Research Article

A COMPUTER-AIDED BRAIN GLIOMA IDENTIFICATION USING MRI BASED TEXTURE ANALYSIS

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Abstract

Brain gliomas are deadly tumors that are discovered after a stressful, lengthy, and difficult procedure. Radiology is a broad and varied field that detects brain tumors, but interpreting radiological pictures of the brain needs advanced training, experience, and subject-matter expertise. The endeavor is challenging due to the wide variation in brain tumor tissues among individuals and similar cases within normal tissues. Magnetic resonance imaging (MRI)-based computer-aided biomedical image processing solves the challenges associated with brain tumor localization and identification while simultaneously addressing the shortage of qualified radiologists. This study proposes a computer-aided brain glioma identification (CABGD) model for brain glioma identification using the texture analysis of brain MRIs. The proposed model makes use of machine learning classifiers and brain MRI data. There were 200 MRIs of both normal and glioma brains in the experimental dataset. Firstly, the MRI dataset was pre-processed to crop the MRIs, size equalization, and gray-level conversion. Next, noises were removed by applying filters. Two ROIs of the sizes (10×10) were taken on each MRI after the tumor region was segmented. After extracting COM texture features from each ROI, thirty optimal features were obtained through a compound supervised feature selection, blend of Fisher (FSHR), probabilistic model of error (POE), average correlation (AVC), and mutual information (MUI). The optimal feature brain MRI dataset was classified into glioma and normal brain by applying machine learning classifiers named Bayas Net (BN), logistic model tree (LMT), and partial decision tree (PART); the classification results of the NB, LMT, and PART classifiers were 79.75%, 82.75, and 85%, respectively.

1. INTRODUCTION

Tumors can destroy any critical human organ, like the lungs, liver, stomach, or brain. Just in the year 2018 millions of cases were identified by the International Agency for Research on Cancer (Bray et al., 2018). These abnormalities in the brain cells are identified as a neoplasm or brain tumor (Nawaz et al., 2022). Benign and malignant are the two main types of brain tumors. Brain tumors are either primary or secondary (Sinha, 2018). The primary tumors originate within the brain, whereas the secondary brain tumors grow in the brain from some other body organ (Bianconi et al., 2013).

Gliomas are the most prevalent form of brain tumors, which may be malignant or benign. More than one hundred brain tumors have been identified (D.N. et al., 2016). The process for accurately diagnosing a glioma brain tumor involves several steps carried out by radiologists, comprising physical examination, review of medical history, contrast agents, and biopsies (J Strong & Garces, 2016). The main objective is to determine the accurate location, area, and orientation of the

abnormal tissue. Imaging scans, which follow physical examination and historical analysis, are essential for creating digital brain images. Magnetic Resonance Imaging (MRI) is preferred for its superior contrast and resolution (Bauer et al., 2013). While Computed Tomography (CT) scans are also used, they are not as effective as MRIs. Other diagnostic methods include perfusion MRI, functional MRI, positron emission tomography (PET), and flu-orthodoxy-glucose PET/CT (FDG-PET/CT) (Perkins,A. Liu, 2016).

Manual brain tumor diagnosis is a complex, time-consuming, and stressful process, with the potential for human error due to factors like fatigue and data overload. Early and precise diagnosis of brain tumors is crucial and spurs ongoing research. Accurate measurement of the tumor area is also vital for targeted treatment. Machine Learning (ML) methods are significantly advancing the field of medical image analysis. Recent developments in ML have led to the creation of automated systems for diagnosing brain tumors. These systems provide vital support (Nawaz et al., 2022).

This research study focuses on development of automated identification of glioma brain tumors. For the purpose, the research proposed a computer-aided brain glioma identification (CABGD) model to identify a brain glioma using the texture analysis of MR images. The proposed model makes use of state-of-the-art machine learning techniques.

2. Literature Review

The following section provides a precise survey of the different techniques that have been used for brain tumor identification.

