

Computerised Brain Tumours Classification using MRI Images

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Abstract: The categories of the brain tumours into four categories no tumour, glioma, meningioma, and pituitary are exploited in this study to propose a unique representation for magnetic resonance image analysis. MRI images are the input in this investigation. Radiologists manually interpret MRI scans to find abnormalities in the brain. Interpreting a large number of images by hand is difficult and time-consuming. However, because of the complexity of the MRI equipment, this undertaking is not easy. Particularly, it can be difficult and very subjective to differentiate between various tumour forms, such as gliomas, meningiomas, and pituitary tumours. Computer-based detection aids in the precise, quick, and accurate identification of the disease to address this issue. The suggested study employs CNN and SVM models. Using HOG characteristics, the SVM classifier categorises the brain MRI picture. Three convolutional layers were used in the CNN model's training, and the softmax classifier is used to categorise the image. The four forms of brain tumours identified by the SVM and CNN models are no tumour, glioma, meningioma, and pituitary. By comparing the outcomes, CNN estimates accuracy to be 97%, whereas SVM estimates accuracy to be 92%.

Keywords: CNN, SVM, HOG, Glioma, Meningioma, Pituitary, and Magnetic Resonance Imaging (MRI)

Introduction

The lumps created by aberrant brain cell growth are referred to as brain tumours [1]. The vast and complex brain is the central nervous system regulator. It has over 100 billion nerve cells [2]. People's health may be at risk due to the kind of aberration present in the brain.

Brain tumours are among the most common cancer-related causes of mortality in the world, affecting

both adults and children. For an accurate prognosis and effective treatment planning, a brain tumour must be identified accurately and early [3]. Benign and malignant brain tumours are the two different forms. The healthy tissues are impacted by the growth of a benign tumour. While brain cancer refers to malignant tumours that develop outside the brain [4].

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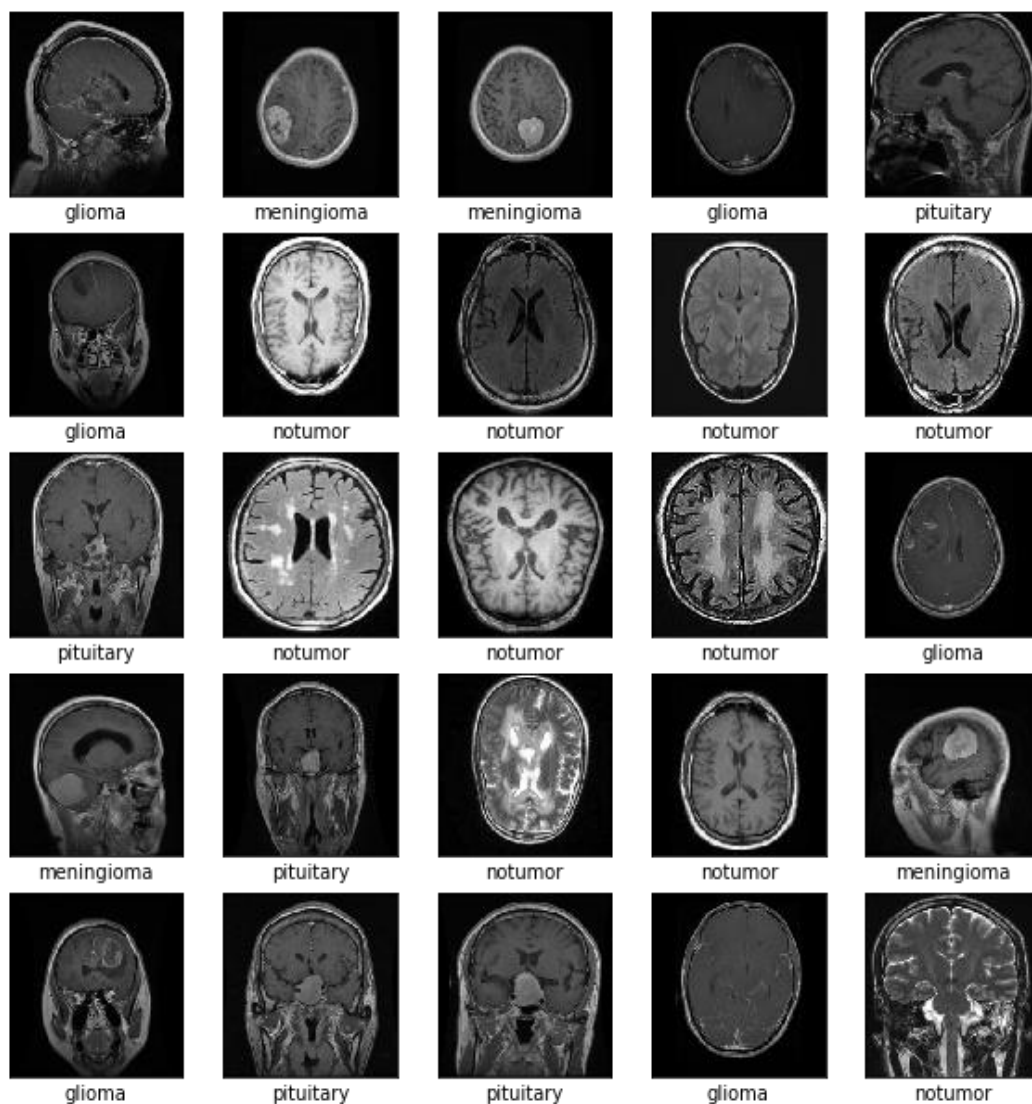


