



Binary and Multi-class Classification of Brain Tumors using MRI Images

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Abstract: A dangerous and potentially fatal condition is a brain tumor. Early detection of this disease is critical for determining the best course of treatment. Tumor detection and classification by human inspection is a time consuming, error-prone task involving huge amounts of data. Computer-assisted machine learning and image analysis techniques have achieved significant results in image processing. In this study, we use supervised and deep learning classifiers to detect and classify tumors using the MRI images from the BRATS 2020 dataset. At the outset, the proposed system classifies images as healthy or normal brains and brain having tumorous growth. We employ four supervised machine learning classifiers SVM, Decision tree, Naïve Bayes and Linear Regression, for the binary classification. Highest accuracy (96%) was achieved with SVM and DT, with SVM giving a better Recall rate of 98%. Thereafter, categorization of the tumor as Pituitary adenoma, Meningioma, or Glioma, is performed using supervised (SVM, DT) classifiers and a 6-layer Convolution Neural Network. CNN performs better than the other classifiers, with a 93% accuracy and 92% recall rate. The suggested system is employable as a powerful decision-support tool to assist radiologists and oncologists in clinical diagnosis without requiring invasive procedures like a biopsy.

Introduction

Medical image processing makes use of various types of scans such as CT (Computer Tomography), Ultrasound, PET (Positron Emission Tomography), MRI (Magnetic Resonance Imaging), Spectroscopy, etc. Among these, MRI is most widely used for diagnosis as it is sensitive and powerful while also being noninvasive (Badža et al., 2020; Khan et al., 2020). MRI scans provide detailed information as they use effective radio waves and magnetic fields are used to create pictures of the inside organs, effectively detecting cysts, tumors, swelling or bleeding of organs. Analysis and classification of these scans lead to the identification of any irregular growth. Early detection of abnormal tissue growth is one of the main issues in medical image processing. Precise estimation of the abnormal tissue growth aids in a better prognosis and post-operative

treatment. Any disease can be cured, and patients have a higher chance of surviving with early and correct detection.

The fundamental unit of the human body is a cell. Tumor formation is caused by the body's cells growing irregularly or abnormally. These tumorous regions may have different shapes and sizes. Different image intensities in the scan capture these regions. Figure 1 shows an MRI scan of a normal brain and a brain with tumorous growth. A tumor can be benign or malignant. The differentiating feature among them is their structure. While benign tumors have a uniform homogenous structure, malignant or cancerous tumors form heterogenous structures. Benign tumors are non-cancerous and can be surgically removed, as they seldom grow back. Malignant tumors, however, contain cancer cells and are a cause of much concern. These cells tend to

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invade healthy cells in their proximity as well. Also, a benign tumor can later become cancerous. A low-grade tumor can metamorphose into a higher-grade tumor. Therefore, timely detection and diagnosis of the exact stage and grade of tumors are crucial for proper treatment.

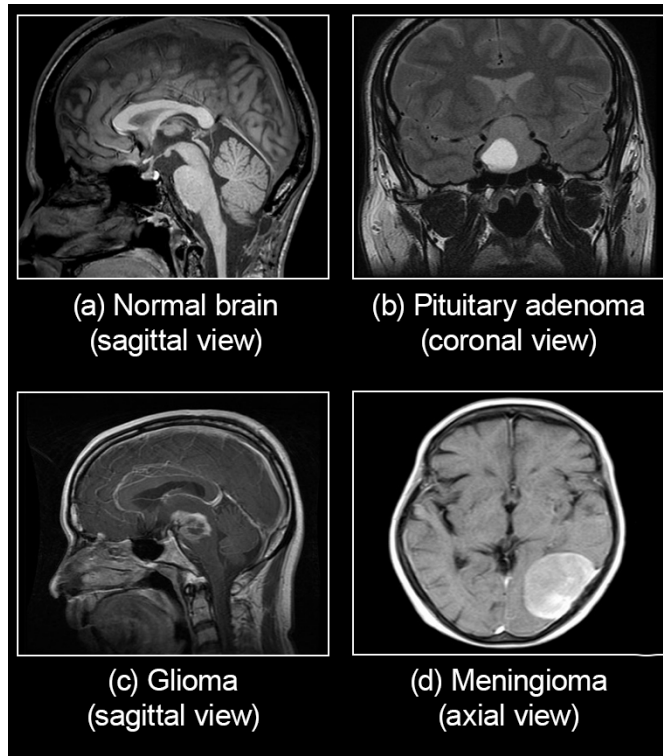


Figure 1. MRI scans of the normal brain and brain have different tumorous growth types.

