporated spectrum features were fed into support vector machines. However, in this paper, the dataset that contains 90 T2-weighted MR brain images is relatively small. Although it has obtained good performance. It is not adapted to a larger dataset.

2.3 ImageNet

A CNN trained by ImageNet to identify different types of abnormalities in magnetic resonance brain images. They achieved the best accuracy performance by combining the features extracted from a CNN and handcrafted features [7].

2.4 DT-CNNS

A method that combined domain-transferred convolutional neural networks (DT-CNNS) [8] with a sparse spatial pyramid (SSP) to classify medical images. In this paper, they used VGG19 (19 layers CNN) proposed by as the transferred network, which could ignore the medical image characteristics. However, this approach provided a new train of thought to solve this problem. All the above algorithms have some problems in that they used transferred convolutional neural networks or directly employed traditional method to classify the medical images. In traditional methods, regardless of which features (color features, texture features, or shape features) are used, it is not adequate to classify the medical images solely by those features that are gained through experience. For deep models, the transfer-learning network finds it very easy to ignore the characteristics of medical images. In addition, most of the literature about medical image classification is on binary classification. In practice, we usually need to perform a multiclass classification task. To solve these problems and improve the performance of medical image classification, we present our new algorithm. Currently wide research is going on the brain tumour detection using CNN in so many countries in the worldwide shown in the below Figure 1. The following country names are USA, Brazil, Peru, Germany, UK, France, Spain, Switzerland, Italy, India, Uganda and South Africa.

2. Proposed Algorithm

2.1 Fuzzy C – Means

Fuzzy C-means (FCM) is a method of clustering data into a specified number of clusters. It is similar to the k-means algorithm but allows for "fuzzy" membership of data points to multiple clusters, rather than requiring a strict assignment to one cluster. This is done by introducing a "fuzzy membership" value for each data point, indicating the degree to which it belongs to each cluster. The algorithm iteratively updates the cluster centroids and the fuzzy membership values until convergence. FCM is useful in situations where data points may belong to multiple clusters, or where the number of clusters is not known a priori.

2.1.1 Membership function

The membership function in Fuzzy C-Means (FCM) algorithm is used to determine the degree of membership of a data point to each cluster which is shown in Figure 2. It is defined as a continuous function that maps each data point to a value between 0 and 1, where 1 represents full membership and 0 represents no membership.

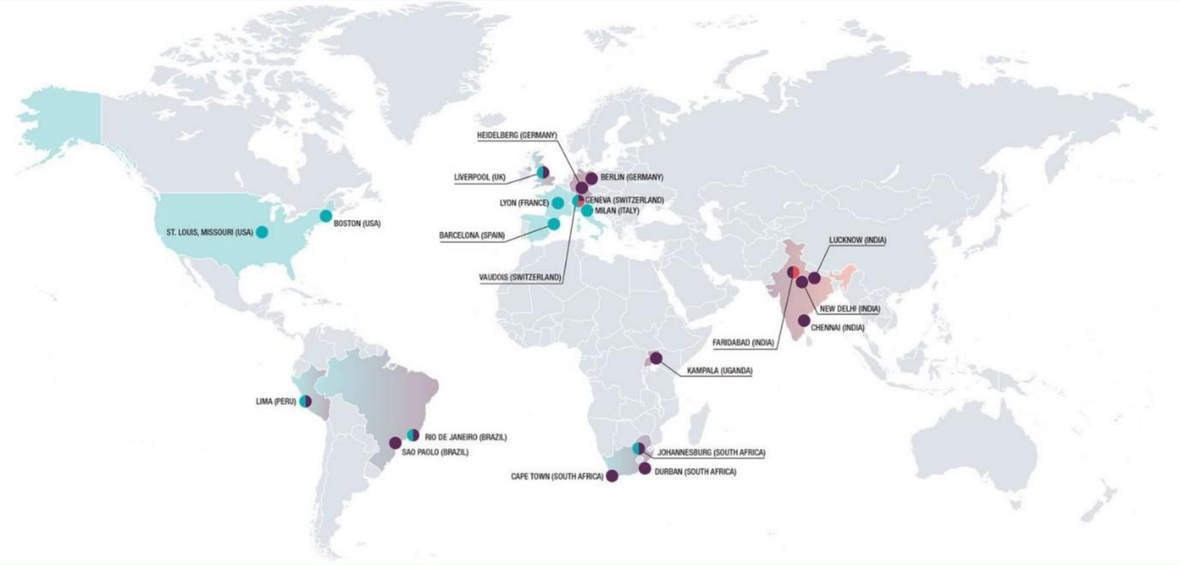

Figure 1: World map showing different countries in the world doing research currently on brain tumour detection [9]