Fig. 1 sample MRI image of human brain image.

Brain tumours are the term for the uncontrolled and unnatural proliferation of brain cells. It is typically divided into primary tumours and secondary tumours. The brain contains the primary cancer, whereas the secondary tumour spreads through the bloodstream to the brain tissue in other parts of the body [5]. Meningioma and gliomas are two different types of primary tumours. These are the two primary kinds of brain tumours that can be lethal if they are not found in their early stages. The Glioma type is the most prevalent [6]. The brain's MRI scan in Fig. 1 displays tumor-free, glioma, meningioma, and pituitary tissue.

The World Health Organisation (WHO) assigns four classifications to brain tumours. Meningiomas are classified as grade 1 and grade 2 because they are regarded as lower-level tumours. Since gliomas are thought to be severe, they are graded at the Grade 3 and Grade 4 levels. The incidence rates of meningioma, pituitary, and glioma tumours are around 15%, 15%, and 45%, respectively [7]. The suggested work's block diagram is shown in Fig. 2.

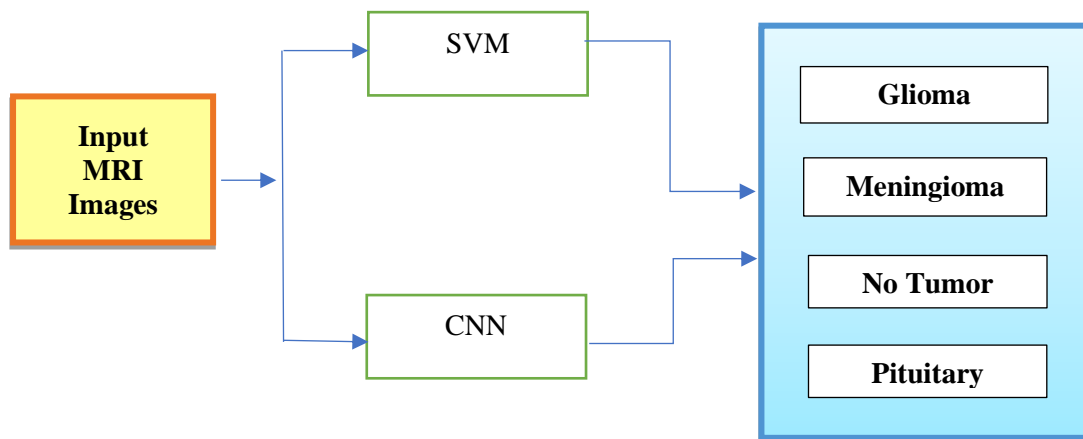


Fig. 2 Block Diagram of the Proposed Work

Literatures Of The Work

In the field of machine learning, an automated approach was developed to identify irregularities in brain tissue, namely lumps or masses, and to classify them as possibly cancerous (suggesting marginal adhesion) or benign (suggesting clump thickness). This classification task was described in reference [8]. A novel two-phase multi-model automated diagnostic approach was developed to achieve precise localisation and prediction of brain tumours.

A number of crucial actions were made throughout the system's first development period. The reference [9] states that these procedures comprised preprocessing the data, utilising a Convolutional Neural Network (CNN) to extract relevant features, and classifying the features through the application of the Error-Correcting Output Codes Support Vector Machine (ECOC-SVM) approach. As mentioned in reference [10], this suggested deep learning-based system performed remarkably well in tumour identification when compared to non-deep learning methods covered in the literature. The outcomes also show how effective the recommended strategy is at localising and detecting tumours.

Furthermore, a novel method for categorising brain tumors into multiple grades based on convolutional neural networks was introduced. Initially, deep learning techniques were employed to segment tumor regions from MRI images, as detailed in reference [11]. As noted in reference [12], the research also tackled a practical issue by assessing the system's performance with a small

number of training instances. The study findings suggest that transfer learning can be a valuable strategy when medical image availability is constrained. The paper also offers a detailed analytical discussion of misclassifications.