An artificial neural network (ANN) model has been employed for the identification of brain tumors in MR images. The dataset comprised the normal and abnormal brain MR images. Gray Level Co-occurrence Matrix (GLCM) texture features were extracted for texture analysis of brain tissues. The research work identified the brain tumor mess with an acceptable classification accuracy of 81.4%. This research emphasizes the potential of ANN machine learning model and the texture analysis to achieve brain tumor classification (Jain, 2013).

In another research study, Santhosh and his research fellows presented a machine learning classification model to classify normal and abnormal brain tissues. The dataset used this research study, contained the normal and abnormal brain MR images. After the pre-processing, threshold and watershed segmentation was applied to isolate the brain mess. Geometric, intensity and texture properties were extracted from the isolated regions and machine learning algorithm, support vector machine (SVM) was trained on the featured dataset. The SVM classifier gave an overall 85.32% classification accuracy (Hatcholli Seere & Karibasappa, 2020).

A research experiment has been conducted under Ranji with his research fellows (Rajni et al., 2020), for the identification of brain tumor. This research study proposed a Bayesian classification model for the identification of brain tumor based on MR images. The 114 MR images were collected comprising both normal and tumorous MRIs, and the basic image pre-processing techniques were applied. To isolate the tumor region Otsu's threshold segmentation scheme was used. Morphological operations were performed to extract the geometric properties of the MR images. A Naïve Bayes classifier was trained on 64 images and was tested on 50 images to classify the normal and abnormal images. The proposed model gave a noteworthy classification accuracy.

In a research experiment, Kaur with his research fellows explored and demonstrated the impacts of various image segmentation techniques in medical imaging modalities. Major segmentation categories described were model-based, partial_differential_equation based, threshold-based, edge_detection based, region_growing based, clustering-based, and watershed-based. Thresholding, edge detection, region growing, and watershed

seemed more promising (Kaur & Kaur, 2014).

Another research work has been presented by MRI-based classification using machine learning models to classify brain tumor. The research work highlights the importance of feature selection and the potential impact of image quantization levels on classification accuracy in a non-invasive and fast diagnostic approach for brain lesions. After extracting the texture features, the model applied feature selection scheme to get a subset of 32 the most optimized features. The proposed model employed SVM classifier to discriminate the brain lesion with the normal brain images. The resultant model showed a significant classification accuracy using support vector machine (Ortiz-Ramón et al., 2020).

Afshar with his co-authors proposed an automated breast cancer diagnosis model by devising the ANN classification model to differentiate between benign and malignant breast tumors. The authors collected 184 breast cancer MR images comprising benign and malignant breast tumors. The research team implemented a breast tumors diagnosis model using multi-fractal dimensions and backpropagation neural networks. The model was trained on 184 breast cancer MRI of benign and malignant types. The research experiment gained high accuracy in classifying breast tumors, by showing a precision of 82.04% (Afshar et al., 2019).

Least-square-support-vector-machine (LS-SVM classification model is proposed by Selvaraj with his co-authors for the diagnosis of brain tumor, where LS-SVM is a variation of SVM. MRI dataset was collected for the normal and healthy brain, and then basic image pre-processing was applied for the next processing. GLCM texture features were extracted from the normal brain and the tumorous brain MR images for texture analysis. The research experiment tried different machine classifiers, including MLP, radial-basis-function, k-nearest-neighbor, and LS-SVM.

The LS-SVM got the better of the other classifiers and gave noteworthy classification accuracy. The proposed model discriminated against the normal brain and the tumorous brain images successfully (Selvaraj et al., 2007).

Arsa, with her research participants, suggested a brain tumor segmentation model based on Sobel operator plus thresholding scheme. The research model comprised several steps, which include dataset collection, preprocessing. After computing the initial gradient, the threshold value was fixed, which helped to differentiate between the background pixel and the edge pixel. A closed contour algorithm was applied recursively to implement seeded-growing and separate tumor regions. The proposed brain tumor segmentation model worked better than others (Aslam et al., 2015).

The survey of the literature elaborated that most of the research work is based on a suitable feature selection method, and irrelevant features impact the reliability of the underlying model. Datasets are also small, and most surveyed schemes don't focus on a specific dataset. Almost no work was found to identify the glioma brain tumor separately. In this research work, a novel computer-aided brain glioma identification (CABGD) model has been designed. The proposed model identifies the brain glioma by classifying the brain MRI dataset using machine learning classifiers.