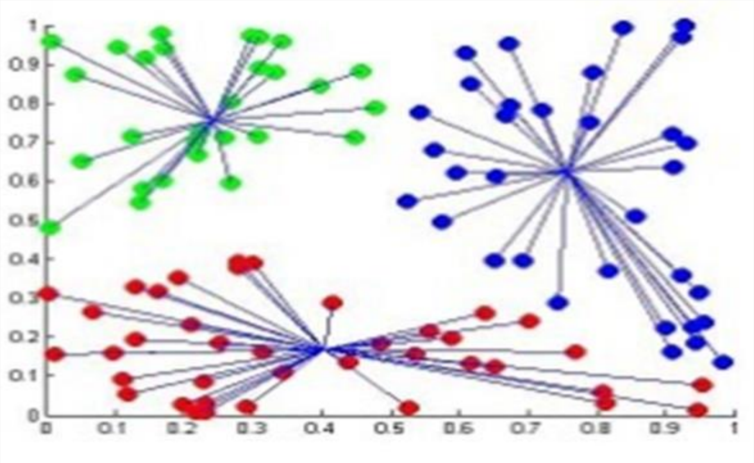

Figure 2: FCM membership function [10]

The membership value of a data point i to cluster j is calculated using the following formula:

$$U_{ij} = \left(\frac{1}{sum\_k(1/(\| x_i - c_j \|^2 / \| x_i - c_k \|^2))} \right)^{\frac{1}{(m-1)}}$$

Equation 1

Where:

U_{ij} is the membership value of data point i to cluster j

x_i is the ith data point

c_j is the center of cluster j

c_k is the center of cluster k

$\left\| x_i - c_k \right\|^2$ ||x_i – c_k||^2 is the Euclidean distance between data point i and center j

m is the fuzzy ness parameter, usually set to 2:

$$U_{ij} = \frac{1}{\sum_{k=1}^{c} \left(\frac{d_{ij}}{d_{ik}} \right)^{\left(2/_{m-1} \right)}}$$

Equation 2

Step 3: Initialize the fuzzy cluster centers V_j using the formula:

$$V_j = \frac{\sum_{j=1}^{n} \left(U_{ij} \right)^m X_i}{\sum_{j=1}^{n} \left(U_{ij} \right)^m}, \forall_j = 1, 2, 3....c$$

Equation 3

Step 4: Update the cluster centers by taking the weighted average of all data points for each cluster, where the weight is the degree of membership of the data point for that cluster.

Step 5: Update the degree of membership of each data point for each cluster.

Step 6: Repeat steps 3 and 4 until the cluster centers and degree of membership of the data points no longer change or a maximum number of iterations is reached.

Step 7: Once the algorithm converges, the final cluster assignment for each data point is determined by the cluster centre with the highest degree of membership.

Note that the parameter m is a degree of fuzziness, the higher the value of m, the fuzzier the clusters will be.

2.1.3 FCM for Image Segmentation

Fuzzy C-means (FCM) can be used for image segmentation, which is the process of partitioning an image into multiple segments or regions. The goal of image segmentation is to separate the image into meaningful regions that correspond to different objects or regions of interest. In FCM-based image segmentation, each pixel in the image is treated as a data point and is assigned a degree of membership for each cluster. The clusters represent different regions or segments in the image. The algorithm proceeds by initializing the cluster centers, updating the cluster centers, and updating the degree of membership for each pixel until convergence.

The process of segmenting an image into various areas or segments, each of which corresponds to a different object or portion of the image, is known as image segmentation. The results of FCM image segmentation depend on the parameters used, the quality of the input image, and the desired output.

