Multiclass Brain Tumor Classification using GA-SVM

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***Abstract* — The objective of this study is to develop a CAD system for assisting radiologists in multiclass classification of brain tumors. A new hybrid machine learning system based on the Genetic Algorithm (GA) and Support Vector Machine (SVM) for brain tumor classification is proposed. Texture and intensity features of tumors are taken as input. Genetic algorithm has been used to select the set of most informative input features. The study is performed on real 428 post contrast T1- weighted MR images of 55 patients. Primary brain tumors such as Astrocytoma (AS), Glioblastoma Multiforme (GBM), Meningioma (MEN), and child tumor -Medulloblastoma (MED) along with secondary tumor- Metastatic (MET) are classified by GA-SVM classifier. Test results showed that the GA optimization technique has enhanced the overall accuracy of SVM from 56.3 % to 91.7%. Individual class accuracies obtained are: AS-89.8%, GBM - 83.3%, MEN -96%, MET-91.8%, MED-97.1%. A comparative study with earlier methods is also done. The study reveals that GA-SVM provides more accurate results than earlier methods and is tested on more diversified dataset.**

Keywords-classification, brain tumor, MRI,GA-SVM

I. INTRODUCTION

Brain tumor classification includes categorization of primary and secondary tumors into different classes. Primary tumors are tumors that originate in the brain itself like Astrocytoma (AS), Glioblastoma Multiforme (GBM), Meningioma (MEN), child tumor- Medulloblastoma (MED). Secondary brain tumors are the cancer cells that originate from another part of the body and have spread to the brain like Metastatic (MET) tumors.

Different computer aided techniques proposed for brain tumor classification either uses MR spectroscopy signals or MR image sequences. Many researchers [4] [5] [6] [7] have used MR spectroscopy data for classifying brain tumors and have obtained substantial results. Researchers [1] [2] [3] have also used MR images for classification. Both these techniques give comparable results and could be used equally for classification purpose. However, MR spectroscopy data requires expertise in signal conditioning and also is difficult to collect. Therefore, this paper focuses on development of a CAD system to improve and assist radiologists in multiclass brain tumor classification using MR images.

MR images obtained from different excitation sequences like T1, T2, post contrast T1, FLAIR provide texture and intensity information of brain tumors. From these sequences, post contrast T1 weighted MR images provide better visualization of brain tumors than other sequences. These post contrast images are obtained by inducing, 0.15-0.20 ml/kg of contrast material-Gadolinium in patients. Even though the quantity induced is same, the degree of enhancement of tumor obtained (of same and different class) is different (show full/peripheral/no enhancement) for different subjects. These post contrast T1 weighted MR images are used for classification.

Segmented Region of interest (SROI) or tumor on images can be manually marked by the radiologists [1] [2] [3] or Computer aided techniques (CAT) - automatic and semi-automatic methods [15] [16] [17] [18] [19] [20], can also be used for segmentation of brain tumors. However, CATs have been developed for segmentation of specific type of tumor images. None of the CATs seems to segment all different tumor types.

Many researchers have developed classifiers for brain tumor classification. Binary classifiers separating benign from malignant have been proposed [21] [22]. Classifiers distinguishing normal slices from abnormal ones are also there [23] [24]. Multiclass classification models for brain tumors are proposed by Georgiadis et al. [1] [2]. Metastases, Meningiomas and Gliomas are classified in his two studies using LSFT-PNN classifier. In the first study, experiment is performed on 75 images achieving an accuracy of 87.50% for Metastases, 95.24% for Meningiomas and 96.67% for Gliomas. In the second study, dataset of 67 images is considered. The individual class accuracy is increased by developing a two stage classifier. In the first stage, primary and Metastases (secondary tumors) are separated delivering an accuracy of 95.24% and 93.48% respectively. In the second stage, primary tumors are classified delivering an accuracy of 100% for Meningiomas and 88.89% for Gliomas.

Similar study was performed by Zacharaki et al. on 98 images [3]. Accuracy obtained for each class is: Metastasis - 91.7%, Low-grade glioma -90.9%, Glioblastoma Multiforme - 41.2% and Glioma Grade III -33.4%.

