DETECTION AND CLASSIFICATION OF MRI-BASED BRAIN TUMOR VIA JAYA ALGORITHM AND TWIN SUPPORT VECTOR MACHINE

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Abstract

Brain tumor detection and classification is one of the challenging tasks in the medical image application. Early detection of a brain tumor can help diagnosis and treatment of the patients. Magnetic Resonance Imaging (MRI) is widely used for the detection of brain tumor. Manual analysis of brain MRI, and classification of brain tumor is tedious and time-consuming job. This paper introduces the new novel approach of brain tumor segmentation and classification using BRATS 2015 datasets. Our system exploits the benefits of Jaya Algorithm (JA) as optimization technique for finding multi-level thresholds to segment the tumor part from the MRI. Feature extraction is implemented by Gray Level Co-occurrence Matrix (GLCM), followed by Principal Component Analysis (PCA) for feature reduction. Due to its inherent distinct feature and advantages, a machine-learning approach, Twin Support Vector Machine (TSVM) is used as a classifier. The prediction accuracy of proposed system yielded up to 97.89 % with sensitivity 96.48%, 98.97 precision, 97.91% F1 Score and 0.0798 MSE. The accuracy, sensitivity, F1 Score and MSE are found comparable to the other state-of-arts machine learning methods.

Keywords*: Brain Tumor, Gray Level Occurrence Matrix, Jaya Algorithm, Principal Component Analysis, Twin Support Vector Machine*

1. Introduction

Cancer is termed as the abnormal growth of cells in the body that can even spread to other parts, causing the untimely demise of a person if not treated at its early stage. It is likely the second leading cause of death on the earth. Twenty million death has been recorded in 2020 (*Cancer*, n.d.). Brain tumor is a type of cancer in which tumor cells reproduce uncontrollably inside the brain. It is classified as primary and metastasis. Primary brain tumor is due to the growth of brain tissue itself, while if it is caused by spread of cancer from elsewhere in the body, it is metastasis. A primary brain tumor is further classified as benign and malignant. The benign brain tumor develops gradually, has distinct contours, and infrequently spread; while the malignant, which is quite dangerous compared to benign, develops rapidly, has non-patterned boundaries, and spreads to close by mind regions.

MRI is a non-invasive technology that is widely used in the medical study for the detection of tumor. It produces 3-D detailed anatomical images with clear clarity without use of damaging ionizing radiation. MRI represents the excellent method for brain study where it is able to distinguish tissue with a high spatial resolution. (Ayadi et al., 2019).

Several machine learning techniques have been employed for brain tumor classification such as support vector machine (SVM) (Bahadure et al., 2017; Deepak & Ameer, 2019; Tandel et al., 2020; Toğaçar et al., 2020), k-nearest neighbors (KNN) (Jha et al., 2017; Mir & Nasiri, 2018; Özyurt et al., 2019), fuzzy-clustering (FC) (Alagarsamy et al., 2019; Geetha & Gomathi, 2020; Sumathi et al., 2018), random-forest (RF) (Nayak et al., 2016) etc. SVM (Cortes & Vapnik, 1995) is one of the most

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widely used supervised algorithms for classification and regression problems in many domains. Convectional SVM outperforms for a small datasets and can even solve non-linear problems using different kernel functions such as Polynomial, Gaussian, Sigmoid etc. However, it fails to solve to obtain the solution for Quadratic Programming Problem (QPP). TSVM (Jayadeva et al., 2007) was developed to overcome the problems of SVM whose computational complexity is four time faster than that of SVM. The variations of TSVM can be found in (Ding et al., 2017; Tanveer et al., 2021). A lot of research on Twin Support Vector Machine have been carried out for classification purpose. The researchers have investigated the pathological MRI using Twin Support Vector Machine, Generalized Eigenvalue Proximal SVM (GEPSVM) and SVM being trained with features extracted from Hu Moment Invariant (HMI) and with 5 x 5 fold cross validation (Zhang et al., 2017). In the paper (Mir & Nasiri, 2018), the authors have predicted brain tumor using a modified form of TSVM, Least Square Twin SVM (LSTSVM) in conjunction with KNN.

Segmentation of tumor region from brain MRI is one of the difficult tasks in medical image processing. Mostly, thresholding method is employed, but the finding out the correct thresholds takes an endeavoring labor, for which optimization algorithm is used to get optimal thresholds. Particle Swarm Optimization (PSO) has been in employed in the papers (Kaur et al., 2018; Khairuzzaman & Chaudhury, 2019). V. Ranjinikath *et al.* (Rajinikanth et al., 2017) have analyzed Teaching Learning Based Optimization (TBLO) with three entropies as objective functions to get the optimal thresholds from brain MRI.

In the paper, (Tarkhaneh & Shen, 2019), the researchers have investigated the adaptive differential evolution algorithm. An adaptive wind drive optimization has been experimented with brain MRI to get thresholds in (Kotte et al., 2018). Bahar Khorram *et al.* (Khorram & Yazdi, 2018) has investigated biologically inspired ant colony algorithm on T1-weighted brain MRI. Sanjay Agrawal *et al.* (Agrawal et al., 2020) used the new hybrid evolutionary computing techniques called Adaptive Cuckoo Search-Squirrel Search Algorithm (ACS-SS) as optimization algorithm to find the thresholds values to segment the tumor part. In (Narmatha et al., 2020) a fuzzy brain-storm optimization (FBSO) is used for segmentation of brain tumor.