3. Material and Method

This section demonstrates the complete introduction to the designed CAGBD model. The model incorporated the fundamental steps of knowledge discoveries from databases using machine learning classification. In the first step, the brain MR images were collected. In the second step, the collected brain MR images were pre-processed. In the third step, the tumour area was marked by the expert radiologists to confirm the ground truth value. In the fourth step, GLCM features were drawn out for texture analysis. In the

fifth step, the most critical features were selected by applying a composite feature selection technique. In the sixth step, three machine learning classifiers were deployed to identify the glioma brain tumour. The complete methodology model is shown in Figure # 1.
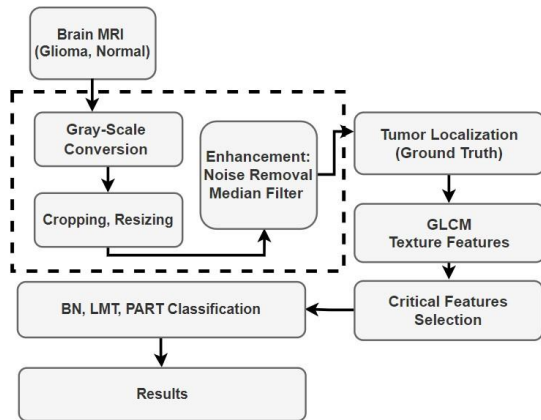

Figure 1. CABGD Methodology Diagram

3.1 Dataset

The brain MRI digital scans dataset for this research study was collected from the BVH-RDL(QMC-BVH, 2020). Brain MRI dataset of 200 persons was collected, where 100 MR scans were of normal brain and 100 MR scans were of glioma patients. When we took two ROIs on each MRI scan, it generated an ROI image dataset of 200 healthy brain images and 200 of glioma brain images. Thus, this research study took place on a total 400 ROIs image dataset.

3.2 Pre-processing

During preprocessing, the MR Images were converted into grayscale images, as the color images increase the amount the data massively which introduced not only the complexity but may also increase the computational cost. Next, all the MR images were cropped to remove the unnecessary areas of the image and the private information of the patients to ensure the ethical research norms. Next, all the images were standardized to the size of 512×512, as all the images must be equal sized before further processing. To reduce noise, a median filter is carried out on the pixel values. Ultimately, we obtain normalized, enhanced, and smooth MR images of the brain dataset. The sample brain MRIs of the normal and abnormal slices are shown in Figure # 2.
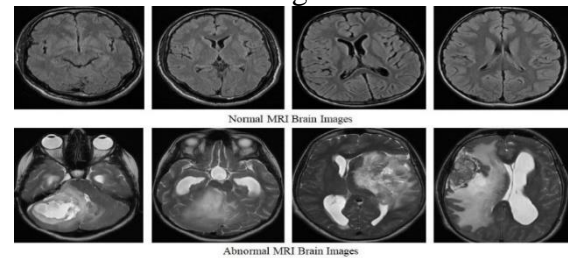

Figure 2. Sample Brain Normal and Glioma (Abnormal) MRIs

3.3 Features Extraction

The feature extraction phase comprised a number of key steps, which included tumour region segmentation by expert radiologists marking the tumour area to ensure the ground truth value. When tumour areas were marked, the process of taking region-of-interest (ROI) on each of the MRI digital scans was initiated. In this research experiment, a couple of equally sized ROIs of sizes 10×10 were taken from each MRI digital scan. For texture analysis, COM texture features were extracted from each of the ROI using Mazda 4.6 (Strzelecki et al., 2013) During this process, the total number of texture features was 88,000 ($200 \times 2 \times 220$). All the extracted features are described precisely.

3.3.1 COM Texture Features:

COM texture features are commonly used MRI based medical image analysis and classification. There are several reasons to use COM features for this purpose. MRI images frequently consist of texture patterns that are easy to view but they are difficult to measure accurately using only simple image intensity characteristics. COM texture features can detect texture patterns and spatial properties of the image among the pixel intensities, offering a more comprehensive depiction of image texture. Similarly, the COM features are sensitive to the tissues which are present in the MR images. Additionally, COM texture features provide more robustness against the noise present in the medical images.