In general, FCM can produce high-quality segmentation results, especially when the input image contains clear boundaries between the objects of interest.

However, it may struggle with images that have complex shapes, multiple objects with similar features, or noisy data. In the end, the quality of the FCM image segmentation results can be evaluated using metrics such as accuracy, precision, recall, which compare the output of the segmentation algorithm to the ground truth or reference segmentation. One of the advantages of using FCM for image segmentation is its ability to handle images with non-uniform backgrounds and intensity variations. Since FCM allows for overlapping clusters, it can effectively segment images with multiple objects or regions of interest. It’s also worth noting that FCM is sensitive to initialization, so different initialization methods, such as K-means++, random sampling can be incorporated and the use of pre-processing techniques, such as edge detection and morphological operations, to improve the initialization.

2.2 Transfer Learning

Transfer learning is the use of a pre-trained algorithm on a similar dataset for better output. Transfer learning is a machine learning research issue that focuses on retaining knowledge obtained while resolving one problem and applying it to another that is unrelated but important [7]. For example, weights gained while learning to recognize objects could apply when trying to classify other objects. it is also known as a machine learning method where a model is trained for one task and then used for another task linked to it. In Figure 3 entails applying the knowledge learned in one source task to learn and improve the associated target task. It has been noted that DNNs trained on natural photos exhibit an odd behaviour in which the network's initial layer seems to learn features resembling those of Gabor filters. Many datasets have shown these first layer traits to be generic features. The initial layers' general characteristics are those that ignore the picture dataset, task, and loss function. The filters learned in these levels can be reused by other convnets if some of the convnet's layers pick up on the same kind of feature. Transfer learning [11] solves the issue of limited data availability while saving time and resources for your training. Transfer learning, in other words, is a machine learning technique where we use a previously trained model as the foundation for a model on a new problem. Simply expressed, an optimization that enables quick progress when modelling the second task is applied to a model that was trained on the first, unrelated job. One can attain considerably better performance than training with only a modest quantity of data by applying transfer learning to a new task.

It is uncommon to train a model from scratch for tasks linked to images or natural language processing because transfer learning is so widespread. Instead, data scientists and academics prefer to begin with a model that has already been trained to recognise general features like edges or endpoints or shapes and classify objects.

2.2.1 Classical Machine Learning Vs Transfer Learning

Traditional machine learning models need to be trained from scratch, which is expensive computationally and needs a lot of data to work well. In Figure 4 shown Transfer learning, on the other hand, helps provide better results with less safe word and is computationally efficient. The isolated training strategy used in Classical ML allows each model to be trained separately for a given task without relying on prior information. Transfer learning, on the other hand, leverages the information learned from the previously trained model to carry out the task. Transfer learning models outperform conventional ML models in terms of performance.