Feature extraction extracts the both quantitative and qualitative features of segmented part from the image for classification task. Gray Level Co-occurrence Matrix (GLCM) (Baraldi & Panniggiani, 2019) is one of the widely used tools to extract features. (Agrawal et al., 2020; Birare & Chakkarwar, 2018; Geetha & Gomathi, 2020; Jabber et al., 2020; Jany Shabu & Jayakumar, 2020; Kshirsagar et al., n.d.) have opted GLCM for feature extraction. In addition, discrete wavelet transform (DWT) (Ayadi et al., 2019; Nayak et al., 2016; Reema Mathew et al., 2018a, 2018b; Sergaki et al., 2018; Srinivas & Sasibhushana Rao, 2019; Zhang et al., 2017) is also popular method for features extraction tool. Apart from these two, Convolution Neural Network (CNN) (Çinar & Yildirim, 2020) and Deep Learning (DL) (Aboelenein et al., 2020; Daimary et al., 2020) methods are widely used these days to extract the features automatically from input images for the large datasets.

In this paper, we proposed a novel method of segmentation of brain tumor from brain MRI using multi-level thresholding techniques. JA with Otsu's class variance as objective function is used to get the optimal thresholds. Then, tumor part is segmented and morphological active contour is employed to process the segmented image. The features extracted from GLCM were input the TSVM classifier for binary classification of tumor as benign and malignant.

The major contributions of this paper is:

i. Implementation of JA with Otsu class variance as its objective function with Fluid Attenuated Inversion Recovery (FLAIR) modality of BRATS 2015 dataset to get optimal thresholds.
ii. Feature extraction using GLCM and feature reduction using Principal Component Analysis (PCA).
iii. TSVM as classifier to predict the brain tumor as benign and malignant.

2. Literature Review

Jaya Algorithm (JA) is a newly invented evolutionary algorithm by Rao (Rao, 2016). The authors (Satapathy & Rajinikanth, 2018) proposed the brain tumor segmentation using JA and Otsu method thresholding with T2 and Flair modality, and Chan-Vese (CV) approach for extraction. The limitation of this algorithm is that it is semi-automated as it required to fix the threshold value during the preprocessing task and, also it requires the operator assistance during the bounding box initiation while implementing the CV segmentation. The same authors with others have used a meta-heuristic optimization approach called Teaching Learning Based Optimization with different types of entropy as objective functions for segmentation of brain tumor using CEREBRIX and BRAINIX dataset, whose validation is carried out using the Multimodal Brain

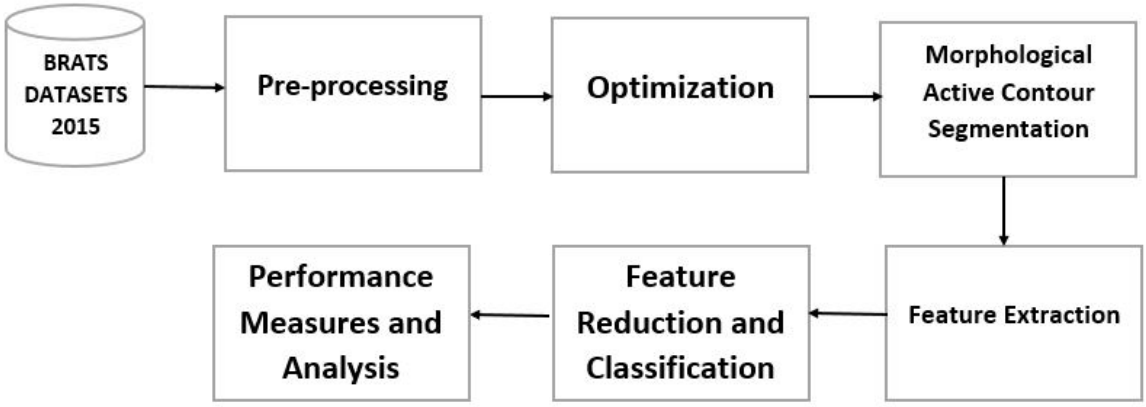


Fig. 1 A generic view of system model of proposed model.

Tumor Image Segmentation Benchmark (BRATS) challenge 2012 datasets (Rajinikanth et al., 2017).

The authors (Bahadure et al., 2017) have investigated Berkely Wavelet Transformation (BWT) based brain tumor segmentation, and used GLCM for feature extraction an Support Vector Machine (SVM) as classifier. The accuracy and dice-coefficient of their proposed system are 96.51% and 0.82 respectively. Adaptive contrast enhancement based on modified sigmoid function was applied as the pre-processing of MRI to increase the signal to noise ratio.
A novel approach called Adaptive Convex Region Contour (ACRC) algorithm has been used for brain segmentation, and GLCM and SVM with Gaussian Kernel function as feature extraction tool and classifier respectively (Pandiselvi & Maheswaran, 2019). The 2-D segmentation of MRI slices of brain tumor were transformed to 3-D for shape visualization using Rapid Model Image Matching (RMIM) algorithm, and further modeled into 3-D for reconstruction, all implemented in the MATLAB simulation environment.