3.4 Feature Selection

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The extracted 88,000 texture features were not sufficient for efficient classification because a lot of unnecessary features were also becoming part of our obtained feature vector. Thus, in this step, the unnecessary features were eliminated, and the features were kept in hand for further dataset classification. For feature selection, we combined FSHR plus POE plus AVC plus MUI. FSHR applied an indexing method to select the most discriminated features. POE took the probabilistic approach to determine the ratio of improperly classified features between the total number of features. The AVC computed the sums and averages of the old and new selections of the features and the coefficient of correlation. MUI used the ranking of features and densities of the corresponding probabilities of the multiple random variables to select the most critical features. The designated scheme gave the thirty most critical features, which are shown in Table # 1.

anomaly finding, and making predictions. Each node in NB is a random variable, and the edges of the nodes contain the conditional probability for these random variables. Potential advantages are its capability of handling uncertainty occurring in the dataset, effectively handling missing values, and for small dataset their graphical structure is easily understandable. Some of the weaknesses of the Bayesian classifier are as follows. For large scale networks, the learning cost exponentially increases (John & Langley, 2013).

3.5.2 LMT Classifier

The LMT ensembles decision tree learning with logistic regression (LR) with a corresponding supervised training technique. A decision tree with linear regression models at its leaves to form a piecewise linear regression model. It is opposite to regular decision trees with constants at their leaves, which would yield a piecewise constant model and is the

Table 1: Selected Features Set (FSHR+POE+AVC+MUI)

S(0, 2) sum variance	S(2_2) inverse_diff_momentum	S(0, 5) correlation
S(1, 0) sum average	S(0_2) inverse_diff_momentum	S(0, 3) sum average
S(3, 3) entropy	S(0_3) inverse_diff_momentum	S(0, 4) correlation
S(1, 0) correlation	S(3_-3) inverse_diff_momentum	S(0,1) inverse differ momentum
S(5, -5) inverse diff momentum	S(4_-4) inverse_diff_momentum	S(2, 2) correlation
S(0, 1) angle second momentum	S(0_1) inverse_diff_momentum	S(0, 4) sum average
S(5, 5) entropy	S(0_4) inverse_diff_momentum	S(0, 4) correlate
S(1, 1) sum variance	S(5_-5) inverse_diff_momentum	S(0, 5) contrast
Skewness	S(2_-2) inverse_diff_momentum	S(0, 3) correlation
Percent 0.01%	S(0_5) inverse_diff_momentum	S(0, 3) contrast

3.5 Classification

Finally, the most critical selected features were input the machine learning classifiers named Bayesian network (NB), logistic model tree (LMT), and Partial Decision Tree (PART) classifiers applying 10-fold cross-validation approach using the Weka 3.8 software (Bouckaert et al., 2002).

3.5.1 BN Classifier

The BN is a classification model based on the probabilistic approach. They can be used for a wide range of tasks, including disease diagnostics, reason modelling,

foundation of the concept of a logistic plus decision tree technique/ LMT classifier is good for handling nonlinear features, its implicit capability of features selection during the tree building maximizes the generalization process. It is scalable which combines the strengths of decision trees with regression. There are also some disadvantages of LMT classifier, which include suffering from overfitting. Although, they good for classification but poor for regression analysis and they are

Table 2: Machine Learning Classifiers Performance Measure Table

Classifiers	K_Sta	TP Rate	FP Rate	R_O_Chrc	T_N_Ins	Time. (Sec)	Accuracy
PART	0.7	0.850	0.150	0.866	400	0.06	85%
LMT	0.655	0.828	0.173	0.861	400	0.73	82.75%
BN	0.595	0.798	0.203	0.838	400	0.08	79.75%

also affected from the small data variation during the training process (Witten et al., 2011).