The brain is a complex organ of the human body that regulates the biological mechanisms and individual characteristics of the body. Brain tumors occur when the brain cells start multiplying abnormally. Conventionally, image classification and tumor detection are done by human inspection (Hashmi and Osman, 2022). This is a complex, error-prone and time-consuming task, due to the huge amounts of data involved. The results depend on the expertise of the radiologists and are non-reproducible. Researchers have worked diligently to find the most accurate method for classifying tumors from MRI scans.

Advancements in computer-aided image processing and the fields of cancer and biomedicine have benefited greatly from the use of machine-learning techniques. They aid radiologists, and oncologists in improving overall surgical and diagnostic accuracy, help in proper prognosis, dose estimation and preparing a treatment plan for the patient. Image processing techniques help detect the tumour prematurely, limiting the need for a biopsy. Image classification is used to diminish the gap between computer vision and human vision. The main challenge is accurately detecting and classifying tumours from the MRI scan (Irmak, 2021). Timely detection of any disease

helps in better treatment, saving patients' life. For this reason, the detection and classification of Brain tumor are of great importance and has been extensively researched.

This paper uses a Support Vector Machine, Decision Tree, Naïve Bayes and Linear Regression to classify images as normal or tumorous. Thereafter, the tumorous images are further classified as (i) Pituitary, (ii) Meningioma, or (iii) Glioma using SVM, DT and a 6-layer Convolution Neural Network on the BRATS 2020 dataset. We compare the performance of all the classifiers used based on the accuracy, precision, recall and F1 score metrics. Section 2 of the paper sheds light on the work presented in extant literature in the area of brain tumor classification. Section 3 discusses the methodology adopted in this work for preprocessing images and their classification. In Section 4, we discuss the results obtained from our experiments. Confusion matrices and other evaluation measures including accuracy, precision, recall, and F1 score are used to present the results. In Section 5, we wrap up our analysis.

Relevant Work

Research has been done on classifying and segmenting brain tumors from MRI images extensively using supervised and unsupervised techniques. Zacharaki et al. (2009) apply ranking-based feature selection on Region of Interest (ROI) and classify using support vector machine recursive feature elimination (SVMRFE). Their proposed method achieved 98.2 % accuracy for GL2-GL4 (glioma grade II and IV). González-Navarro et al. (2010) use Magnetic Resonance Spectrograph (MRS) images for classification using LOO bootstrap and Naïve Bayes, Logistic Regression, Linear Discriminant, Quadratic Discriminant, SVM with Linear and quadratic Kernel (SVM-L and SVM-2) and SVM Radial (SVM-R). Feature selection using Entropic filtering improved classifier performance. They could achieve better results for Short Echo Time data, with SVM-R giving the best accuracy of 55.5, 88.2, 87.2 (LET, SET, LSET data). Naik et al. (2014) performed a comparison of Naïve Bayes and Decision Tree classifiers to classify CT-Scan brain images into normal, benign and malignant. They used Median Filtering with 3x3 median filter for denoising, and Morphological Opening, Power law Transformation for Image enhancement. Their experiments conclude that Decision Tree gave better accuracy of 96% compared to NB. Kumar et al. (2017) also compared K-NN, SVM and Decision Trees for classifying brain MRI scans. RGB preprocessed the images to gray scale conversion, Gaussian filtering for denoising. The dataset was trained on a neural network,

segmented using morphology and clustering, and classification using K-NN, SVM and Decision Trees. Their results affirm better performance by the SVM classifier. In another study, Kumar et al. (2017) worked on SICAS Medical Image Repository. They apply DWT for feature extraction, PCA for feature selection, and SVM for classification achieving linear accuracy varying from 80%-90%. Abd-Ellah et al. (2016) experimented on data from Harvard Medical School, MICCAI 2014 Machine Learning Challenge (MLC). The MRI images were preprocessed for noise removal, features extracted by DWT, dimensionality reduction by PCA, and classification by kernel support vector machine (KSVM). They could achieve maximum classification accuracy of 100% using Gaussian radial basis function (GRB) kernel with a default scaling factor. Alfonse et al. (2016) make use of Expectation Maximization (EM) for segmentation, Fast Fourier Transform (FFT) for feature extraction, Minimal-Redundancy-Maximal-Relevance criterion (MRMR) for feature selection, and finally, SVM for classification. They could achieve an accuracy of 98.9% with their proposed model. Deepa et al. (2011) Present a survey of ML techniques used till 2011 for medical image classification and segmentation. Their survey noted that SVM and ANN for classification, FCM and K-means for segmentation, and GA and PSO for feature extraction are used effectively.