In (Ahmed et al., 2019), a meta-heuristic approach Gray Wolf Optimizer (GWO) was presented to find the optimal value of radial basis function parameter and an error penalty parameter of SVM. Their model produced an accuracy of 98.75%, however only 80 T2-weighted images were considered. D.R. Nayak *et al.* (Ayadi et al., 2019) have investigated the two feature extraction techniques, Discrete Wavelet Transform (DWT) and Bag-of-Words; SVM, K-NN, and Adaboost were used as classifiers. Three The different datasets were used, D-66, D-160, and D-255. The authors (Narmatha et al., 2020) employed FBSO to reduce the segmentation task in MRI images of BRATS 2018 datasets.

Recently, many researchers are found to be using Convolution Neural Network (CNN) and Deep Neural Network (DNN) for detection and classification tasks of brain tumor. Deep Belief Network has been implemented for binary classification of brain MRI in which Gray Wolf Optimization (GWO) was used to optimize the features and hidden layer of it, and it was being carried out in MATLAB 2014a with 48 datasets (Geetha & Gomathi, 2020). Genetic Algorithm has been employed to find the optimized parameters CNN to identify the different grades of glioma (Anaraki et al., 2019). CNN with VGG19 model was explored to classify CE-MRI dataset into three types of brain tumor in which min-max normalization and resizing of images were done as pre-processing method (Swati et al., 2019). Auto-encoders techniques are explored to detect the brain tumor in (Amin et al., 2020; Balamurugan et al., 2021; Siva Raja & rani, 2020).

3. Methodology

3.1 System Model

Fig. 1 depicts the generic view of system model of the proposed system in the form of block diagram. It consists of pre-processing of datasets, optimization algorithm, feature extraction, feature reduction and classification process. Then model is analyzed with different performance measures. The detailed process in the system model is described as follows:

3.1.1 Image Acquisition and Pre-processing

We have used BRATS 2015 challenge datasets, as it is easily accessible from the internet and moreover it has ground truth images. The dataset is downloaded from the site (*BRATS - SICAS Medical Image Repository*, n.d.) . Each MRI image is volumetric in size and consists of different modality such as T1, T1C, T2, DW, and FLAIR. For our research, we considered FLAIR modality only due to the clarity it

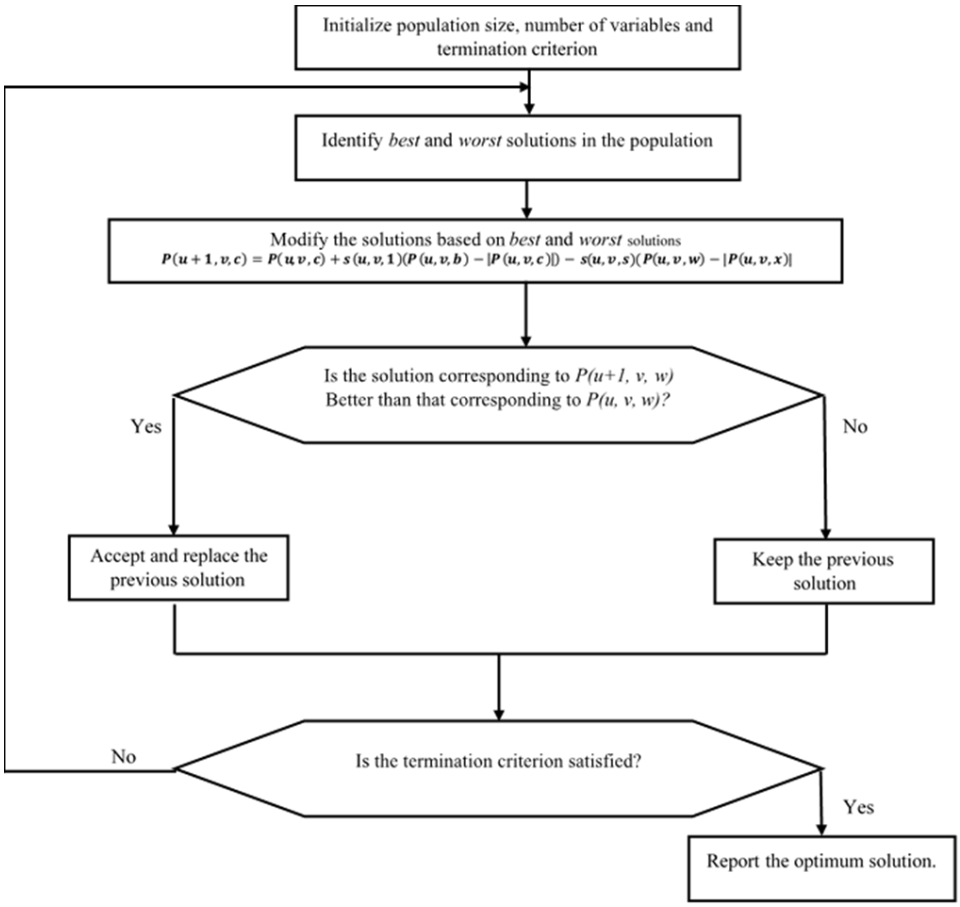


Fig. 2 Flow chart of JA.

produces than others modalities. So, the 3-D volumetric image was first converted to 2-D Slices of gray-scale. To remove noise, median filter of window size 3 x 3 was applied to the sliced image.