The literature studies reported so far reveals that there are very few studies for multi-class classification. There exists no MR images based classification method separating all different types of tumors viz. Primary tumors- Astrocytoma, Glioblastoma Multiforme, Meningioma, child tumor- Medulloblastoma and secondary tumor- Metastatic by single model (as per knowledge of the author). Generally

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Meningiomas, Gliomas and Metastatic tumors are classified. Moreover, the datasets used for classification by the earlier proposed methods were very small. There has been no attempt to classify child tumors (Medulloblastoma) and to separate Astrocytoma from Glioblastoma. Very low accuracy has been obtained specifically in identification of Glioblastoma Multiforme (41.2%).

In this paper, we have developed a hybrid GA-SVM based classification model which overcomes these limitations. Routinely taken post contrast T1 MR images are used to extract texture and intensity information. The implementation is carried out by using GA-SVM approach on 428 images to classify five classes of brain tumors. These classes are: Primary tumors- AS, GBM, MEN, child tumor- MED and secondary tumor-MET. A CAD system is developed to assist radiologists in multiclass brain tumor classification.

This paper is organized in the following main sections. Section 2 provides the detail method used. In Section 2 feature extraction, feature selection using genetic algorithms and the classifier (SVM) modules are discussed. Standard classifier is given in Section 3. Dataset is illustrated in Section 4. In Section 5 experimental results are given. Discussions including comparative study with earlier methods are given and Section 6 respectively. The paper is concluded in Section 7.

II. METHOD

The proposed system developed to assist radiologists in classifying brain tumors in MR images is shown in Figure1. The system consists of three modules: (i) feature extraction module from tumor regions (ii) feature selection using Genetic Algorithm (GA) where GA is used to select a set of salient features from input features (iii) classification module using SVM. The selected features are used as inputs to SVM.

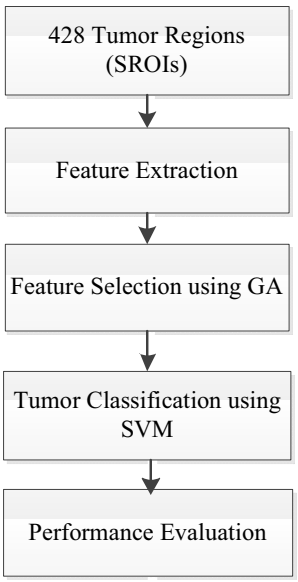

Figure1. Flow diagram of the proposed scheme

A. Feature Extraction

Relevant set of 71 intensity and texture features extracted from tumors are discussed below:

1.) Gray Level Co-occurrence Matrix: Four different features namely Contrast', 'Homogeneity', 'Correlation' and 'Energy' for four different offsets are calculated, contributing 16 features in feature pool [8].

2.) Laplacian of Gaussian Features: Four different values of Gaussian widths viz. (0.25, 0.50, 1, and 2) for LoG filters are considered, and are convoluted with the input image. The mean values of output in the tumor segment region are retrieved which count as four features and are added in the feature pool.

3.) Directional Gabor Texture Features: The λ (in pixels) and θ (in degrees)are varied for five different values viz. (2√2,4,4√2,8,8√2) and θ (0°, 22.5°, 45°, 67.5°, 90°) resulting in 25 different Gabor filter features [9].

4.) Rotation Invariant Circular Gabor Features: At five values of λ (in pixels) viz. (2√2, 4, 4√2, 8, 8√2) and two values of ψ i.e. 0°and 90°, 10 rotation invariant circular Gabor features are retrieved [10].

5.) Rotation invariant Local Binary Patterns: Intensity pattern in tumor region is modeled using histograms. Four intensity-statistical parameters namely: mean intensity, standard deviation; skewness and kurtosis from the histogram of an image within the tumor segment are calculated [11].

6.) Intensity based features: Four intensity-statistical parameters namely: mean intensity, standard deviation; skewness and kurtosis from the histogram of an image within the tumor segment are calculated. Image range feature and mean of local entropy is taken as fifth and sixth intensity feature.

7.) Shape based Feature: The regularity parameter R is used to characterize shape of the tumor. The regularity for a binary segment B is defined as:

$$R = \frac{\sqrt{4\pi \times area(B)}}{perimeter(B)} \quad (1)$$

The value of R is 1 for pure circular segments and it decreases to a limiting value 0 as the shape becomes irregular.