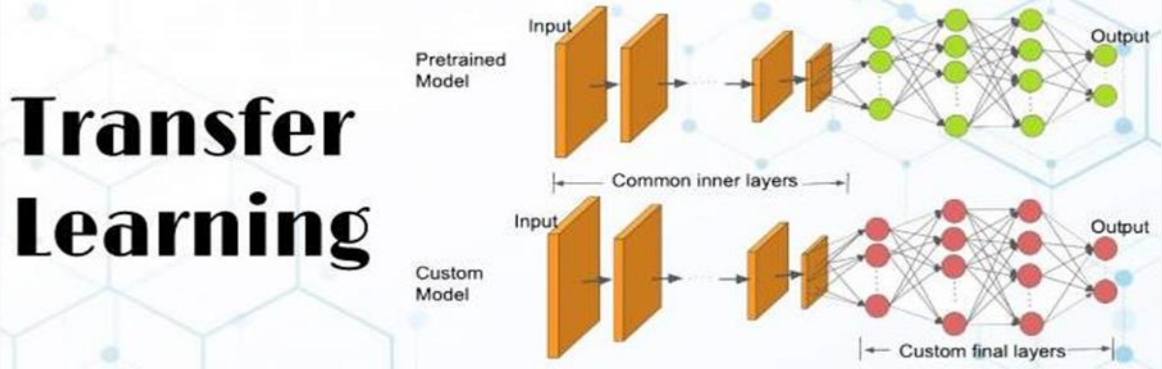

Figure 3: Transfer learning pre trained and custom models

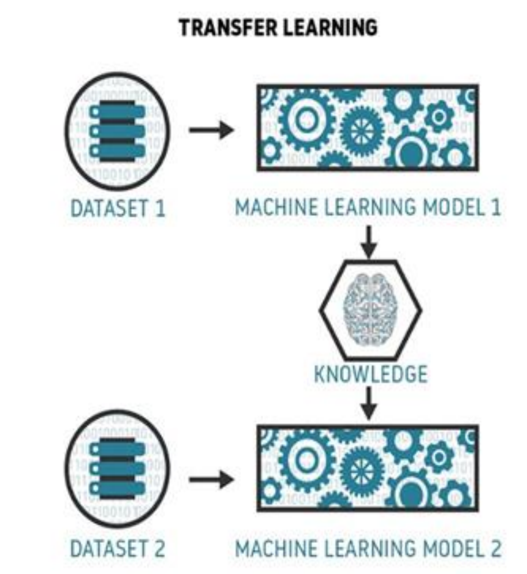

Figure 4: Transfer learning and machine learning models

The reason for this is that the models that use information (features, weights, etc.) from previously trained models already have a thorough understanding of the features. It expedites the process compared to building neural networks from scratch.

2.2.2 Types of Transfer Learning

Definite Transfer Learning: Despite the fact that the exact tasks the model is working on differ, Definite transfer learning demands that the source and target domains be the same. The algorithms try to enhance the target task by applying the knowledge from the source model. The pre-trained model is starting from a stronger position than if we were to train it from scratch because it already has knowledge of the domain's features. The presence or absence of labelled data in the source domain further divides Definite transfer learning into two types. These include learning while multitasking and learning on your own, respectively.

Natural Transfer Learning

The Natural Transfer Learning approach is used in situations when the source and target task domains are related but not identical. The source and target tasks are comparable in certain ways. In these cases, the source domain typically has a large amount of labelled data while the target domain only contains unlabeled data.

3. Methodology

In this we are using two types of methods to solve the problem stated above the first one is a supervised and the other is an unsupervised method in the first method we are using Transfer Learning which is a supervised learning and in this, we are using a pre-trained model named vgg19 or also called visual geometric group 19 its number denotes about the layers it contains within a variation of the vgg model called vgg19 has 19 layers in total (16 convolution layers, 3 fully connected layers, 5 max pool layers and 1 softmax layer). This model has been trained using the ImageNet database which is a large database of over 10 million samples which is why this model reaches around 92 percent of accuracy in training as well as testing. It can classify 1000 classes.

The Architecture of VGG19 is shown in the Figure 5, the block wise explanation is given below. VGG-19 is so beneficial, and it simply uses 3 × 3 convnet arranged as above to extend the depth. To decrease the size, max-pooling layers are applied as a handler. FCN (fully connected layers) layers are two in number to which have 4096 neurons applied. VGG is trained based on individual lesions and for testing all types of lesions were considered to reduce the number of false positives. Convolution layers perform convolution process over images at every pixel, allowing outcome to pass through the subsequent layer. Filters are used in convolution layer is of 3 × 3 dimension which are trained for feature extraction. Every stacked convolution layer is subsequently added with Rectified Linear Unit (ReLU) layer and max-pooling layer. ReLU is presently the best-known non-linear activation function which allows only the positive portion of the input.

Input: this network received a fixed-size (224 * 224) RGB picture as input i.e zebra image, indicating that the matrix was shaped (224,224,3). The mean RGB value of each pixel, calculated throughout the whole training set, was the only pre-processing that was carried out. They were able to cover the entirety of the image by using kernels that were (3 * 3) in size with a stride size of 1 pixel. To maintain the image's spatial resolution, spatial padding was applied. Stride 2 was used to conduct max pooling over a 2 * 2-pixel window.