3.1.2 Multi-level Threshold Segmentation

Segmentation is the process of dividing an image into number of classes that will have some homogenous features. Thresholding is one of the simplest methods for segmentation, but the process of finding the optimal values of threshold is very challenging and difficult job. Here, we use a newly developed optimization algorithm, Jaya Algorithm (Venkata Rao, 2019). Compared with other existing optimization algorithm, it only needs few initial parameters to be tuned, so we have opted for our research. Its main equation is shown in Equation (1).

$$\begin{aligned} \boldsymbol{P(u+1,v,c)} = \boldsymbol{P(u,v,c)} \\ + \boldsymbol{s(u,v,1)(P(u,v,b)} \\ - \boldsymbol{|P(u,v,c)|)} \\ - \boldsymbol{s(u,v,s)(P(u,v,w)} \\ - \boldsymbol{|P(u,v,x)|} \end{aligned} \quad (1)$$

where,

- *b* and *w* represent the best and worst solution among current populations,
- *u, v, and c* are the index of iteration, variable, and candidate solution,
- *P(u, v, c)* represent the v^{th} variable and c^{th} candidate in v^{th} iteration,
- *s(u, v,1)* and *s(u, v,2)* are numbers generated randomly in the range of [0,1] and acts as scaling factor.

Fig. 2 depicts the flow chart of JA. JA tries to result with the best solution after each iteration and updates the values correspondingly. We used Otsu's class variance as its objective function (Otsu, 1979); the objective function which is to be maximized is given by the Equation (2):

$$f(T) = \sum_{i=0}^{m-1} \sigma_i \quad (2)$$

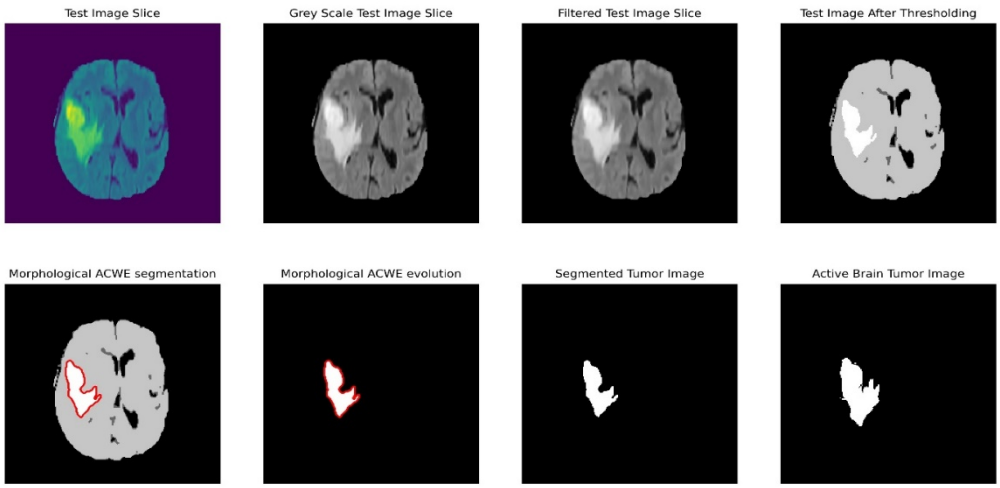


Fig. 3 Segmentation of tumor area from a test MRI image.

3.1.3 Morphological Active Contour

Chan-Vese model for active contour (Chan & Vese, 2001) is one of the widely used for image segmentation methods. Active contour model, based on energy minimization problem is mostly employed in medial image segmentation In compare to the traditional functional gradient descent method, morphological active contour model is simple in implementation, fewer model parameters to be tuned initially, no required of well-defined boundary in the image to be segmented, no numerical instability and one-order of magnitude faster (Marquez-Neila et al., 2014).

3.1.4 Feature Extraction: GLCM

Feature extraction refers to the way of extracting major quantitative information out of color, texture, shape, contrast, contours etc. contained in the image. The features extracted quantitatively help determine the detection of object in the image. GLCM is used as feature extraction tool. The followings features are then calculated from GLCM, which are then used to train the classifier:

$$\textbf{\textit{Mean (}}\boldsymbol{\mu}\textbf{\textit{)}} = \sum_{q,r}(q,r)p(q,r) \quad (3)$$

$$\textbf{\textit{Standard Deviation (}}\boldsymbol{\sigma}\textbf{\textit{)}} = \sqrt{\sum_{q,r}\frac{\left((q,r)-\mu\right)^2}{p(q,r)}} \quad (4)$$

$$\textbf{\textit{Variance}} = \sum_{q,r}\left((q,r)-\mu\right)^2\ p(q,r) \quad (5)$$

$$\textbf{\textit{Kurtosis}} = \sum_{q,r}|q-r|^4\,p(q,r) \quad (6)$$

$$\textbf{\textit{Skewness}} = \sum_{q,r}\frac{\left((q,r)-\mu\right)^3}{\sigma^3} \quad (7)$$

$$\textbf{\textit{Energy}} = \sum_{q,r}p^2(q,r) \quad (8)$$

$$\textbf{\textit{Entropy}} = -\sum_{q,r}p(q,r)\log_2 p(q,r) \quad (9)$$

$$\textbf{\textit{Homogeneity}} = \sum_{q,r}\frac{p(q,r)}{1+|q-r|^2} \quad (10)$$

$$\textbf{\textit{Contrast}} = \sum_{q,r}|q-r|^2\,p(q,r) \quad (11)$$

$$\textbf{\textit{Correlation}} = \sum_{q,r}\frac{(q,r)p(q,r)-\mu_x\mu_y}{\sigma_x\sigma_y} \quad (12)$$

where q and r indices in x and y direction of GLCM and $p(q, r)$ is the probability of occurrence of value at (q, r) in the GLCM.