3 Methodologies

Feature Extraction (HOG)

The domains of computer vision and artificial intelligence are where HOG (Histogram of Oriented Gradients) descriptors are mainly used for object recognition [13]. However, HOG descriptors can also be applied to measure and represent both shape and texture.

In essence, the process of creating HOG descriptors involves five key stages:

1. Normalizing the image before feature extraction.
2. Calculating gradients in both the x and y directions.
3. Compiling votes that are weighted in orientation and spatial cells.
4. Normalising gradients in spatial cells that overlap.
5. To create the final feature vector, combining all of the Oriented Gradient Histograms.

Among the parameters that significantly influence the HOG descriptor are orientations, pixels per cell, and cells per block. These three variables, along with the input image's size, effectively regulate the feature vector's dimensionality. In the proposed work, the following values are utilized for HOG feature vector generation: Orientations - 9, Pixels-per-cell - 10X10, Cells-per-block - 2X2, and the image size is set to 224 X 224. It is important to note

that the HOG descriptor produces a feature vector with real-valued components.

SVM (Support Vector Machine)

In the presented research, HOG (Histograms of Oriented Gradients) features are extracted from brain tumour images and utilized as input data for a machine learning classifier, specifically Support Vector Machine (SVM). Support Vector Machine is also denoted to as Support Vector Classification, and it is a supervised and rectilinear machine learning technique commonly employed for solving classification problems. It aims to find an optimal decision boundary that best separates data points belonging to different classes.

Additionally, there is a variant of SVM called Support Vector Regression (SVR), which applies the same principles to address regression problems, aiming to predict continuous numeric values rather than class labels.

One of the noteworthy features of SVM is its support for the kernel method, known as kernel SVM. This methodology allows the SVM to handle non-linear data by transforming it into a higher-dimensional space where linear separation becomes feasible.

The diagram presented in Figure 3 illustrates the block diagram of the Support Vector Machine, which outlines its key components and how it functions in the context of the research.

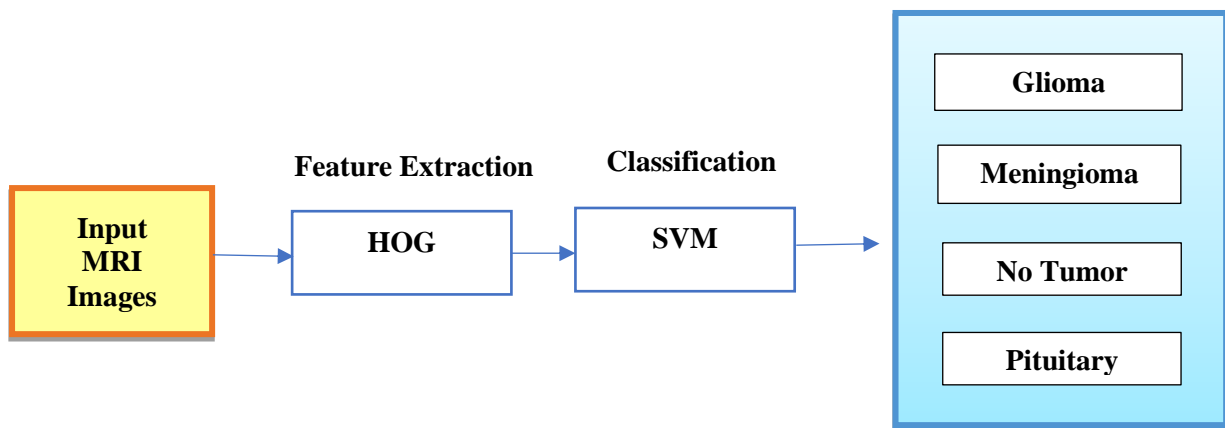


Fig. 3 Block Diagram of SVM

Support Vector Machine (SVM) is a versatile machine learning technique that can be functional to equally classification and regression problems. Its prime use case is indeed classification, but it can also effectively explain regression tasks.

SVM operates by constructing a hyperplane in a multidimensional space to separate different classes of data points. This hyperplane is iteratively optimized to minimize classification errors. The objective of SVM is to find a Maximum Marginal

Hyperplane (MMH) that splits a dataset into classes as distinctly as possible [14].

The term "maximum marginal hyperplane" refers to the hyperplane that maximizes the margin (the distance) between data points of different classes. This approach aims to achieve the best possible separation between classes, making SVM a powerful tool for various machine learning tasks, including both classification and regression.