Relu (Rectified leaner units): was used after this to add non-linearity to the model in order to increase classification accuracy and computing efficiency because earlier models had relied on tanh or sigmoid functions and as we are required to classify between 2 classes probability works better than all other methods so SoftMax function is used [4] and [12].

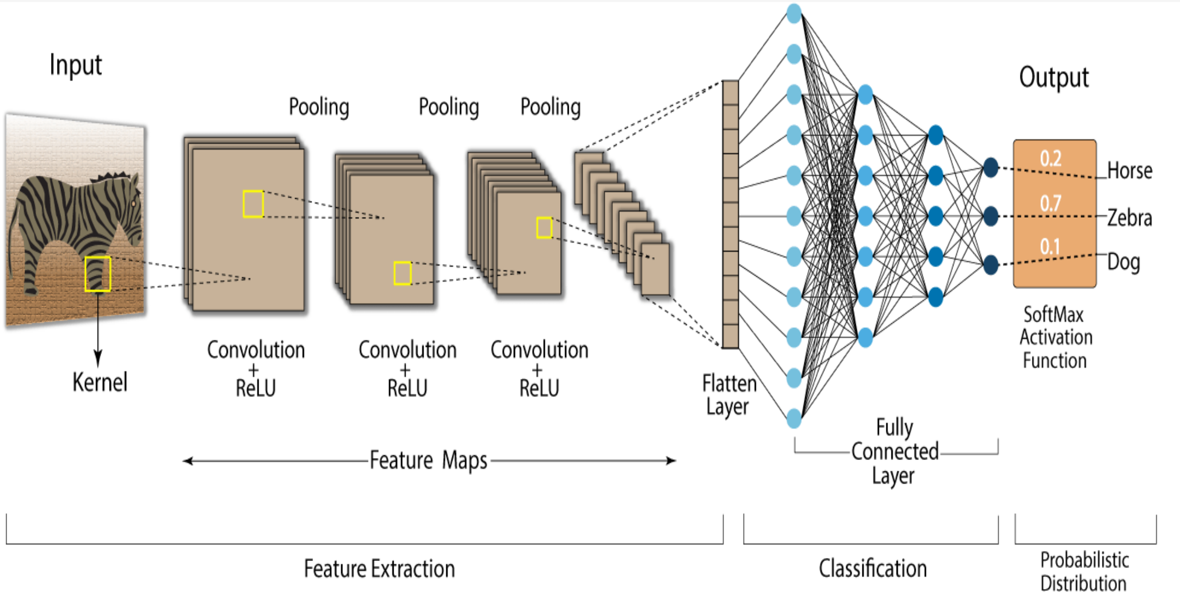

Figure 5: The architecture of VGG19

The layers in the VGG19 model are as follows:

- A fixed size of (224 * 224) RGB image was given as input to this network which means that the matrix was of shape (224,224,3).
- The only pre-processing that was done is that they subtracted the mean RGB value from each pixel, computed over the whole training set.
- Used kernels of (3 * 3) size with a stride size of 1 pixel, this enabled them to cover the whole notion of the image.
- spatial padding was used to preserve the spatial resolution of the image.
- max pooling was performed over a 2 * 2-pixel windows with sride 2.
- this was followed by Rectified linear unit (ReLu) to introduce non-linearity to make the model classify better and to improve computational time as the previous models used tanh or sigmoid functions this proved much better than those.
- implemented three fully connected layers from which first two were of size 4096 and after that a layer with 1000 channels for 1000-way *ILSVRC* classification and the final layer is a softmax function.

The column E in the following table is for VGG19 (other columns are for other variants of VGG models).

Comparison and explanation of the columns (Architecture) in Table 1 so let me first explain the column **E** as that is the VGG19 architecture, it contained 16 layers of CNNs and three fully connected layers and a final layer for softmax function, the fully connected layers and the final layer are going to remain the same for all the network architectures.

A: Contains 8 CNN layers so total of 11 layers including the fully connected (FC) layers and has no difference internally except the number of layers.