Havaei et al. (2016) used the BRATS2013 and compared *k*-nearest neighbor classifier (kNN), support vector machines (SVM), random forests and boosted decision trees. They claim that SVMs gave superior results. Chavan et al. (2015) used the WHO (World Health Organization) data from WBA (World Brain Atlas) Website. They studied the performance of K-NN classifier. After denoising the images using a Gaussian filter, contrast enhancement using Histogram Equalization, segmentation using Thresholding and feature extraction by GLCM (gray-level cooccurrence matrix), K-NN classifier gave 96.15% classification accuracy. Ain et al. (2014) employ an ensemble-based SVM classifier using weighted majority voting to combine results. They applied Fast Discrete Curvelet Transform for denoising, histogram-based and co-occurrence matrix-based textural feature extraction, and FCM for segmentation. Their ensemble classifier gave higher accuracy as compared to SVM and ANN. Keerthana (2018) propose a SVM-GA model wherein they employ a Median filter for noise removal, Feature extraction GLCM (Gray Level Co-occurrence Matrix), and SVM RBF (Radial Basis Function) for classification.

A genetic algorithm optimizes extracted features and SVM parameters to improve classification performance.

Researchers have also employed many unsupervised techniques. Logeswari et al. (2010) propose a model that uses Weighted Median (WM) filters for noise reduction and HSOM (Hierarchical Self Organizing Map) for image segmentation. Akil et al. (2020) propose a fully CNN architecture with Overlapping Patches inspired by the Occipito-Temporal Pathway (OTP) for the segmentation of high- and low-grade Glioblastomas on the BRATS 2018 dataset. They applied the class-weighting technique to segmentation results to overcome the unbalanced data problem. They concluded that CNN with Overlapping Patches provided good segmentation results compared to adjacent patches (Basheera and Ram, 2019; Mohan et al., 2022). Khan et al. (2021) apply k-means clustering for segmenting tumorous areas in the BRATS 2015 dataset. The preprocessed image is classified into two categories, benign or malignant, by a CNN model using VGG19 (Visual Geometric Graph). They also use synthetic data augmentation to increase the available data size. Ari and Hanbay (2018) propose an ELM-LRF (Extreme Learning Machine local receptive fields) framework for classification. The model selects random weights for convolution and pooling in the input layer, the least square method for calculating weights between the hidden layer and output layer. Tumor detection is done by Watershed segmentation. They compared the performance of their model with the Gabor wavelets-based method, statistical features-based method, and 6-layer CNN. They could achieve 97.18% accuracy on the BRATS 2013 dataset with their proposed method, which outperformed the other methods. Krizhevsky et al. (2012) also employ CNN, having five convolutional and three fully-connected layers for classification. They used data augmentation to reduce overfitting. They could achieve top-1 and top-5 test set error rates of 37.5% and 17.0%, which outperforms state-of-art techniques. Zhang et al. (2001) developed a Hidden Markov Random Field (HMRF) model combined with an expectation-maximization (EM) algorithm for fitting model parameters to segment normal brain images into three tissue categories - Gray Matter (GM), White Matter (WM) and Cerebral Spinal Fluid CSF. Abdel-Maksoud (2015) employs K-means clustering integrated with Fuzzy C means for brain tumor segmentation.

Materials and methods

Dataset and preprocessing

The image dataset used for experimentation in this study is the BraTS 2020 dataset available on Kaggle. The

dataset contains around 2870 MRI scans in the Digital Imaging and Communications in Medicine (DICOM) standard format, with 395 images of the healthy or normal brain without tumorous growth, 827 images of pituitary tumor, 822 images of meningioma, and 826 of

and Linear Regression, are used for this purpose. We found the best accuracy (96%) with SVM-RBF and Decision Tree classifiers, with SVM having an edge with a better Recall rate of 98%. Hence, we use these two supervised learning classifiers and a 6-layer CNN to