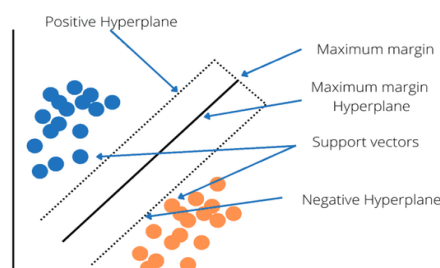


Fig. 4 SVM Hyperplane split

Support vectors are specific data points that hold a special significance in Support Vector Machines (SVM). These data points are the closest ones to the hyperplane, and they play a crucial role in shaping the classifier. By calculating margins and aiding in the definition of the separating hyperplane, support vectors contribute significantly to the construction of an effective classifier.

Speaking of hyperplanes, in the SVM context, a hyperplane acts as a decision boundary. Its purpose is to separate a collection of objects or data points belonging to different classes. SVM's goal is to find the ideal hyperplane that exploits the margin between these classes, ensuring the most effective separation possible. The support vectors, as mentioned earlier, are instrumental in determining the position and orientation of this crucial decision plane. Understanding these concepts is vital for comprehending the inner workings and effectiveness of SVM in classification tasks.

The margin, in the context of Support Vector Machines (SVM), represents the distance among the two lines formed by the closest data points from different classes. It's determined as the vertical distance from this line to the support vectors or the adjacent data points. A wider border is preferred, indicating a clearer separation between classes, while a narrower margin is less desirable.

When constructing a nonlinear support vector classifier, an essential step involves replacement the inner product (x, y) with a kernel function denoted as $K(x, y)$. This kernel function enhances the SVM's capability to handle complex data patterns where a simple linear separation boundary is inadequate. By using this kernel function, SVM can effectively capture intricate relationships within the data.

$$f(x) = \text{sgn}\left(\sum_{i=1}^l \alpha_i y_i K(x_i, x) + b\right) \quad (1)$$

The Support Vector Machine (SVM) consists of two layers in its learning process. In the initial layer, it selects the basis $K(x_i, x)$ for $i = 1, 2, \dots, N$, from a predefined set of bases determined by the chosen kernel function. Subsequently, in the second layer, it builds a linear function within this feature space. This process is entirely corresponding to the task of constructing the optimal hyperplane within the corresponding feature space.

The SVM algorithm possesses the capability to create various learning models by utilizing different kernel functions. Typically, three different types of kernel functions are commonly employed. These three types are as follows:

1. Linear Kernel

$$K(X, Y) = (X + Y) \quad (2)$$

2. Polynomial Kernel of degree d

$$K(X, Y) = ((X, Y) + 1)^d \quad (3)$$

3. Radial basis function with Gaussian kernel of width $C > 0$

$$K(X, Y) = \exp\left(\frac{-\|X - Y\|^2}{c}\right) \quad (4)$$

In the presented research, a linear kernel is employed to classify brain tumor images into four different classes, which are Glioma tumor, Meningioma tumor, No tumor, and Pituitary tumor. The use of the linear kernel in this context allows for the effective separation and categorization of these different types of brain tumors.

Convolutional Neural Network (Cnn)

Deep learning is branch of machine learning that has expanded significant consideration and application in various domains. One of the greatest prominent deep learning architectures is the Convolutional Neural Network (CNN), which is primarily employed for the tasks such as image recognition, image classification, video labeling, natural language processing, and analysis medical image, among others. A CNN is composed of multiple layers, including an Input Layer, Output Layer, and several hidden layers [15]. These hidden layers are typically comprised of convolutional layers, which are fundamental to the network's operations.

In a CNN architecture, the Rectified Linear Activation Unit (ReLU) layer serves as a common activation function. Following this, you often find pooling layers, fully connected layers, and normalization layers. The convolutional layer plays a central role and frequently employs backpropagation for enhancing the accuracy of the results.

Figure 4 provides an illustrative depiction of the architecture of the Proposed Convolutional Neural Network model. Each convolution layer within a

neural network follows a series of steps to abstract meaningful features from the data.