A-LRN: This is also similar to the column A but has one extra step of Local response normalization (LRN) which implements lateral inhibition in the layer by which i mean that it makes a significant peak and thus creating a local maximum which increases the sensory perception which we may want in our CNN but it was seen that for this specific case that is ILSVRC it wasn't increasing accuracy and the overall network was taking more time to train.

C: This contains 13 CNN layers and 16 including the FC layers, in this architecture authors have used a conv filter of (1 * 1) just to introduce non-linearity and thus better discrimination.

B and D: These columns just add extra CNN layers and are of 13 layers and 16 layers respectively.

Table 1: Actual configuration of the networks, the ReLu layers are not shown for the sake of brevity

Convolution Neural Network Configuration					
A	**A-LRN**	**B**	**C**	**D**	**E**
11 weight layers	11 weight layers	13 weight layers	16 weight layers	16 weight layers	19 weight layers
Input (224x224 RGB Image)					
Conv3-64	Conv3-64 **LRN**	Conv3-64 Conv3-64	Conv3-64 Conv3-64	Conv3-64 Conv3-64	Conv3-64 Conv3-64
maxpool					
Conv3-128	Conv3-256 Conv3-256	Conv3-256 Conv3-256	Conv3-256 Conv3-256	Conv3-256 Conv3-256	Conv3-256 Conv3-256
maxpool					
Conv3-256 Conv3-256 Conv3-256	Conv3-256 Conv3-256 Conv3-256	Conv3-256 Conv3-256 Conv3-256	Conv3-256 Conv3-256 Conv3-256 **Conv1-256**	Conv3-256 Conv3-256 Conv3-256 **Conv3-256**	Conv3-256 Conv3-256 Conv3-256 Conv3-256 **Conv3-256**
maxpool					
Conv3-512 Conv3-512	Conv3-512 Conv3-512	Conv3-512 Conv3-512	Conv3-512 Conv3-512 **Conv1-512**	Conv3-512 Conv3-512 **Conv3-512**	Conv3-512 Conv3-512 Conv3-512 **Conv3-512**
maxpoll					
Conv3-512 Conv3-512	Conv3-512 Conv3-512	Conv3-512 Conv3-512	Conv3-512 Conv3-512 **Conv1-512**	Conv3-512 Conv3-512 **Conv3-512**	Conv3-512 Conv3-512 Conv3-512 **Conv3-512**
maxpool					
FC-4096					
FC-4096					
FC-1000					
Soft -max					

4. Results

We have applied the MRI scans of both healthy and affected brain images for the algorithms and obtained the results as mentioned below.

4.1 Software's Utilized

Python: Python is an interpreted, high-level, general purpose programming language created by Guido Van Rossum and first released in 1991, Python's design philosophy emphasizes code Readability with its notable use of significant Whitespace. Its language constructs and object-oriented approach aim to help programmers write clear, logical code for small and large-scale projects. Python is dynamically typed and garbage collected. It supports multiple programming paradigms, including procedural, object-oriented, and functional programming.

Anaconda: Anaconda is a free and open-source distribution of the Python and R programming languages for scientific computing that aims to simplify package management and deployment. Package versions are managed by the package management system conda. The Anaconda distribution includes data-science packages suitable for Windows, Linux, and macOS. Anaconda distribution comes with 1,500 packages selected from PyPI as well as the conda package and virtual environment manager. It also includes a GUI, Anaconda Navigator, as a graphical alternative to the command-line interface (CLI).

Jupyter Notebook: Anaconda distribution comes with 1,500 packages selected from PyPI as well as the conda package and virtual environment manager. It also includes a GUI, Anaconda Navigator, as a graphical alternative to the command line interface

(CLI). A Jupyter Notebook document is a JSON document, following a versioned schema, and containing an ordered list of input/output cells which can contain code, text mathematics, plots and rich media, usually ending with the “.ipynb" extension

4.2 Fuzzy C Means Clustering

After pre-processing, we segment the abnormal tissues which are the brain tumor from the MRI Using Fuzzy C Means segmentation algorithm. we distinguish between the normal cells and abnormal cells. We used FCM clustering method. Which gives us the improved result as it ensures that one piece of data to belong to two or more clusters which are important for Brain MRI. In Figure 6 healthy brain MRI image has shown is given as input image for VGG19 using FCM as experiment-1. The segmented brain image is shown in the Figure 7 which is determined as No tumour detected. Because no tumour contour has detected, the black area in the image shows that normal brain white region is skull. so that for normal brain images are given as input to trained VGG-19 as No tumour detected.