B. Feature selection using GA

As explained above, we obtain a set of 71 features. The purpose here is to obtain an optimal subset of features which produce the best possible results [12]. The various steps in GA are described below:

Representation: We represent a chromosome by a binary vector size of 71 features, where each bit of the chromosomes represents whether the corresponding input feature is selected or not. 1 represents the presence and 0 represents the absence of the specific feature.

Fitness Evaluation: The fitness function A (i) is used for evaluating the fitness of a chromosome I where, A (i) is the

classification accuracy obtained by the SVM with the input feature set.

$$\text{Fitness}=A(i) \tag{2}$$

Selection: Roulette Wheel selection is used for parent selection. In Roulette Wheel selection, fitness level is used to associate a probability of selection with each individual chromosome. If f_i is the fitness of individual i in the population, its probability of being selected is:

$$p_i = f_i / \sum_{j=1}^{n} f_j \tag{3}$$

where, N is the number of individuals in the population. The value of N=10 is taken in this study. The candidates with higher fitness are more likely to be selected. There is a still a chance that some weaker solutions may survive the selection process; this is an advantage, as though the solution may be weak, it may include some component which would prove useful following the recombination process.

Crossover: The crossover operates by swapping corresponding segments of a string representation of the parents. A crossover point is randomly selected and the bits to the left of the crossover point in parent and the bits to the right of the crossover point in the second parent are combined to get a new offspring. By manual optimization the values of crossover rate is taken as 0.70.

Mutation: Mutation refers to flipping of the bits in the chromosome. Every time the genetic evolution occurs, the bits in the chromosome are flipped with a probability of 0.01.

Fitness Check: A fitness check has been introduced before transferring new generation to next iteration. Only those changed chromosomes are forwarded to the next iteration, which show improvement in the fitness values. Therefore if the reproduction process decreases the fitness value of a chromosome then the corresponding chromosome before reproduction is retained for next iteration and hence GA leads monotonously towards improvement in fitness values. The GA terminates when there is no improvement in fitness value for subsequent iterations or when maximum iteration count is reached.

C. Classification Module

The optimal set of features are selected by the genetic algorithm above is then used as input to the SVM. The original input features are scaled to the range of [0, 1]. The goal of the linear scaling is to independently normalize each feature component to the specified range. It ensures the larger value input attributes do not overwhelm smaller value inputs, and thus helps to reduce prediction error.

The MATLAB software package 8.0 is used to perform the experimentation. The proposed system uses non-linear support vector machine. Support Vector Machine (SVM) in MATLAB implements Vapnik's SVM for solving problems of classification, regression, and the problems of learning a ranking function. The kernel function used for transforming the input space to the higher dimension space is the Gaussian radial basis function kernel. This kernel is selected as it gave better experimental results than the other common kernel functions.

III. CLASSIFIER

A. Standard Support Vector Machine(SVM)

SVMs perform classification by projecting the data points into higher dimensional hyper plane through Kernel trick. SVM uses structural risk minimization to determine the decision boundary in the given data space. A simple binary SVM classifier identifies few data points as support vectors, which best identifies and separates the data points in terms of their classes. The training data $\boldsymbol{x}$ consists of n data samples each of m dimensions and belonging to class y, is expressed as:

$$(x_1, y_1)\ldots(x_i, y_i)\ldots(x_n, y_n),\ \ \boldsymbol{x}\in\mathbb{R}^m, y\in\{+1,-1\} \tag{4}$$

SVM projects data ($\mathbf{x_i}$,y) into an infinite dimensional hyper plane $\boldsymbol{\varphi}(\mathbf{x_i}$,y) by using Gaussian kernel function and defines its decision rule as sign(f($\mathbf{x}$)). The discriminant function f($\mathbf{x}$) creates the optimum hyper plane decision boundary by using weight vector $\boldsymbol{w}^*$ and bias b^*.