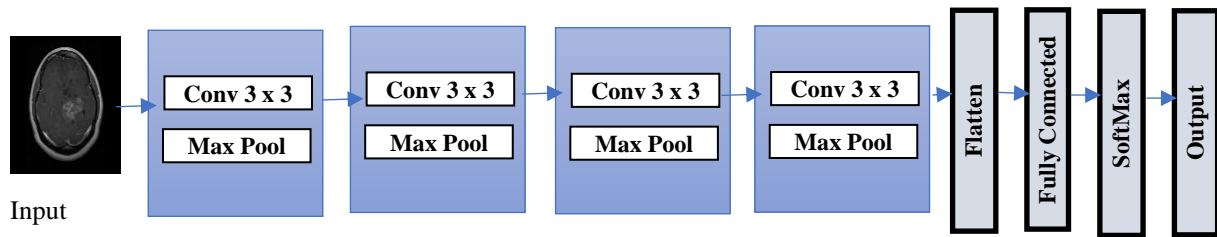


Fig. 4 CNN Architecture Diagram

Convolutional Layer

The convolutional layer is a fundamental component of a CNN and plays a crucial role in its architecture. Within this layer, there are parameters known as filters or kernels. These filters have a small receptive field, but they extend into the depth of the input image. In the process, each filter is systematically applied across the width and height of the input image, and by calculating the dot product between the filter and the input data at each position, a two-dimensional activation map specific to that filter is generated [16]. This activation map reflects how the filter responds to different features or patterns within the input data.

Pooling Layer

Pooling layers serve to decrease the dimensions of data in a CNN by consolidating the output neurons into a single layer, subsequently passing this layer as a single neuron to the next stage. In the realm of data processing in convolutional networks, pooling can be considered into two main types: local pooling and global pooling. Local pooling brings together all the smaller clusters of data, while global pooling essentially functions as a neuron integrated within the convolutional layer.

Pooling operations encompass three essential techniques: Min Pooling, Max Pooling, and Average Pooling [17]. Min Pooling involves selecting the minimum value from separately neuron group in the previous layer, Max Pooling captures the maximum value from separately neuron group in the previous layer, and Average Pooling computes the average value from each neuron group in the previous layer. These pooling strategies contribute significantly to reducing the complexity of data and retaining essential information for subsequent stages of processing.

Fully-Connected Layers

This approach utilizes the fundamental concept of the Multi-Layer Perceptron (MLP). In this design, each neuron in one layer is connected to each neuron in another layer, forming a dense network of connections. These fully connected layers play a key role in image classification tasks by processing data in the form of a flattened matrix, where each element corresponds to a specific feature or aspect of the image. This comprehensive interconnection of neurons agrees the network to learn and extract complex patterns and relationships in the data, ultimately aiding in accurate image classification.

Activation function

The activation function plays a crucial role in neural networks by computing a weighted sum of inputs and adding a bias, which determines whether a neuron should be activated or not. Its primary purpose is to introduce non-linearity into a neuron's output, enabling the network to model complex relationships and make it capable of learning effectively [18].

Various types of activation functions are existing, including sigmoid, ReLu (Rectified Linear Unit), leaky ReLu, and tanh (hyperbolic tangent). In this particular research project, the ReLu activation function is employed. ReLu is known for its simplicity and effectiveness in introducing non-linearity by allowing positive values to pass through while setting negative values to zero. This activation function has been found to perform well in many deep learning applications.

ReLU Layer

The full form of ReLU is the rectilinear unit which is used for the unsaturated activation function defined as [19]

$$f(x) = \max(0, x) \quad (5)$$

It removes the negative values from the activation function by placing them to zero.

Softmax Layer

The last layer is the Softmax layer. The softmax function specifies a discrete probability assignment for the K classes $\sum_{k=1}^K P_k$. The last layers of CNN are fully connected and the last layer handles the softmax role at its input so we get probabilities for each single image. The parameters of the network are trained with a backpropagation algorithm as in the usual neural networks.

Steps of CNN

1. Provide the input image within the convolution layer.
2. Select parameters, apply filters along with strides, padding if necessary.
3. Perform convolution on the image and use ReLU activation on the matrix.
4. Render pooling to decrease dimensionality size.
5. Add convolutional layers as needed until the desired level of feature extraction is achieved.
6. Flatten the output from the convolutional layers to create a one-dimensional vector, which is then given into a fully connected (FC) layer.
7. Design the output layer to handle the activation function for generating class predictions.

In this work three convolutional layers are created to classify the MRI images into four different types such as no tumour, Glioma, Meningioma and Pituitary tumour with the soft max classifier.

4 Experimental Results

4.1 Datasets Description

MRI images used in the study were sourced from Kaggle datasets, specifically T2-weighted MRI images. The dataset comprised a total of 5712 images, all in jpg format. For the testing phase of the research, 1311 of these images were selected and utilized.

4.2 Environmental setup

The deep learning environment was established by configuring the following components:

1. Python 3.6: Python version 3.6 was installed and set up as the core programming language.

2. Anaconda: The Anaconda library was installed, providing a comprehensive environment for data science and machine learning tasks.
3. OpenCV Contrib (version 3.3.0): OpenCV Contrib, version 3.3.0, was effectively integrated with the Python 3.6 interpreter to support computer vision and image processing operations.
4. TensorFlow and Keras: These critical deep learning frameworks were installed using the **conda install** command, enabling the development of neural networks.
5. Required Libraries: Various essential libraries were installed using **pip install**. These libraries include NumPy, PIL (Python Imaging Library), Scikit-learn, SciPy, Scikit-learn (a variation of Scikit-learn), and h5py, which are essential for data manipulation, image processing, and machine learning tasks.