Figure 8 illustrated tumour affected brain MRI image which is given as input image for VGG19 using FCM as experiment-2. The tumour has spread surrounded by white region. As running FCM the output MRI brain image is shown in the Figure 9 which is determined as tumour detected. In the output image tumour is surrounded by white region which is segmented by using FCM.

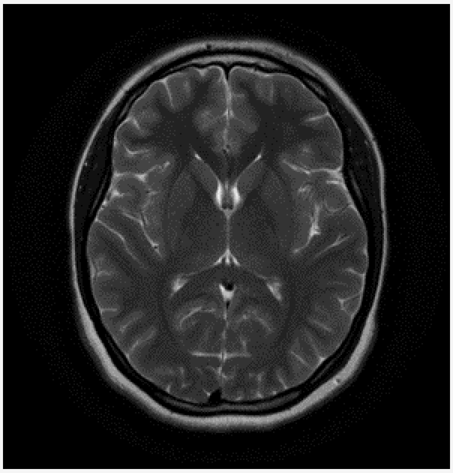

Figure 6: MRI image of a healthy brain as input image for experiment -1

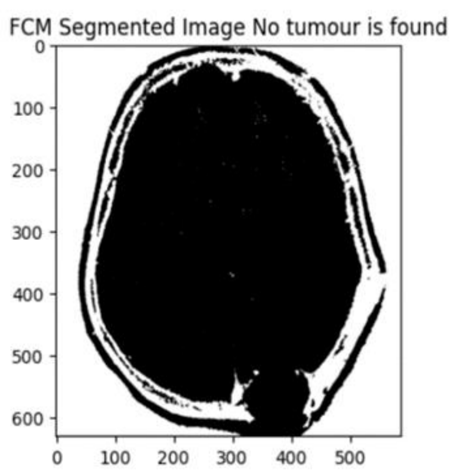

Figure 7: FCM segmented output image for experiment -1

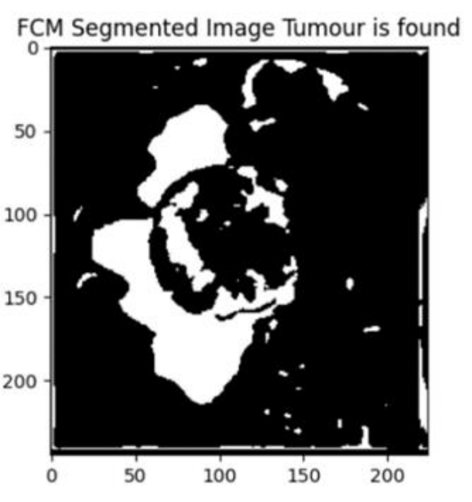

Figure 8: MRI image of an affected brain as input image for experiment -2

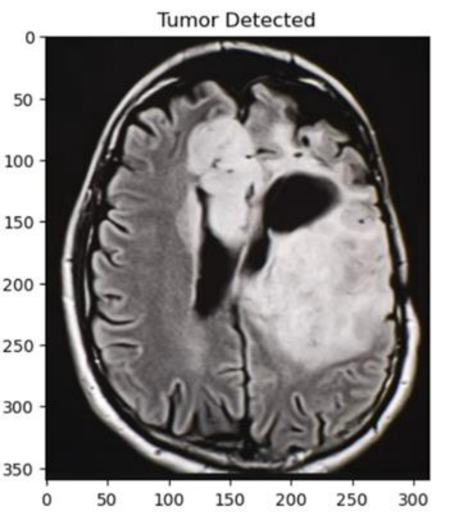

Figure 9: FCM segmented image output image for experiment -2

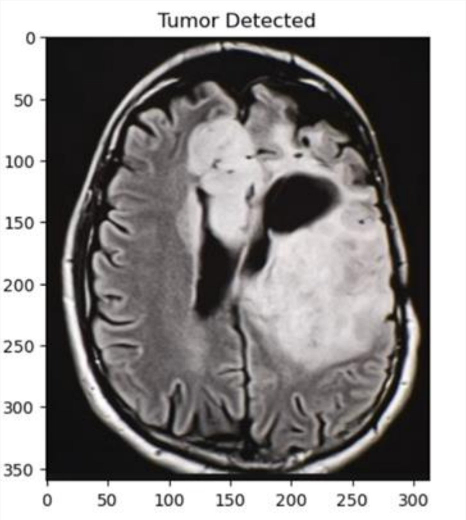

Figure 10: Model predicted as affected brain in transfer learning

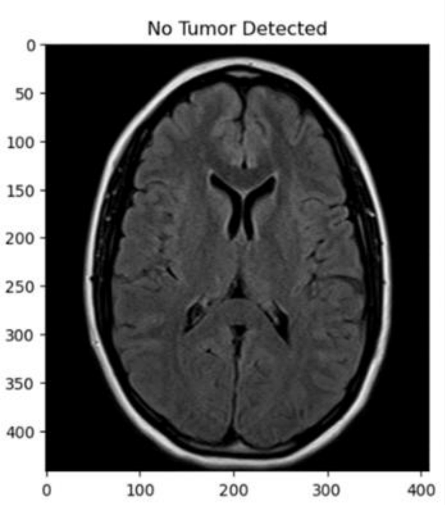

Figure 11: Model predicted as healthy brain

Table 2: Performance comparison of proposed method with previous work

S. No	Method	Accuracy
1	Probabilistic Neural Network	95%
2	Five Layer CNN Model	97.87%
3	VGG19 with FCM	97.9%
4	VGG19 with Transfer Learning	98.3%

4.3 Transfer Learning

Transfer learning for machine learning is when existing models are reused to solve a new challenge or problem. Transfer learning is not a distinct type of machine learning algorithm, instead it’s a technique or method used whilst training models. The knowledge developed from previous training is recycled to help perform a new task. The new task will be related in some way to the previously trained task, which could be to categorise objects in a specific file type. The original trained model usually requires a high level of generalisation to adapt to the new unseen data.

Transfer learning means that training won’t need to be restarted from scratch for every new task. Training new machine learning models can be resource-intensive, so transfer learning saves both resources and time. The accurate labelling of large datasets also takes a huge amount of time. Most of the data encountered by organisations can often be unlabelled, especially with the extensive datasets required to train a machine