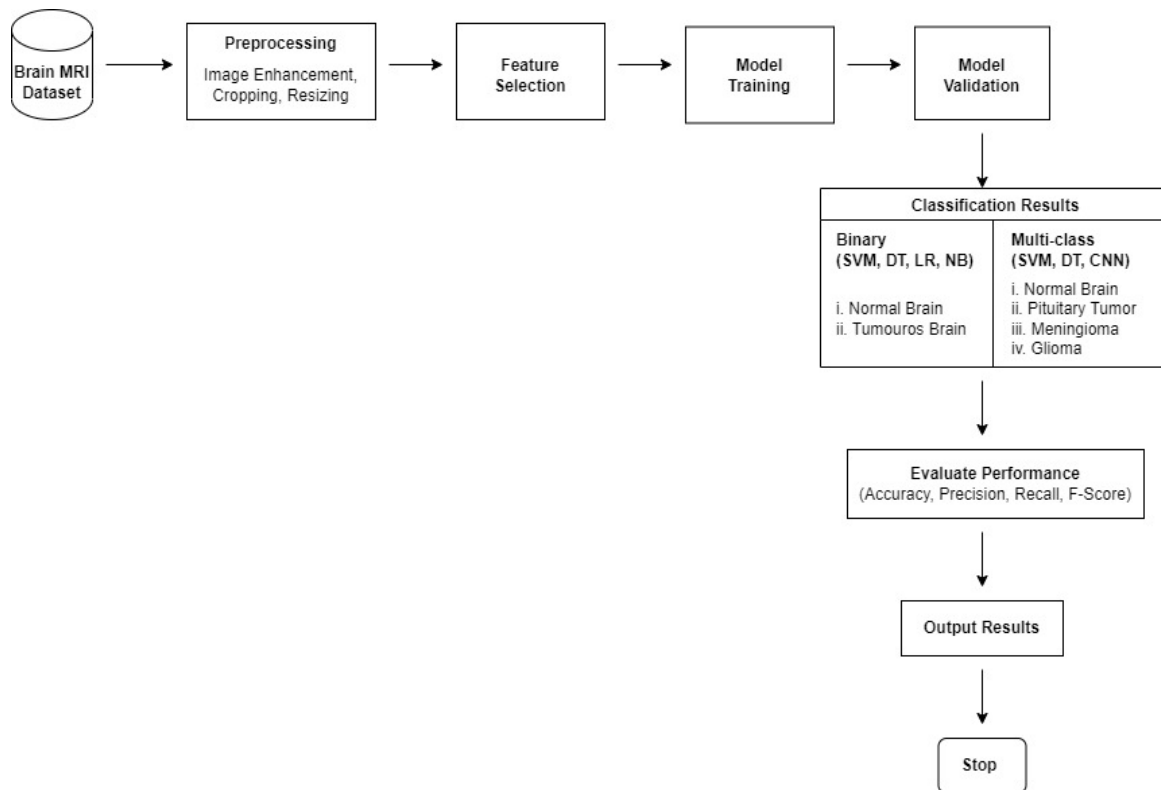


Figure 2. Overview of proposed methodology.

glioma.

One of the most important tasks for accurate tumor detection and classification is enhancing the image through preprocessing techniques. The images were preprocessed and cropped for image enhancement to aid in the accurate detection and classification of tumorous regions. Each input image was normalized and resized from 256 x 256 to 128 x 128 and rescaled by dividing each pixel by 255. Selection of effective features plays a key role in classification performance. An optimum feature set helps in achieving good classifier accuracy. We use PCA (Principal Component Analysis) for selecting optimum features and dimensionality reduction. We conducted classification experiments with and without feature selection and found that the accuracy of classifiers increased with PCA with 1100 features.

Overview of proposed methodology

The preprocessed dataset is split into training and validation datasets. Binary classification involves classifying images as Normal or no tumor brain and Brain containing tumor. Four supervised machine learning classifiers-SVM, Decision tree, Naïve Bayes,

further classify images into four categories – (i) No tumor, (ii) Pituitary tumor, (iii) Meningioma, (iv) Glioma. On comparing the performance of the classifiers based on our experiments, we found that CNN outperforms the other two classifiers with an accuracy of 93% and a Recall rate of 92%. An overview of the proposed methodology is presented in Figure 2.

Binary classification

We employ four supervised machine learning classifiers to categorize preprocessed MRI images as normal or tumorous. Binary classification (class 0 – No tumor, 1- Brain containing tumor) is performed using SVM with RBF (Radial Basis Function) kernel, Decision tree, Naïve Bayes and Linear Regression, with SVM yielding highest accuracy of 96% and Recall rate of 98%. In medical diagnosis, it is very important to see that the false negative rate is as low as possible, as it is comparatively better to misclassify a normal image than the other way around. Hence Recall plays an important role in such cases. Out of 1222 images, 977 were used for training and 245 for testing. After classification, 827

normal brain images were detected, and 395 were detected with tumors.