3.5.3 PART classifier

The PART algorithm creates decision rules, and it recursively divides the input dataset into smaller groups in order to construct a partial decision tree. It is a hybrid algorithm that combines aspects of decision tree-based and rule-based learning of the C4.5 and RIPPER algorithms. The algorithm's approach is recursively splitting the input space into distinct, non-overlapping subsets and then formulating decision rules for each of the splatted subsets. The potential advantages of PART classifier are its interoperability, capability of handling missing values in the datasets, scalability, equally handling discrete and continuous values, and it is also able to make a balance between bias and variance. There are also some disadvantages of PART classifier, which include that its generated rules may overlap, it is more sensitive to the noisy datasets, it requires manual tunning, and it is good for binary classification and for multiclass classification it requires to be extended (Ali & Smith, 2006) (Witten et al., 2011) (Pereira et al., 2016).

3.6 Evaluation

Performance measuring parameters include kappa statistics (K_Sta), receiver operating characteristic (R_O_Chrc), total number of instances (T_N_Ins), and time and confusion matrix. Proportions of true and false cases were described by sensitivity, specificity, and accuracy parameters. The parameters are defined by TP (true positive) rate and FP (false positive) rate (Pereira et al., 2016) .

3.6.1 K-Fold Cross Validation

Machine learning models are evaluated using k-fold cross validation, where the value of the parameter k is set accordingly.

Our model has been evaluated with k = 10, means dataset is rondomnly divided into ten equal folds and this divide is done iteratively ten times. Each time one fold out of ten folds is set for tesing and remaining nine folds are set for set for training. During each turn, the above mentioned evaluation metrics are rocorded, and at the end average values are computed for the maximum accuracy and minimizing the dataset biases. This technique is widely used for the evaluation of machine learning models and provides the maximum utilization of the dataset items (Bouckaert et al., 2002) .

4. Results and Discussion

In the research experiment, 400 ROI brain MR images were collected comprising the normal and brain glioma. Our preprocessing techniques refined all the images, and next we extracted COM texture features form these ROIs images. After applying a fused features optimization, we got thirty most optimized texture features for the glioma diagnosis. Next, three machine learning classifiers, namely PART, LMT, and BN, were deployed to classify normal and abnormal brain MRI datasets. The results of the classifiers are shown in Table 2.

The performance measure table shows that the BN classifier achieved a minimum classification accuracy of 79.75% to classify glioma-infected brain tumours from the healthy ones, among the other classifiers. The confusion matrix table for the BN classifier is given below in Table 3.

Table 3: Confusion Matrix Table for NB Classifier

Classes	Normal	Abnormal
Normal	**164**	36
Abnormal	45	**155**

Next, the LMT classifier gained second overall classification accuracy of 82.75% to classify the glioma brain tumour from the healthy brain. The confusion matrix table for the LMT classification is given below in Table 4.

Table 4: Confusion Matrix Table for LMT Classifier

Classes	Normal	Abnormal
Normal	**177**	23
Abnormal	46	**154**

The performance measure table shows that the PART classifier achieved the highest accuracy of 85% in discriminating the glioma brain tumour from the normal brain. The confusion matrix table for the PART classifier is given below in Table 5.

Table 5: Confusion Matrix Table for LMT Classifier

Classes	Normal	Abnormal
Normal	**186**	14
Abnormal	46	**154**

The overall combined performance comparison graph of PART, LMT, and BN classifiers is given below in Figure 3.

82.75% classification accuracy, and the PART classifier gave the maximum over classification accuracy. The comparison with other state-of-the-art techniques is given in the Table 6., given below.

The above table has three four columns. The first column displays the source of the research work, and next three columns highlights the main comparision factors of different schemes. The above table clearly shows that our proposed CABGD model has multiple superior factors as compare to some other state-of-the-art techniques.