3.1.5 Feature Reduction: Principal Component Analysis

Feature reduction is the technique of reducing 'n' dimensional feature space into 'd' dimension such that $n<d$. PCA is widely used tool for feature reduction (Abdi & Williams, 2010). It is linear transformation that convert possibly correlated samples to linearly uncorrelated variables called principal components, successively maximizing variance. PCA is obtained as a solution to the eigen-value problem, being based on covariance matrix.

3.1.6 Classification

3.1.6.1 Support Vector Machine

SVM is supervised linear binary classifier, which classified data according to a hyperplane. A hyperplane divides classes in such a way that the maximum margin between classes is set.

Consider the N training $\{x_i, t_i\}$ where, x_i is the input pattern for the i^{th} example and t_i is the corresponding desired response. With assumption, the pattern classes represented by $t_i = \pm 1$, are linearly separable, the equation of a decision surface in the form of a hyperplane that does the separation is given by

Equation (13):

$$w^T + b = 0 \tag{13}$$

where, x is an input vector, w is adjustable weight vector and b is a bias.

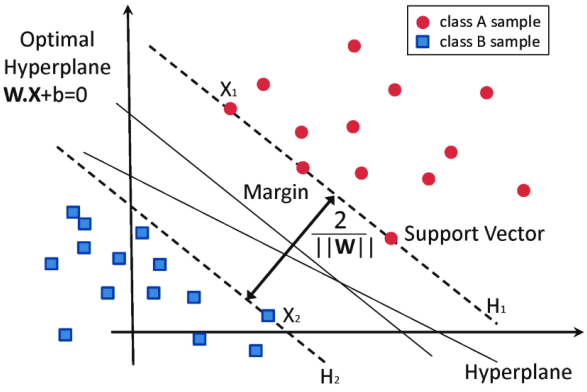


Fig. 4 Illustrating the concept of hyperplane in SVM.

3.1.6.2 Twin Support Vector Machine

The major drawback of SVM is the computational time it takes while solving complex quadratic programming problems (QPPs). First proposed by Jaydev and Khemchandani in 2007 (Jayadeva et al., 2007), TSVM complexity is four time faster than conventional SVM, and offers good generalization. TSVM classifies the patterns into two classes by finding two non-parallel hyperplanes which formed by solving a pair of QPPs instead to single complex constraint like in SVM.

Given n training data and m_1 representing samples belong to class +1 and m_2 representing samples belong to -1. Let a matrix A of size m_1 x n represents the training points of class +1 and a matrix B of size m_2 x n represents the training point of class -1.

TSVM seeks two non-parallel hyperplanes proximal separating hyperplane by training data set whose equation are given by Equation (14):

$$x^T w_1 + b_1 = 0, x^T w_2 + b_2 = 0 \tag{14}$$

The two separating hyperplanes of TSVM classifier is obtained by solving the following pairs of quadratic programming language.

$$\begin{aligned} &\text{(TSVM1)}\ \ min \tfrac{1}{2}(Aw_1 + e_1 b_1)^T (Aw_1 + e_1 b_1) + c_1 e_1^T \xi \\ &\text{Subject to: } -(Bw_1 + e_2 b_1) + \xi \geq 0 \\ &\text{(TSVM2)}\ min \tfrac{1}{2}(Bw_2 + e_2 b_2)^T (Bw_2 + e_2 b_2) + c_2 e_2^T \xi \\ &\text{Subject to: } -(Aw_2 + e_1 b_2) + \xi \geq 0 \end{aligned} \tag{15}$$

where c_1, $c_2 > 0$ are parameters, e_1 is a vector of ones of m_1 dimension, e_2 is a vector of one of m_2 dimensions and ξ is the slack variable.

A new test sample is assigned to the class which of the two planes given it lies closest to.

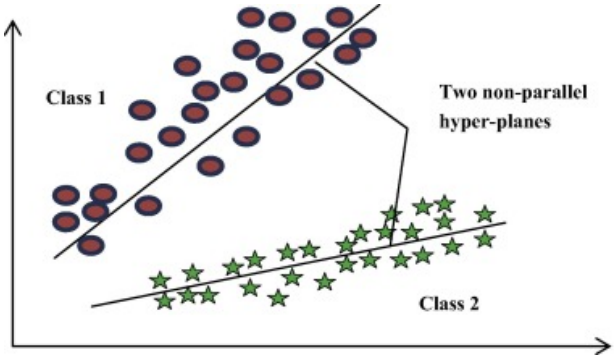


Fig. 5 Illustration of non-parallel hyperplane of TSVM.