Multi-class classification

As the next step, we perform multi-class classification using SVM-RBF, Decision tree classifier and a 6-layer CNN to classify images into one of four categories – (i) No tumor (0), (ii) Pituitary adenoma (1), (iii) Meningioma (3), & (iv) Glioma (4). The input set of 2870 MRI images is split into two subsets in the ratio 80:20 for training, and testing, respectively. 2296 images were used for the training dataset and 574 for validation. After classification, we obtained 395 with no tumor, 827 with a pituitary tumor, 822 with meningioma and 826 with glioma tumor images.

connected layer equals the number of classes the model predicts.

We use a 6-layer CNN model with five convolution layers with different kernel sizes and one fully connected layer. The first layer uses a kernel size of 5 x 5, while the second and third layers use a kernel size of 3 x 3. The fourth and fifth layers employ a 2 x 2 size kernel. Activation function ReLU is used across all five convolution layers. Stride is the difference between two successive kernel positions. Stride has been kept at 1, as it is the most common choice for stride, and padding is kept at zero in the experiments. The main function of the Pooling layer is to cut down on the number of learnable parameters in order to improve model performance, increase computation speed, reduce memory, and avoid

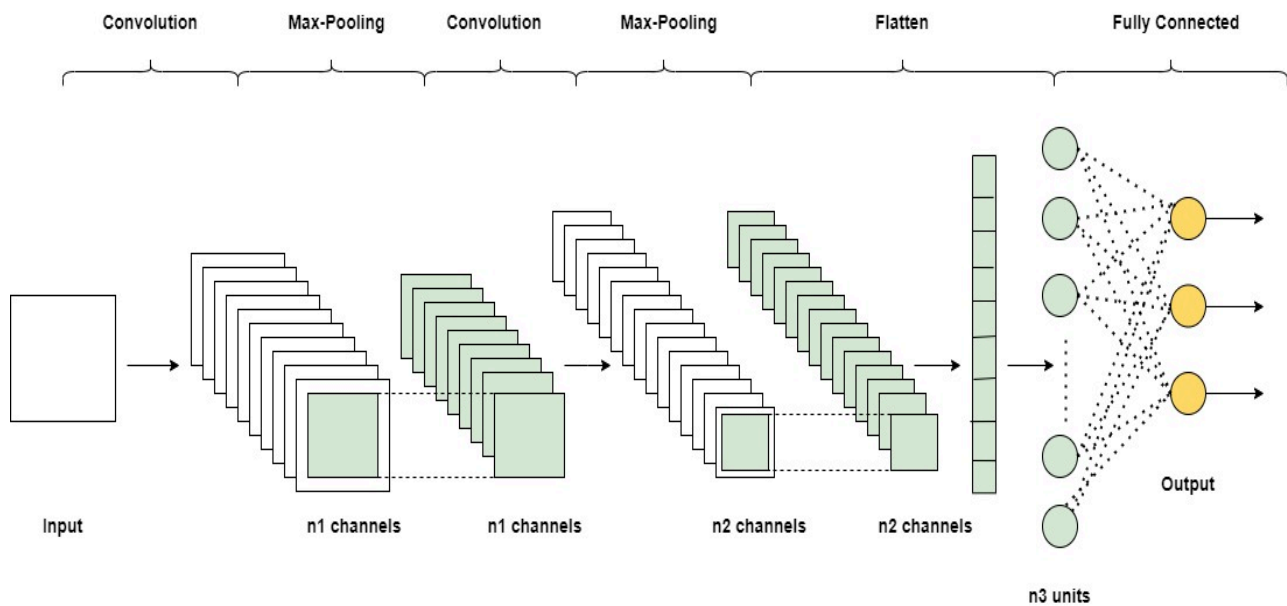


Figure 3. Proposed CNN model.

