A Comparison Study of Various Machine Learning Models for Classifying Tumors in Brain MRI

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ABSTRACT
Magnetic Resonance Imaging is a non-invasive tool used for exploring the internal physique of human body. Machine learning models play a vital role in diagnosing anomalies in early stages so that treatment procedure can be planned accordingly to the category of tumor. In this paper, a comparison study is executed on various machine learning models to classify brain tumors in MR images. For conducting experiments, the data is collected from publicly available dataset. Principal Component Analysis (PCA) is used to extract features from the input brain MR images. The machine learning models classify the images into two categories namely Glioma tumor and Pituitary tumor.

General Terms
Brain Tumor, Machine Learning, Classification, Glioma Tumor, Pituitary Tumor

Keywords
Support Vector Machine, Random Forest Classifier, Normalization, Gray Level Co-occurrence Matrix, Principal Component Analysis, XGBoost Classifier

1. INTRODUCTION
Research says that the growth rate of brain tumor is increasing 12% every year [1]. Tumors are of two types, Benign and Malignant. The former is less harmful whereas the latter is deadly and are more likely to span across other tissues. World Health Organization indexed brain tumors into 120 classes of tumors. They are ranked from grade I to IV (low risk to high risk). The prevailing tumors are Glioma, Meningioma, Pituitary and Astrocytoma [2]. Glioma tumors represent about 52 percent of all dominant tumors whereas Pituitary tumors make 15 percent. Hence early detection of brain tumors are pivotal for prognosis.

Manual classification of brain tumor MRI depends on the reachability and expertise of a radiologist. The medical practitioner locates whether the brain MRI is normal or unusual. The abnormal images are further classified into various tumor types. For huge volumes of MRI data, manual involvement is time consuming and tedious task. Automating tumor image analysis improves the accuracy of image processing dramatically.

Machine learning approaches contribute much to the field of medical image analysis during clinical diagnosis. Traditional machine learning techniques involves several steps with preprocessing, feature extraction, dimension reduction, segmentation, classification and many more. The crux is feature extraction as the accuracy of classification task highly counts on it. The most important features of brain tumors are correlated to the position of tumor region with shape, boundary and texture [6].

2. LITERATURE REVIEW
Different machine learning algorithms are offered for detecting and classifying brain tumors from MRI. Khan I.U et al [7] proposed the concepts of PCA and SVM for classifying tumors as benign and malignant. Second order features are extracted using GLCM to boost feature reduction. The concept of SVM together with wavelet is used for classifying brain MRI either as normal or abnormal in the work suggested by Chaplot S [13].

Krishnakumar S et al [8] used Gabor Wavelet Transform (GWT) for feature extraction and the feature values are given into a K-means clustering algorithm for segmentation. Finally, multi kernel SVM is employed for the classification task.

Kaplan K et al [9] uses Local Binary Patterns (LBP) for feature extraction. The feature matrix is led to a variety of classifiers namely K-Nearest Neighbor (KNN), Random Forest (RF) and Linear Discriminant Analysis (LDA) for classifying tumors as Glioma, Pituitary and Meningioma. The results indicate that KNN achieved highest success rate in classification task.

A hybrid model was proposed by Ramaneswaran S [10] for classifying acute lymphoblastic leukaemia from microscopic white blood cell images. The CNN based Inception v3 [14] is used as feature extractor and finally XGBoost model performs classification.In [11] and [12] Random Forest algorithm is utilized as classifier as well as a segmentation tool for different image processing applications.

3. PROPOSED METHOD
The initial goal of the proposed work is to classify brain MR images into Glioma and Pituitary tumors. Fig (1) gives a picture of the flow chart of the proposed framework. First, the input image is preprocessed to prepare it for classification. The preprocessed images are directed to a feature extractor. Here Principal Component Analysis (PCA) is employed for feature extraction and reduction. The extracted features are given to four classifiers namely Logistic Regression, Support Vector Machine, XGBoost classifier and Random Forest classifier. The experimental results shows that SVM and Random Forest classifier gives effective classification of brain tumors.
3.3 Classification

In a machine learning environment, features are given as input to the ML models which in turn notice the patterns within features. These patterns are used to identify ‘labels’ that successively categorize data. For the classification of Glioma and Pituitary tumors from brain MRI, several machine learning algorithms were implemented including SVM, XGBoost classifier, Logistic Regression, and Random Forest classifier. Scikit-Learn library of Python is used for executing different classifiers in this work.

4. DATASET

Magnetic Resonance Imaging is a structured technique to show brain tissues. The powerful magnets of MRI scanner aligns the protons present in every cell to the direction of magnetic field. When the radio frequency pulse is removed, the protons returned back to equilibrium and the response action is captured as MRI. The intensity of pixels in the image relies on the type of brain tissues.

For the current study, the models are assessed on the publicly available dataset from Kaggle [4]. The dataset contains 2-D slices of Glioma tumors and Pituitary tumors. The training data comprises 1653 subjects that include 826 Glioma and 827 Pituitary tumors. The training data used in this study is further divided as train data and validation data in the ratio 80:20 without overlap. Thus the train data contains 1322 subjects and validation data contains 331 subjects. Finally, the trained machine learning model is subjected to test data with 174 subjects containing both types of tumors.