3.2 Evaluation and Validation Measures

3.2.1 Confusion Matrix

Confusion matrix, also known as *error matrix*, is mostly implemented tool to evaluate the performance of the proposed model of classification, for the given set of known test values. It is a two-dimensional matrix that provides the values of True Negative (TN), False Positive (FP), False Negative (FN) and True Positive (TP). Table 1 illustrates a concept of a confusion matrix. From the confusion matrix, then following performance matrices are evaluated:

$$\textbf{\textit{Accuracy}} = \frac{TP+TN}{TP+TN+FP+FN} \tag{16}$$

$$\textbf{\textit{Sensitivity}} = \frac{TP}{TP+TN} \tag{17}$$

$$\textbf{\textit{Specificity}} = \frac{TN}{TN+FP} \tag{18}$$

$$\textbf{\textit{Precision}} = \frac{TP}{TP+FP} \tag{19}$$

$$\textbf{\textit{F1 Score}} = 2\frac{Precision*Sensitivity}{Presicion+Sensitivity} \tag{20}$$

$$\textbf{\textit{Balanced Error Rate (BER)}} = 1 - \frac{1}{2(Sensitivity+Specificity)} \tag{21}$$

where,

TP = represents the number of pixels that belongs to the segmented tumor region,

TN = represents the number of pixels that do not belong to the segmented tumor region,

FP = represents the number of pixels that do not belong to the segmented tumor region, but segmented into the tumor part,

FN = represents the number of pixels that belongs to the segmented tumor region, but not segmented into the tumor part.

Table 1: Illustration of confusion matrix.

		Predicted		
		Predicted Healthy	***Predicted Tumor***	***Total***
Actual	***Is Healthy***	*TN* = 18	*FP* = 22	40
	Is Tumor	*FN* = 11	*TP* = 279	290
	Total	29	301	*N* = 330

3.3 Environment and Tools

The coding of the proposed system is carried out in the "python" programming language version 3.6 and executed in Intel® Core(TM) i7-7500U CPU @2.7 GHz.

4. Results and Discussions

The dataset experimented in this research are used from MICCA Brain Tumor Image Segmentation Benchmark (BRATS) Challenge 2015 (https://www.smir.ch/BRATS/Start2015). BRATS 2015 training dataset consists of 220 subjects' each of size 240 x 240 x 150. Each image is sliced along z-axis to convert into 2D slice of MRI images. About 6,012 two dimensional gray-scaled filtered images are generated for the study purpose.

For Jaya Algorithm, the three parameters, *viz*, number of iterations, number of candidates and design parameters (i.e. number of thresholds), are initialized whose values are set 1000, 20 and 3 respectively, after which morphological active contour in applied to segment the tumor part using thresholding segmentation techniques. The sample example for a test image is shown in **Fig. 3**.

For classification of brain tumor, we had 2,639 data samples belong to the abnormal, that is, tumor samples, while 3,333 belongs to the normal samples. The features of those images are only taken whose dice-coefficient is greater or equal to 60 during segmentation process, which is the constraint of this study. The dataset is then split into 70% training and 30% for testing the model. The 5-fold cross-validation is done on testing the model. The optimal parameters for SVM and TSVM are tunes using hyper tuning techniques. With this, SVM was trained with the error penalty factor, *C = 100* and *gamma = 0.001* and radial basis function. Using PCA, the features were reduced to four dimensions and then trained with SVM with same parameters as that of SVM. In case of TSVM, it generated best result using linear kernel function with the error penalty factors*, C1 =4.0*, and *C2 = 3.0* and *gamma = 0.0039*.

Table 2: Confusion matrix parameters for different classification models obtained using 5-fold cross-validation**.**

	Confusion Matrix Parameters			
Models	***TN***	***FP***	***FN***	***TP***
SVM	945	64	95	700
PCA + SVM	939	70	105	690
TSVM	1001	8	31	763
PCA + TSVM	1001	8	28	767

Table 3: Validation measures obtained from 5 fold cross-validation.

	Models			
Validations Measures	***SVM***	***PCA + SVM***	***TSVM***	***PCA + TSVM***
Accuracy	0.9119	0.9030	0.9784	0.9800
Sensitivity	0.8805	0.8679	0.9610	0.9648
Specificity	0.9366	0.9306	0.9921	0.9921
Precision	0.9162	0.9079	0.9751	0.9897
F1 Score	0.8980	0.8875	0.9751	0.9771
BER	0.0915	0.1007	0.0235	0.0216
MSE	0.3525	0.3880	0.0640	0.0798

Table 2 shows the confusion matrix parameters for different classification models. From these parameters, the validation measures i.e. accuracy, sensitivity, specificity, precision, F1 Score and BER are calculated, whose results are shown in Table 3. Also mean square error (MSE) is also evaluated for every classifiers models. From, we can observe that the accuracy, sensitivity, precision and F1 Score that of TSVM after feature reduction are highest of all four models. The specificity is same as that of TSVM after PCA. The MSE of TSVM is least of all.

Our system is compared with other state-of-arts found in literature in terms of accuracy. From Table 4 we can find that the proposed system is competitive with others in better prediction ability of brain tumor. It is trained with large training data with BRATS datasets in contrast with other models which are trained with only limited number of training samples.

In addition, the performance of classifiers was observed by plotting learning curves. Learning curve

is a plot of two errors, training error of training set and validation error of validation set as a function of training set; it shows how these error changes as the training set size increases.