The CNN model has been used widely in image classification problems. A CNN uses convolution, pooling and fully connected layers. Convolution and pooling layers are used for feature extraction, where the image is resized, rescaled, and denoised. In the convolution layer a linear operation is applied to extract features using a kernel as a small array of weights. The kernel is applied all over the input to obtain an activation map. This activation map is taken as input by the Pooling layer, which further samples the dataset to reduce dimensionality and speed up computation. After repetitive sequences of convolution and pooling, the Flattening layer converts the dataset into a long continuous vector. This vector contains high-level image features which are used by the Fully-connected layer for classifying the image into various classes based on the training data. The number of hidden units in the Fully

overfitting. In our experiments, we employ Max pooling using a 3 x 3 kernel, zero padding and stride = 1. The Fully connected layer, also known as dense layer, has one-to-one connections between the layers and is used for output. Every input is connected to every output by some weight in this layer. The final task of classification of images is performed here. Once the convolution layer extracts all significant features and the pooling layer samples the dataset, the fully connected layer is used for the final classification output. A ReLU function follows every fully connected layer. Softmax activation function is used for multi-class classification. This function gives output values ranging from 0 to 1, a sum of all values being 1.

We import Tensor flow and Keras to build the CNN Model. The input consists of 2870 MRI images. Each image was divided by 255 to normalise, resale, and resize to 128 x 128.

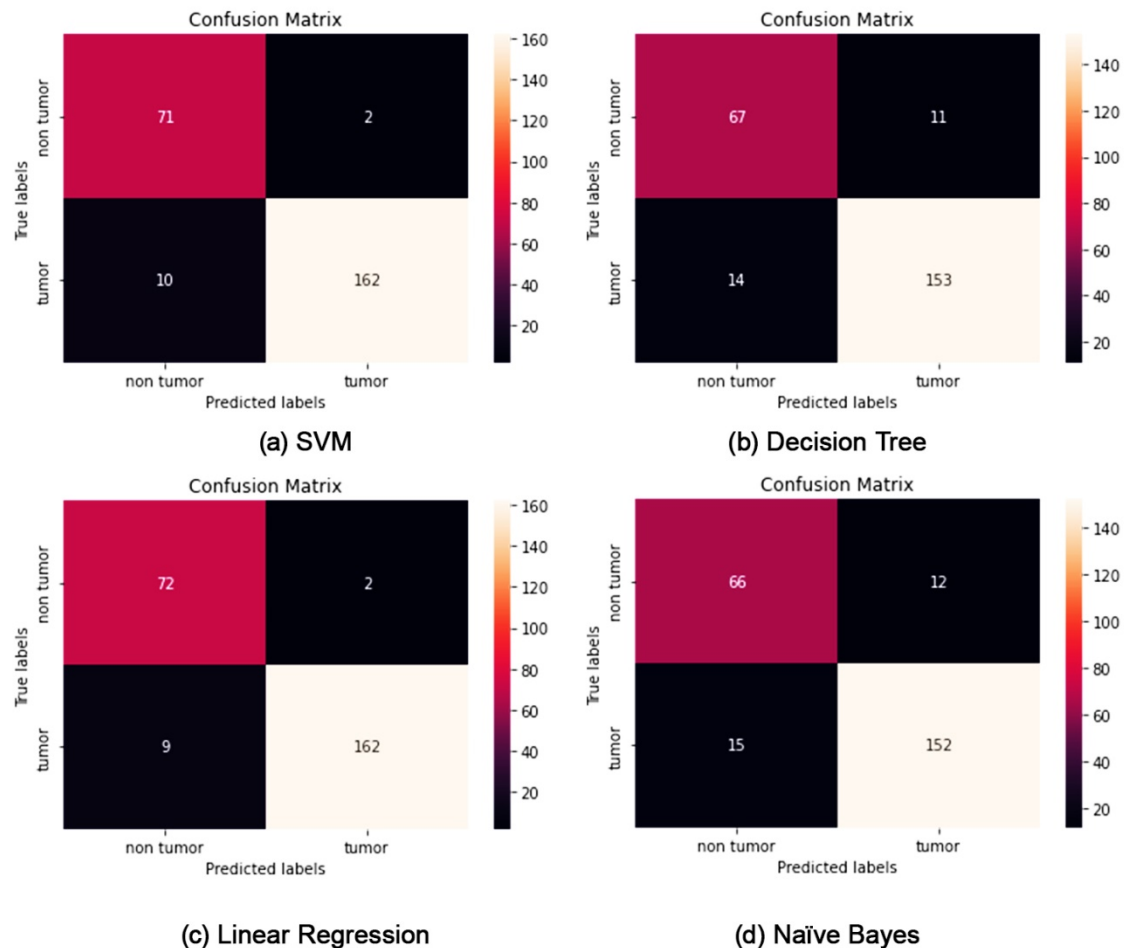


Figure 4. Comparison of classifiers using confusion matrix.