$$f(\boldsymbol{x}) = \boldsymbol{w}^*\Phi(\mathbf{x}) + b^* \tag{5}$$

The optimum values of $\boldsymbol{w}^*$ and b are estimated by solving following optimization problem

$$\min_{w,\xi}\left\{\frac{1}{2}\boldsymbol{w}^2 + C\sum_{i=1}^{n}\xi_i\right\};\ \ y_i(\boldsymbol{w}.\Phi(\mathbf{x}_i)+\mathrm{b}))\geq 1-\xi_i, \xi_i \geq 0 \tag{6}$$

where, C is regularization parameter and ξ is are slack variables allowing inseparable data. This problem is solved using Lagrange optimization through dual formation, which finally yields optimum value for weight vector $\boldsymbol{w}^*$ and bias b^*[13] [14]. Since SVM estimates an infinite dimensional optimum hyper plane, usually it performs better than the other supervised learning algorithms in solving classification problems even on high dimensional input features.

IV. DATASET

In the present study, 428 brain tumor MR images are acquired from 55 different patients at Department of Radiodiagnosis, Postgraduate Institute of Medical Education & Research (PGIMER), Chandigarh, India, over the time period March 2010 to May 2011. These MR images include- 118 AS, 59 GBM, 97 MEN, 88 MED, 66 MET. Contrast and brightness as characteristics of gray scale images are influenced by machine and/or technology used for their generation. Therefore, images are obtained using two MRI equipment (Siemens Verio, Erlangen Germany, 3Tesla and 1.5 Tesla MR Scanners). However, this study is being done separately by taking images from different machines. These tumors are graded and manually segmented by the radiologists based on their knowledge on visual image interpretation of brain tumors, clinical history of the patient, and disease confirmation by the biopsy/dynamic helical CT/MRI/pathological examinations. Distribution of each class data for testing and training is given in Table 1.

TABLE I. DISTRIBUTION OF CLASS DATA FOR TRAINING AND TESTING

50% Training data includes	50% Testing data includes
AS-59	AS-59
GBM-29	GBM-30
MEN-48	MEN-49
MED-44	MED-44
MET-33	MET-33

V. EXPERIMENTAL RESULTS

A. Evaluation Matrix

Matrix used to analyze the performance of the proposed model is overall classification Accuracy. The basic data structure used for evaluation is Confusion Matrix.

Given a Confusion Matrix shown in Table 2, in context of brain tumor classification system,

Class (i) =True instances of class (i) in dataset (7)

Individual Class Accuracy for i^{th} class = TP (i) /class (i) (8)

where, TP(i) is correctly classified instances of class (i)

Overall Classification Accuracy=

$$(\sum_i TP(i) / \sum_i class(i)) * 100 \quad (9)$$

VI. DISCUSSIONS

Individual class accuracies delivered by GA-SVM for each class is: 89.8% for class 1(AS), 83.3%class 2 (GBM) 94.5%, for class 3 (MEN), 96% for class 4 (MED), 97.1 % in case of class 5 (MET). It has delivered an overall accuracy of 91.7%.

Class1 (AS) and class 4 (MED) have not been considered in the recent studies. GA-SVM has delivered an accuracy of 83.3% for GBMs whereas the accuracy obtained by previous study for class 2 is only 41.2%. Since GBMs are heterogeneous tumors (different texture patterns are present within the tumor itself) these tumors are quite tough to predict. The selection of texture and intensity features and GA optimization has improved (quiet double) GBM's accuracy appreciably. For MEN, 96 % accuracy is achieved and for MET 97.1% accuracy is achieved. It is comparable to the accuracy obtained from the recent studies, Men-95 % to 100% and MET-95%. The results were discussed and validated by the radiologists. A comparative study of the proposed method with previous studies is summarized in Table 3.

The study reveals that:

1.) GA-SVM is tested on more diversified dataset.

2.) Five classes of brain tumors are considered for experimentation whereas earlier methods considered 2 to 3 classes.

3.) Astrocytoma and child tumor-Medulloblastoma have been taken for study. These classes were not considered by the earlier studies. GA-SVM has delivered substantial accuracies for these two classes.

4.) GA-SVM has delivered an accuracy of 83.3% for GBM (much higher as compared to earlier studies (41.2%) and for other classes also comparable results are achieved.

Figure 2 compares the performance of SVM and GA-SVM for multiclass classification of brain tumors. The horizontal axis shows the GA iterations and vertical axis shows the classification accuracy achieved. It can be seen that GA-SVM boosts the system performance. The accuracy obtained by SVM is 56.3 % whereas with GA, the accuracy obtained is 91.7%.