5. EVALUATION

The performance of the model is measured in terms of Accuracy, Precision, Recall and F1 score. The terms are defined as follows where TP (True Positive) represents the cases in which actual output and predicted output are positive, TN (True Negative) denotes the cases when both actual output and predicted output are negative, FN (False Negative) shows the cases in which the actual output is true and predicted output is incorrect, FP (False Positive) represents the cases where the prediction is true and actual output is incorrect.

\[
\text{Accuracy} = \frac{TP + TN}{TP + TN + FP + FN} \quad (2)
\]
\[
\text{Precision} = \frac{TP}{TP + FP} \quad (3)
\]
\[
\text{Recall} = \frac{TP}{TP + FN} \quad (4)
\]
\[
F1 \text{ score} = 2 \cdot \frac{\text{Precision} \cdot \text{Recall}}{\text{Precision} + \text{Recall}} \quad (5)
\]

6. EXPERIMENTAL RESULTS

In this section, the results obtained using the proposed method is presented. The experiments in this work use Jupyter Notebook with a Core i3 CPU @ 1.99 GHz and 4GB RAM. Fig 2 and Fig 3 illustrates the outputs of the proposed framework on MRI slices from Glioma and Pituitary tumor patients respectively. The label ‘misclassified’ denote incorrect classification result. A Pituitary tumor is misclassified as Glioma tumor and vice versa.
A comparative study has been carried out to evaluate different classifiers’ performances such as Support Vector Machine, Random Forest classifier, XGBoost and Logistic Regression. The classifiers are investigated with PCA and without PCA. Table 1 and Table 2 reports the obtained classification accuracy and execution time without and with PCA respectively. Table 3 illustrates the precision, recall and F1 score of different classifiers on Glioma and Pituitary tumors. Random Forest classifier shows best performance (97.88%) when PCA is not applied to the dataset while SVM achieved an accuracy of 97.58% with PCA, which is ahead of other classifiers. It is also noted that PCA reduces the execution time of all classifiers.

Table 1. Comparative accuracy and execution time for different classifiers without PCA

| Model               | Accuracy | Execution time (sec) |
|---------------------|----------|----------------------|
| Random Forest classifier | 97.88%   | 8.57                 |
| SVM                 | 97.28%   | 27.08                |
| Logistic Regression | 95.46%   | 3.97                 |
| XGBoost classifier  | 94.56%   | 27.05                |

Table 2. Comparative accuracy and execution time for different classifiers with PCA

| Model               | Accuracy | Execution time (sec) |
|---------------------|----------|----------------------|
| SVM                 | 97.58%   | 1.72                 |
| Random Forest classifier | 95.56%   | 2.51                 |
| Logistic Regression | 95.46%   | 0.53                 |
| XGBoost classifier  | 89.72%   | 1.69                 |

The tumor classification is evaluated through a confusion matrix with c=2 classes where class 1 belongs to Glioma tumor and class 2 belong to Pituitary tumor. They are measured in terms of accuracy, precision, recall, F1 score and ROC. Receiver Operating Characteristics (ROC) curves provide the ratio among false positive rate and true positive rate. The evaluation metrics with ROC for Random Forest classifier is mentioned in Fig 4.
Fig 4: Receiver Operating Characteristics (ROC) curves for Random Forest Classifier model.

### Table 3. Comparative training performance of different classifiers

| Model               | Glioma Tumor | Pituitary Tumor |
|---------------------|--------------|-----------------|
|                     | Precision    | Recall | F1 score | Precision | Recall | F1 score |
| Logistic Regression | 0.96         | 0.95   | 0.95     | 0.95      | 0.96   | 0.95     |
| SVM                 | 0.98         | 0.97   | 0.97     | 0.97      | 0.98   | 0.97     |
| XGBoost classifier  | 0.93         | 0.96   | 0.94     | 0.96      | 0.94   | 0.95     |
| Random Forest classifier | 0.97 | 0.99 | 0.98 | 0.99 | 0.97 | 0.98 |

### 7. CONCLUSION

This work illustrates a comparison study on different machine learning models that classify input MRI into Glioma and Pituitary tumors. To assess the model performance, the authors carry out experiments with and without feature extraction and reduction techniques. Feature selection helps to remove irrelevant features thereby alleviating the effect of curse of dimensionality. PCA facilitates generalization capability and speed up learning process. The model efficiency improves with PCA where the execution time of the model got improved.

The models SVM and Random Forest classifier provide acceptable results compared to XGBoost and logistic regression. The experimental results show that SVM achieved an accuracy of 98% with PCA in 1.72 seconds. The overall experimental results conclude that the proposed models perform better in classification task. The precision criteria is close to one and hence the proposed model is reliable.

In future, the method needs to be tested on real time patient data with normal brain images. This requires more preprocessing steps which include intensity correction, bias normalization and skullstripping. Also, the current work can be extended using different feature extraction techniques like Discrete Wavelet Transform and Grey Level Co-occurrence Matrix. A comparison study can be performed over these techniques using the same dataset.

Another future work may include the implementation of tumor segmentation from the classified images. Content based Image Retrieval, Watershed algorithm, Gaussian Mixture model, Markov Random Field and many more can be used for the tumor segmentation task. Segmentation of Grey Matter, White Matter and Cerebro Spinal Fluid may also be taken into account as future improvement.

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