Results and discussion

The results for binary and multi-class classification are discussed separately for the sake of clarity. We use the Confusion Matrix, Accuracy, Precision, Recall, and F1 score to evaluate classifiers' performance.

Binary Classification

Four supervised machine learning classifiers – SVM, Decision tree, Linear Regression, Naïve Bayes, have been used for the binary classification of images in the dataset. Confusion matrices show classifier performance across different classes. Confusion matrices of each of these classifiers are depicted in Figure 4. Other performance metrics, such as accuracy, precision, recall and F1 score, are tabulated in Table 1.

F1-score is a harmonic mean of Precision and Recall. As a result of our experiments, SVM and Decision tree were found to yield highest F1-Score of 97% and accuracy of 96%, however, SVM outperforms in terms of Recall. In medical cases, Recall is an important metric.

Hence, we can conclude that SVM is the most suitable classifier in this case.

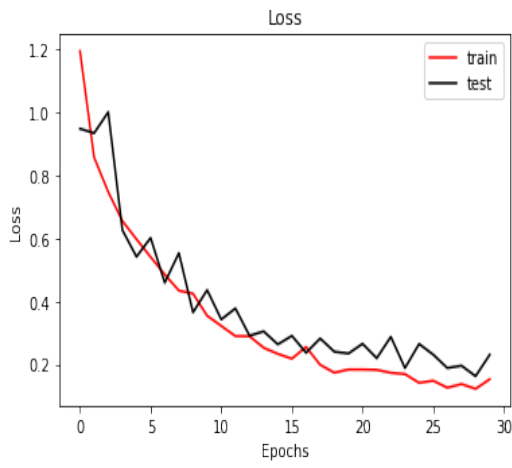
Table 1. Comparison of classifier performance.

| Classifiers | Accuracy | Precision | Recall | F1-score |
|-------------|-------------|-----------|-------------|-------------|
| SVM | 0.96 | 0.96 | 0.98 | 0.97 |
| DT | 0.96 | 0.98 | 0.96 | 0.97 |
| LR | 0.95 | 0.93 | 0.99 | 0.96 |
| NB | 0.88 | 0.89 | 0.95 | 0.92 |

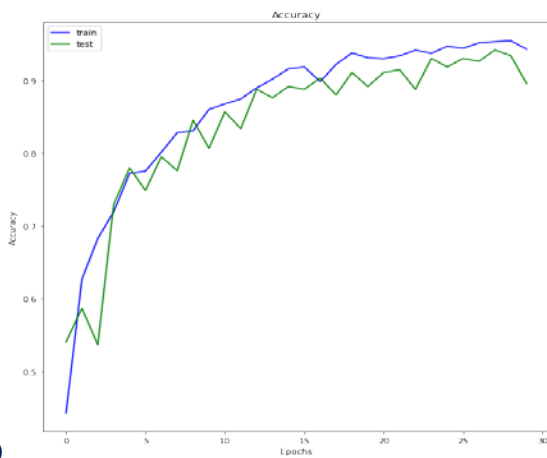
Multi-class classification

We employed SVM, Decision tree and a 6-layer CNN to classify tumours in the Pituitary, Meningioma and Glioma categories. Performance of the classifiers was compared using metrics accuracy, precision, recall and F1 score. These results are tabulated in Table 2. Confusion matrix showing class-wise accuracy, as depicted in Figure 6.

The parameters in CNN were checked with 30 epochs in training and testing. The plot diagram of Figure 5 depicts the loss and accuracy of data with respect to epochs.

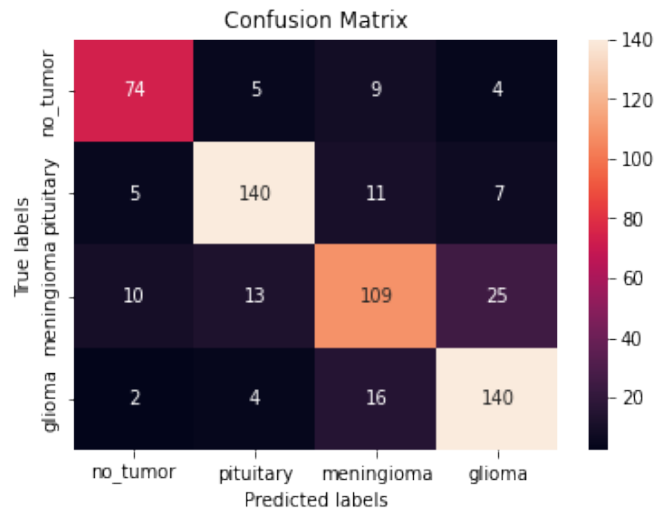


(a)