TABLE II. CONFUSION MATRIX FOR GA-SVM

		Ground truth Class (assigned by Radiologist)				
	Class	AS	GBM	MEN	MED	MET
Predicted Class	AS	53	2	1	0	0
	GBM	2	25	0	0	0
	MEN	3	3	43	2	1
	MED	0	0	0	45	0
	MET	1	0	1	2	33
Individual Class Accuracy		89.8% (53/59)	83.3% (25/30)	96% (43/45)	91.8% (45/49)	97.1% (33/34)
Overall Classification Accuracy		91.7% (199/217)a				

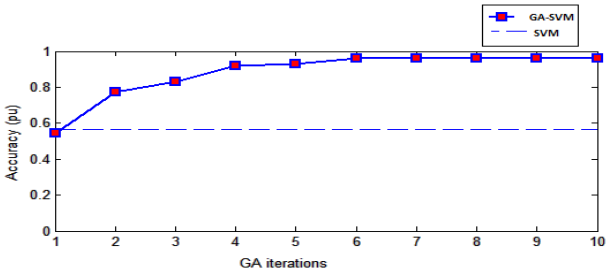

Figure2. Comparison of SVM and GA-SVM for multiclass brain tumor classification

VII. CONCLUSION

In this paper, a hybrid GA-SVM for selection of intensity and texture features and multiclass classification system is proposed. The experiment performed consists of primary tumors and secondary tumors which differ in every aspect in their appearance, location, size and shape. The performance of GA-SVM in terms of individual class and overall accuracy is evaluated for large dataset of 428 images. The high value of

individual class accuracy for each class- AS (89.8%), GBM (83.3%), MEN (96%), MED (91.8%), and MET (97.1%) is achieved. Further, GA-SVM has delivered an overall accuracy of 91.7%. The study reveals that GA-SVM provides more accurate results than previous methods and has been tested on more diversified dataset. It has been observed that the performance of the classifier depends upon the features selected. Thus a medical decision system based on GA-SVM classifier can provide substantially accurate results and can help radiologists in forming a better decision in classifying brain tumors.

In future, dataset comprising of class like Glioma and subclasses like Low Grade Astrocytoma and Higher grade Astrocytoma will be collected for classification and the proposed method will be tested on more diversified dataset.

TABLE III. COMPARISON OF THE PRESENT STUDY WITH PREVIOUS STUDIES ON CLASSIFICATION OF BRAIN TUMORS

Author -Year	**Brain tumor classes / Images per class**	**Total Images**	**Classifier**	**Data distribution for classifier**			**Accuracy obtained per class**
					Train Set	Test Set	
Georgiadis -2007	1-Metastases (24) 2-Meningiomas (21) 3- Gliomas (30)	75	LSFT-PNN	Leave-one-out method			Metastases 87.50% Meningiomas 95.24% Gliomas 96.67%
Georgiadis -2007	1-Metastases (21) 2-Meningiomas (19) 3- Gliomas (27)	67	LSFT-PNN Two Stage Classifier Primary and Metastases Second Stage- Gliomas and Meningiomas		66%	33%	Metastases and Primary 95.24% 93.48% Primary Meningiomas 100% Gliomas 88.8%
				Metastases	14	7	
				Meningiomas	13	6	
				Gliomas	18	9	
Zacharaki -2009	1-Metastasis (24) 2-Grade Gliomas (22) 3-Glioblastomas (34) 4-Gliomas Grade III (18)	98	SVM-RFE	Leave one out cross validation procedure			Metastasis 91.7% Low-grade glioma 90.9% Glioblastoma Multiforme 41.2% Glioma Grade III 33.4%
Present Study -2011	1-Astrocytoma (118) 2-Glioblastoma multiforme (59) 3-Meningioma (97) 4-Medulloblastoma (88) 5- Metastatic (66)	428	GA-SVM	Train Set	Validation Set	Test Set	Astrocytoma 89.8% Glioblastoma Multiforme 83.3% Meningioma 96% Medulloblastoma 91.8% Metastatic 97.1%
				40%	10%	50%	
				47	12	59	
				23	6	30	
				39	10	48	
				35	9	44	
				26	7	33	

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