This setup forms a robust deep learning environment, providing the necessary tools and libraries to work on a wide range of deep learning projects involving image analysis and classification.

4.3 Performance Measures

In this study, numerous evaluation parameters are employed to measure the performance of the classification method. These metrics are designed based on the data gathered from the confusion matrix, which summarizes the results of the classification.

Accuracy

Accuracy serves as a measure of how well a measurement system performs. It signifies the extent to which results are both true (free from systemic errors) and consistent (lacking random errors).

$$Accuracy = \frac{TP + TN}{TP + TN + FP + FN}$$

(6)

Precision

Precision, in the context of classification, pertains to the accuracy of the positive class predictions. It quantifies the number of true positive predictions (correctly identified positive cases) relative to the total number of elements labeled as belonging to the positive class (which includes both true positives and false positives, i.e., items incorrectly labeled as positive).

$$Precision = \frac{TP}{TP+FP} \quad (7)$$

Recall

Recall, represents the number of true positive predictions separated by the total number of elements that genuinely fit to the positive class (comprising true positives and false negatives, i.e., cases that should have been labeled as positive but were not).

$$Recall = \frac{TP}{TP+FN} \quad (8)$$

F-Measure

The F-Measure is a composite metric that associations precision and recall. It is particularly useful when there is an imbalance between positive and negative classes. The F-Measure is designed as

the harmonic mean of precision and recall, providing a composed assessment of the test's accuracy.

$$F-Measure = 2 \frac{Precision * Recall}{Precision + Recall} \quad (9)$$

Performance of SVM

In this proposed work HOG features are extracted from the human brain MRI images. There are 5712 images are trained by using HOG feature extraction technique. Then the trained features are fit into the SVM classifier. The SVM classifier, categorizes the brain MRI images into the classes Glioma tumour, No tumour, Meningioma tumour, and Pituitary tumour. There are 1311 images are used for testing. The SVM with HOG feature model produce the accuracy of 92% for the brain tumour classification. The confusion matrix and classification report for brain tumour classification using SVM with HOG feature are show in the table 1 and table 2.

Table 1: Confusion Matrix for SVM with HOG feature

	Glioma Tumour	Meningioma Tumour	No Tumour	Pituitary Tumour
Glioma Tumour	245	53	0	2
Meningioma Tumour	23	270	3	10
No Tumour	0	0	402	0
Pituitary Tumour	2	11	0	287

Table 2: Classification Report for SVM with HOG feature

	Precision (in %)	Recall (in %)	F1- Score (in %)	Accuracy (in %)
Glioma Tumour	81.66	90.72	85.72	87.78
Meningioma Tumour	88.23	82.31	85.16	88.35
No Tumour	100.00	99.20	99.59	97.77
Pituitary Tumour	95.66	95.94	95.79	94.08

Performance of CNN

The trainable and non-trainable parameters of CNN model is shown in the table 3. There are 130,116 parameters are trainable in CNN model. In this

proposed model four convolutional layers are used with ReLu activation function and softmax classifier. it Classifies the brain images into four classes Glioma tumour, No tumour, Meningioma tumour and Pituitary tumour

Table 3: Parameters of CNN Model

Layer Output Parameters		
Layer (Type)	Output Shape	Param #
(Conv2d)	(None, 222, 222, 32)	896
(Maxpooling2D)	(None, 111, 111, 32)	0
(Conv2d)	(None, 109, 109, 64)	18496
(Maxpooling2D)	(None, 54, 54, 64)	0
(Conv2d)	(None, 52, 52, 64)	36928
(Maxpooling2D)	(None, 26, 26, 64)	0
(Conv2d)	(None, 24, 24, 64)	36928
(Maxpooling2D)	(None, 12, 12, 64)	0
(Flatten)	(None, 9216)	0
(Dense)	(None, 4)	36868
	Total params	130,116
	Trainable params	130,116
	Non-trainable params	0

The proposed model is accomplished for 20 epochs with 5712 images for training. In that 0.1% of data are used for validation. The following figure 5

displays the training and validation loss for every epoch.