From the Fig. 9, we observe that the learning curves of both SVM and SVM after PCA has low training error and high gap between two error curves; that is, the model is of low bias and high variance. This implies that these models fit the training data every well, but it prediction ability is comparatively low compared to TSVM. In the learning curve of TSVM, the validation error decreases and training error increases as training size increases, trying to converge at a point, and resulting in a low variance as the gap between two curves is very narrow. This shows that TSVM fits the training data every well with better prediction results. However, at a certain point i.e. after nearly 2600 samples, the curve tried to intersect. Such is the case for PCA + TSVM model after 1900 samples. This shows that the TSVM model would suffer under fitting problem provided that the parameters are not properly tuned.

Table 4 Comparison of proposed model with other state-of-arts on basis of accuracy.

Models	Accuracy
GWO + SVM (Ahmed et al., 2019)	0.9875
HMI + GEPSVM (Zhang et al., 2017)	0.9889
HMI + TSVM (Zhang et al., 2017)	0.9889
Transfer Learning (Swati et al., 2019)	0.9482
DWT + PCA + ABRF (Nayak et al., 2016)	0.9844
DWT + PPCA + ABRF (Nayak et al., 2016)	0.9953
GLCM + TSVM (Proposed)	0.9806
GLCM + PCA + TSVM (Proposed)	0.9789

From Fig.6 and Fig. 7, we can observe that the MSE of TSVM is very much less than that of SVM model and it's training time is also comparatively very less.

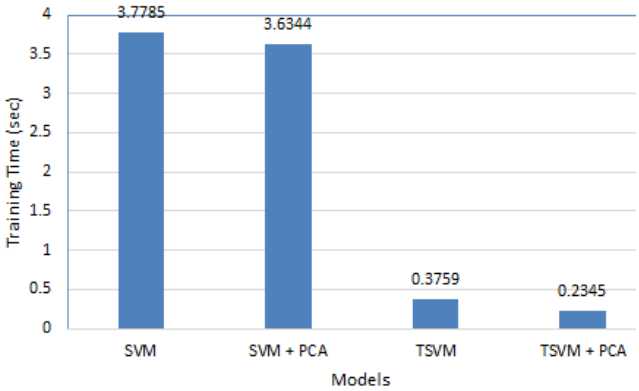


Fig.6 Bar chart representation of MSE of different models.

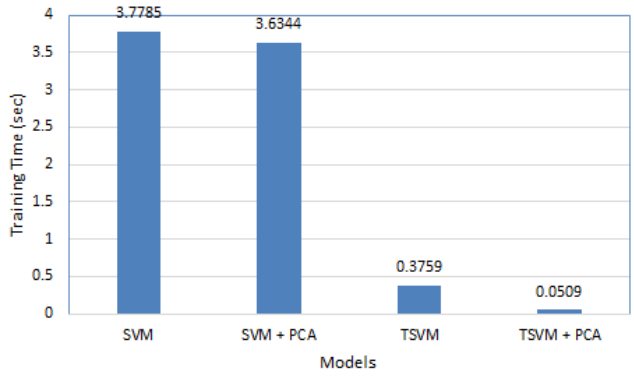


Fig. 7 Bar chart representation of training time of different models.

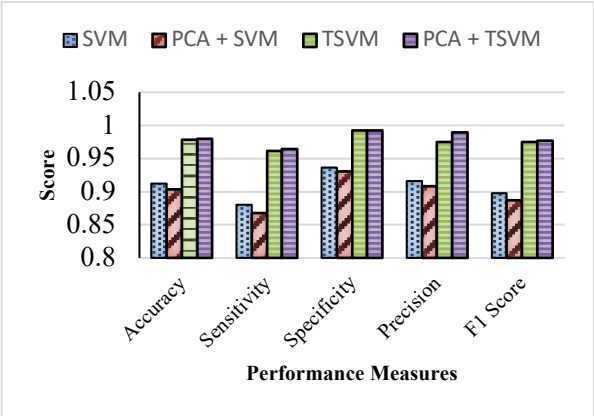
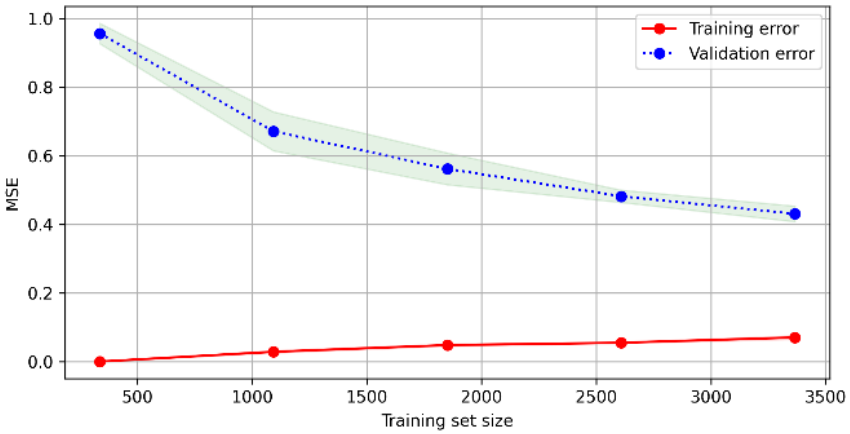


Fig. 8 Bar chart representation of different performance measures of different models.