5. Conclusion

In this research work, a novel computer-aided brain glioma identification model entitled CAGBD has been designed. Firstly, glioma-infected patients and healthy brain MRI datasets were collected from the Radiology of Bahawal Victoria Hospital (BVH-RDL). Histogram equalization, grey-level collection, noise removal, and tumour localization according to the ground truth were the image pre-processing steps. A couple of ROIs of size 10×10 were circled on each of the MRIs, and GLCM features were extracted from each ROI for texture analysis. A composite feature selection scheme comprising FSHR plus
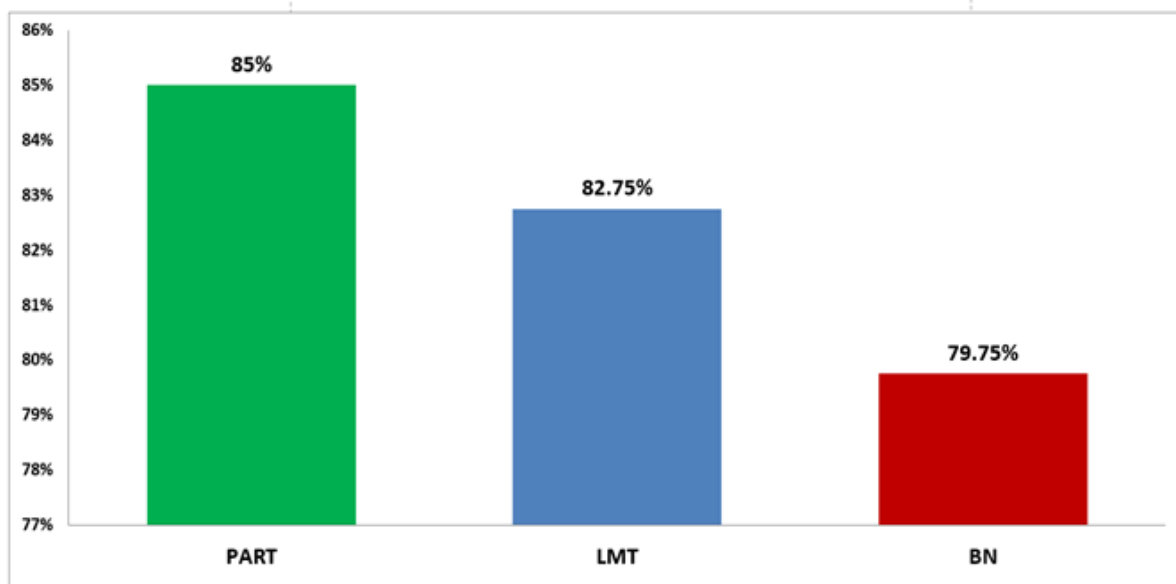

Figure 3. Performance Comparison Graph of Machine Learning Classifiers

The above figure shows that bayesian classifier gave the minimum classification accuracy as 79.75%, logistic classifier gave

POE plus AVC plus MUI gave the thirty most optimal features set. The obtained features were input into three machine

learning classifiers to identify glioma brain tumours. The BN classifier gave 79.75% classification accuracy, The LMT got 82.75%, and finally, the PART classifier achieved a maximum of 85% classification accuracy.

Table 6: Comparison with Other State-of-the-art Techniques

Source	Key Factors	Classification	Max. Accuracy
(Jain, 2013)	Brain MRI, GLCM, ANN, BPN (Back Propagation Network)	Normal ve Abnormal	81.4%
(Syed M. S. Reza, Randall Mays, 2017)	Brain MRI, MFDFA and Texture Features, Random Forest Classifier	LG, vs HG Tumors	83%
(Rajni et al., 2020)	Brain MRI, morphological and texture features, Naïve Bayes Classifier	Normal vs High grade Glioma	81.25%
(Selvaraj et al., 2007)	Brain MRI, Texture Features, SVM, MPL, LS-SVM, RBF,	Normal ve Abnormal	77 to 98%
(Havaei et al., 2016)	Brain MRI, CNN Classification model, SISS training	LG, vs HG Tumors	73% to 79%
Proposed CABGD Model	**Brain MRI, BN, LMT, PART, GLCM texture features. Optimization**	**Normal vs Glioma**	**85%**

6. Future Work

Some of the limitations of the model might be addressed in future research studies. The maximum accuracy of the model remains to 85%, which should be improved in future research studies. Our proposed model is limited to the glioma vs normal brain classification, thus in the future, the designated model can be applied to classify the other brain tumor types. The proposed model is limited only to the COM texture features, whereas in the future research, the proposed model may be extended to add more features, like gray-level-run-length matrix (GLRLM) and gradient features.

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