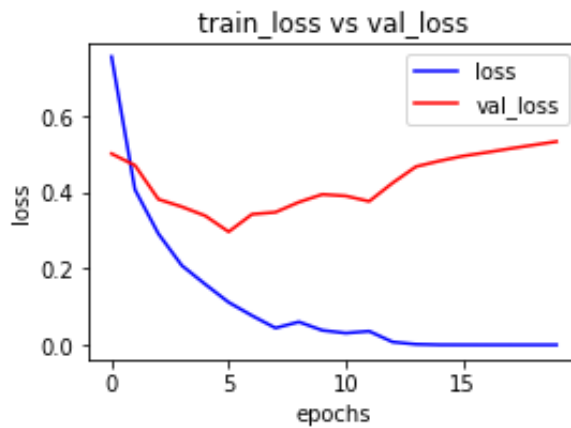


Fig.5 loss of training/validation data for CNN

The validation and training accuracy is shown in the following figure 6. The figure illustrates the epoch wise accuracy for both training and validation.

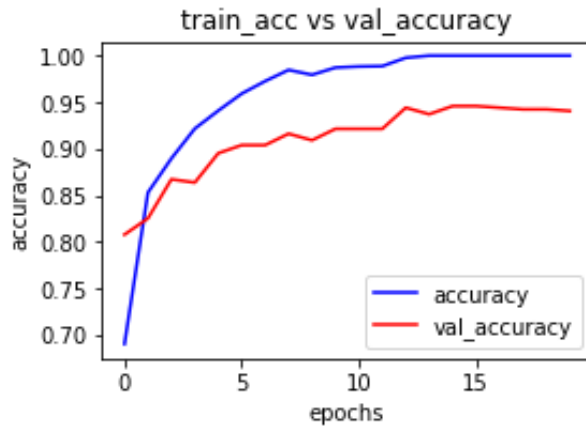


Fig.6 Accuracy of training/validation data for CNN model

For testing there are 1311 images used. The confusion matrix of the projected work is shown in the table 4. The images of each class for testing are

Glioma tumour 300, Meningioma tumour 306, No tumour 405 and Pituitary tumour 300.

Table 4: Confusion matrix of Brain Tumour image using CNN

	Glioma Tumour	Meningioma Tumour	No Tumour	Pituitary Tumour
Glioma Tumour	290	10	0	0
Meningioma Tumour	20	275	7	4
No Tumour	0	3	402	0
Pituitary Tumour	0	1	0	299

The performance of CNN for classifying the brain tumour MRI images is specified in the table 5. The table illustrates the performance metrics precision, recall, f1-score and accuracy of the

classes Glioma tumour, No tumour, Meningioma tumour and Pituitary tumour. The overall accuracy of the CNN for the brain tumours produced 97% accuracy.

Table 5: Performance of Brain Tumour MRI Images using CNN Model

	Precision (in %)	Recall (in %)	F1- Score (in %)	Accuracy (in %)
Glioma Tumour	94.00	97.00	95.00	94.00
Meningioma Tumour	95.00	90.00	92.00	96.00
No Tumour	98.00	99.00	99.00	98.00
Pituitary Tumour	99.00	100.00	99.00	99.00

Performance Comparison

The comparison performance of the proposed model is given in the figure 7. The figure displays the comparison performance of the models SVM

and CNN using brain tumour images. The SVM model provides 92% of accuracy where CNN provides 97% accuracy. Comparison of the both models the CNN outperforms well.

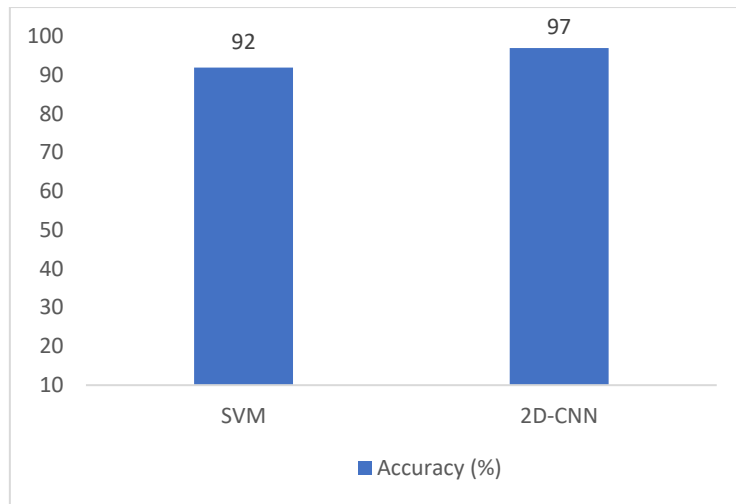


Fig. 7 Performance Comparison of Proposed Model

Testing Sample output

For testing the brain image is given to system and the proposed model detect the type of tumour as

glioma tumour, pituitary tumour, meningioma tumour, and no tumour The following figure 8 shows the sample output for brain tumour classification.