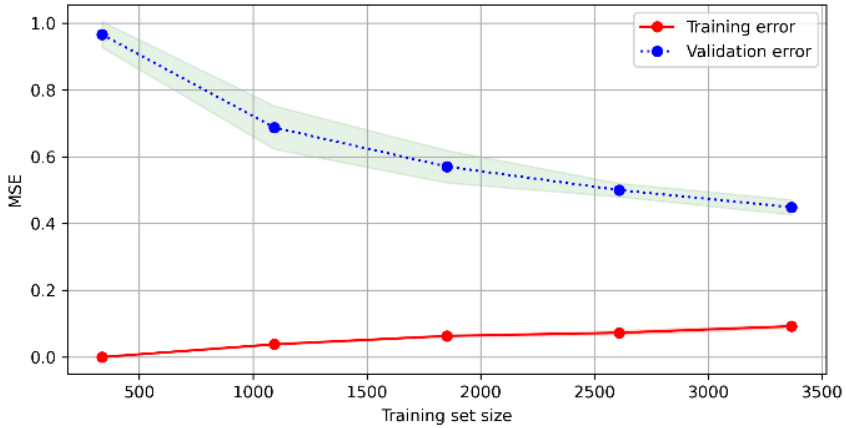
Fig. 8 shows the bar chart representation of performance measures of different models. We can see that TSVM model has better scores in term of different performance metrics.

5. Conclusion and Future Work

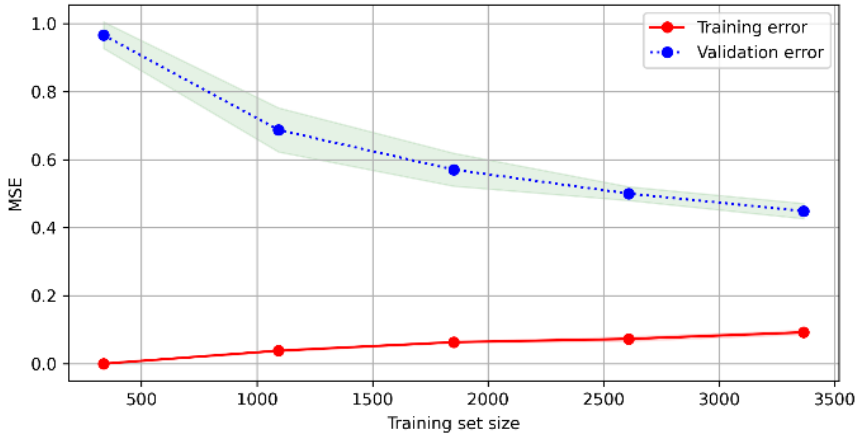
In this research work, segmentation of brain tumor from flair modality of MRI images of BRATS 2015 dataset is done, and binary classification was analyzed with four models. Their performance analysis is compared using different metrics and learning curves. Investigating the performance analysis is compared using different metrics and learning curves. Investigating the performance measures, TSVM performed better in classification task with an accuracy of 97.84% while that of SVM mode was found 91.19%. In addition, the training time and MSE of TSVM are significant compared to SVM. Also, the sensitivity, specificity, precision and F1 score of TSVM are higher than that of SVM. We found out SVM model suffered from overfitting problem while TSVM somewhat suffer underfitting problem for large training set of data.



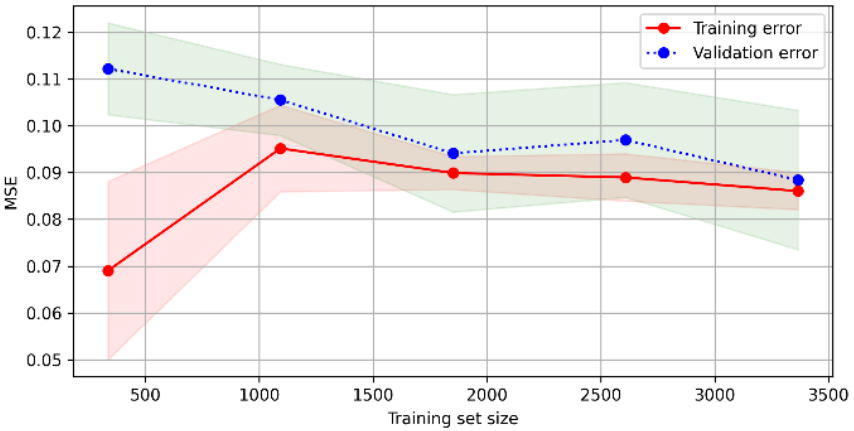
a. Learning curve of SVM



c. Learning curve of TSVM



b. Learning curve of PCA + SVM



d. Learning curve of PCA + TSVM

Fig. 9 Learning curves of different models

It is not necessarily true that, the classification models perform well after the feature reduction; MSE is higher after feature reduction. From the Table 4, we can observe that the proposed method is competitive with other state-of-arts method in terms of accuracy.

The research can be further carried out by latest state-of-arts methods such as convolution neural network, recurrent network, deep neural network and so on. Also, the different variants of TSVM like least square TSVM, fuzzy bounded TSVM etc. can be investigated. In addition, different modalities of BRATS datasets can be analyzed for further investigation.

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