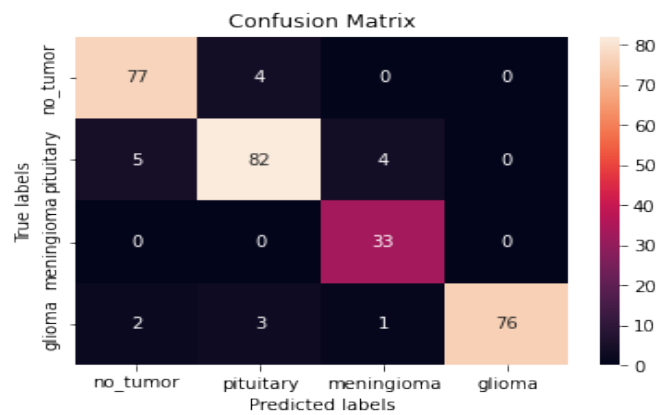


(b)

Figure 5. Loss relation and accuracy with epochs

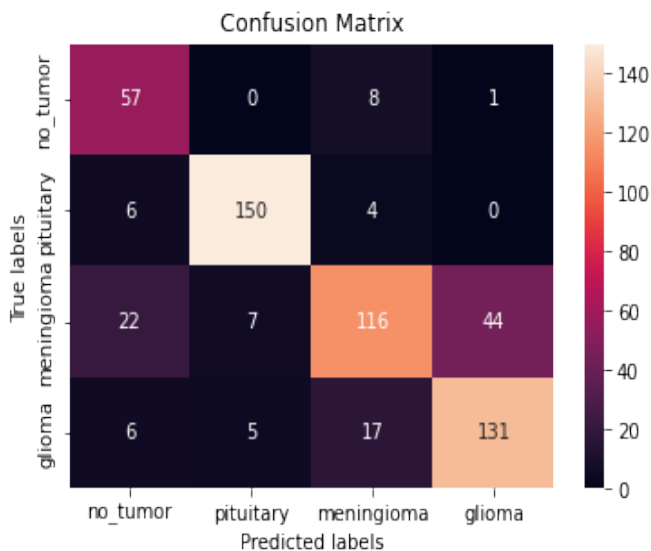


(b) Decision tree



(c) CNN

Figure 6. Multi-class classification confusion matrices.



(a) SVM

Table 2. Performance metrics for multi-class classification.

| Classifiers | Accuracy | Precision | Recall | F1-score |
|-------------|-------------|-------------|-------------|-------------|
| SVM | 0.83 | 0.85 | 0.72 | 0.83 |
| DTC | 0.80 | 0.80 | 0.80 | 0.80 |
| CNN | 0.93 | 0.94 | 0.92 | 0.93 |

Conclusions

Accurate and early detection and classification of brain tumors from MRI scans is imperative for effective and timely treatment. Manual techniques take a lot of time due to the large amount of data involved. Also, the results are non-reproducible as they depend on the radiologist’s expertise. In this study, we make use of brain MRI scans in the BraTS 2020 dataset and classify images as normal brains and brains containing tumorous growth. Supervised machine learning classifiers -

Support Vector Machine, Decision Tree, Linear Regression and Naïve Bayes have been used for binary classification. As a result of our binary classification experiment, we found that SVM outperforms the other classifiers with an accuracy of 96% and Recall rate of 98%. Thereafter, we further categorize images into four classes - (i) No tumor, (ii) Pituitary adenoma, (iii) Meningioma, & (iv) Glioma. We evaluate and compare the performance of SVM-RBF, Decision tree and CNN for multi-class classification. We use a 6-layer CNN model with 5 convolution layers with different filter sizes, ReLU activation function, and one fully connected layer. As a result of our experiments, CNN was found to outperform the other classifiers with an accuracy of 93% and a Recall rate of 92%.

This work can be extended to determine the grade and size of a tumor in tumorous images. This can help surgeons and oncologists to get an accurate estimate of the type of tumor and prescribe the best course of treatment for the patient. Image segmentation algorithms can be applied to the images showing tumorous growth. This can help estimate the area and volume of the tumorous region, which will aid the oncologist to perform surgery accurately and precisely. The accuracy and timeliness of analysis benefit both the patient and the doctor to effect a timely cure or treatment.

Conflicts of interest

There are no conflicts of interest for the authors in the presentation and publication of this work.

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