learning algorithm. With transfer learning, a model can be trained on an available labelled dataset, then be applied to a similar task that may involve unlabelled data. As applying affected brain image to supervised approach transfer learning the output MRI brain image is shown in the Figure 10 which is determined as tumour detected. In the output image tumour is surrounded by white region which is identified due to pre trained CNN.

The segmented brain image is shown in the Figure 11 which is determined as no tumour detected. Because no tumour contour has detected, the black area in the image shows that normal brain white region is skull. so that for normal brain images are given as input to supervised transfer learning it shows No tumour detected with high accuracy. The proposed work aims on transfer learning-based brain tumor detection. In the Table2 shows the performance comparison of the proposed methodology using VGG-19with previous CNN models, achieved maximum accuracy on validation data. In testing phase, accuracy is 98.3% accuracy.

5. Conclusion

In this study, MRI images of brain tumor are identified using a deep learning-based pre-trained convolutional neural network framework. Using transfer learning approaches, the paper investigates several pretrained networks and clustering techniques for enhancing brain tumor's MR image classification. We made a few discoveries through observation. First off, the training outcomes of various pretrained DL networks demonstrate that the type of optimizer selected has a considerable effect on overall model's performance. Although the dataset is too little, picture data augmentation has done well to get better results and thereby overcome this problem. Our suggested solution achieved the highest accuracy of 92.04% while using the provided dataset and performed better than the traditional unsupervised approaches. Future research can be done with a larger dataset to increase accuracy even further while attempting to train the network as quickly as possible utilising cutting-edge computers. Significant impact on a PTN's performance. It has an impact on the network's accuracy and, more crucially, on training time.

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