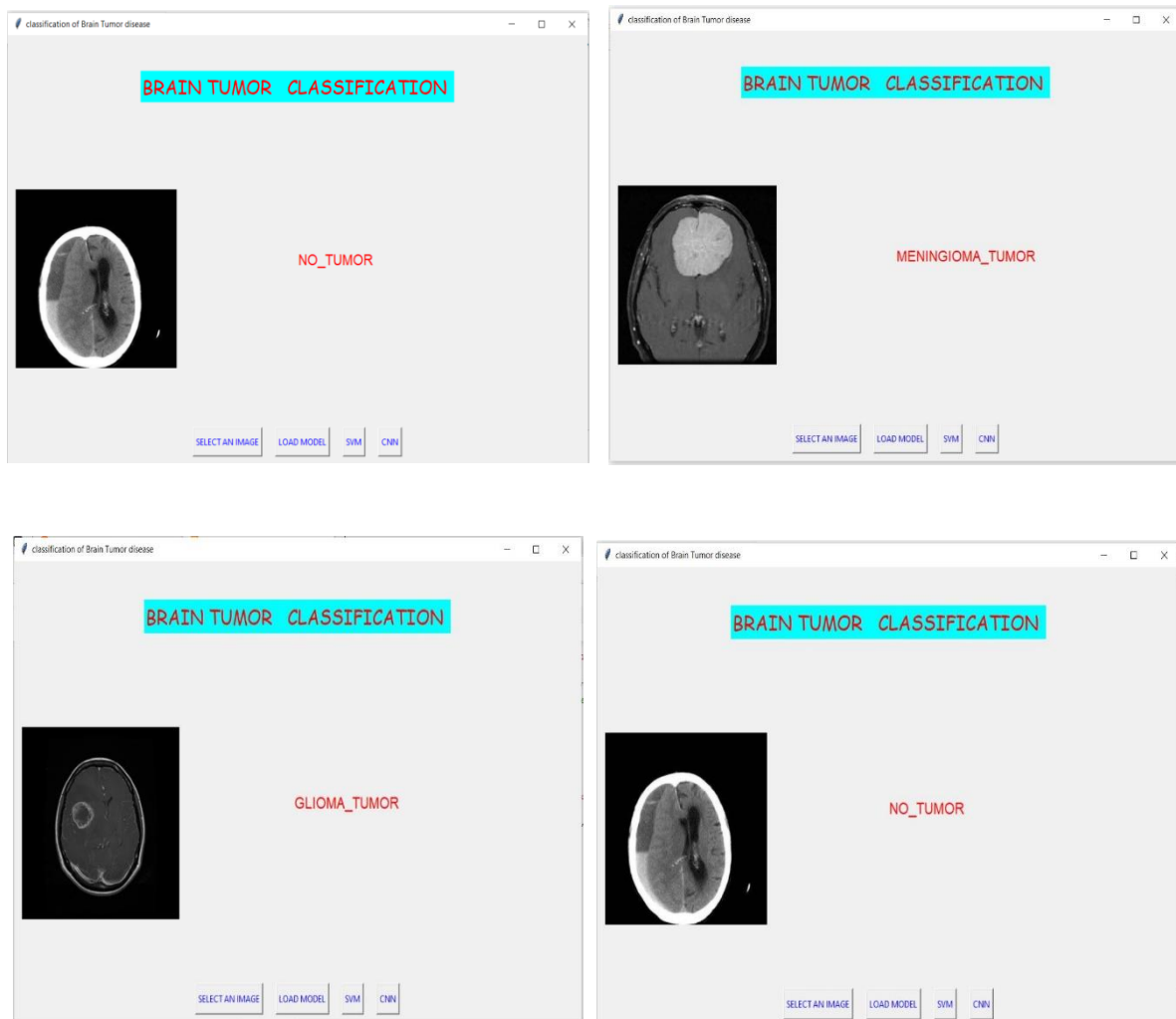


Fig. 8 Sample Outputs of Brain Tumour Classification

Conclusion

In this work a suggested classifier for brain tumours using MRI pictures by using SVM and CNN classifiers. The SVM machine learning classifier used the HOG feature extraction technique. From the brain images, the HOG features are extracted and classify the brain tumours are present in the given image. For training there are 5712 images are used and for testing 1311 images are used. Second the CNN deep learning model is implemented with four convolutional layers.

The convolutional features are extracted and the softmax classifier categorize the brain images into the four different classes as glioma tumour, pituitary tumour, meningioma tumour and no tumour. The CNN trained by 20 epochs. In this proposed work, a machine learning model SVM is compared with deep learning CNN model. The results of both models are estimated by the performance metrics. By comparison of the models, SVM produced 92 % of accuracy and the proposed CNN model produced 97 % of accuracy. Comparison of the both models the CNN outperform well.

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