Comparative Study of Classification System using K-NN, SVM and Ada-boost for Multiple Sclerosis and Tumor Lesions using Brain MRI

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Abstract

Brain Magnetic Resonance Imaging (MRI) plays a very important role for radiologists to diagnose and treat brain tumor/ Multiple Sclerosis (MS) patients. Study of the medical image by the radiologist is a time consuming process and also the accuracy depends upon their experience. Thus, the computer aided systems (CAD) becomes very necessary as they overcome these limitations. This paper presents an automated process of classification of Multiple sclerosis and Tumor lesions from brain MRI in which 3 models for classification of lesions is considered as: i. MS and Normal, ii. MS and Tumor and iii. Benign and Malignant Tumor based on T2-weighted MRI scan. In this work, textural features are extracted using Gray Level Co-occurrence Matrix (GLCM) [13]. Then the classification is done using K-Nearest Neighbor (K-NN), Support Vector Machine (SVM) and Ada-boost classifiers. The performance of the proposed models is evaluated on the basis of accuracy, error rate, sensitivity and specificity. The system performance is also compared with the radiologist's diagnosis for test samples. The developed CAD system is giving 100% accuracy for all three learning algorithms; with SVM outperforming the K-NN and Ada-boost.

1. Introduction

Multiple sclerosis (MS) is one of the most common diseases of the central nervous system (CNS) in young adults, affecting over 2,500,000 patients worldwide. MS is characterized by the destruction of proteins in the myelin surrounding nerve fibers. As a result, multiple areas of scar tissue called sclerosis (also lesions, or plaques) may appear, leading to a progressive decline of motor, vision, sensory, and cognitive function. MRI is a powerful tool for diagnosis of MS and monitoring the disease activity and progression [1].

When most normal cells grow old or get damaged, they die and new cells take their place. Sometimes, this process goes wrong. New cells form when the body doesn't need them and old or damaged cells don't die as they should.

The buildup of extra cells often forms a mass of tissue called a growth or tumor. Primary tumor types are - benign (noncancerous) and Malignant (cancerous).

MR imaging is an important diagnostic tool in the evaluation of intracranial tumors. Its effectiveness is due to its inherent high sensitivity to pathologic alterations of normal parenchymal water content, as demonstrated by abnormal high or low signal intensity on T2- or T1-weighted images, respectively. MR imaging is superior to CT for differentiating between tumor, for defining the extent of tumor, and for showing the relationship of the tumor to critical adjacent structures. T2-weighted sequences are the most sensitive for the detection of tumor. T1 and T2 images give a good image quality and contrast with well distinguishable tumor boundaries.

However, MS lesion can be misdiagnosed as tumor and vice versa.

The sensitivity of the human eye in interpreting large numbers of images decreases with increasing number of cases, particularly when only a small number of slices are affected. Hence there is a need for automated systems for analysis and classification of such medical images [13]. Feature extraction and selection are important steps in automated systems. An optimum feature set should have effective and discriminating features, while mostly reduce the redundancy of feature space to avoid "curse of dimensionality" problem [9].

In this work, textural features are extracted using Gray Level Co-occurrence Matrix (GLCM) method. The supervised machine learning algorithms K-Nearest Neighbor (K-NN), Support Vector Machine (SVM) and Ada-boost are implemented for binary classification of brain MR images. The paper is organized as follows: Section 2 presents the Literature Survey. Section 3 presents the description on classifiers: K-NN, SVM and Ada-boost. Section 4 presents the implemented methodology with a short description for its three stages: feature extraction, cross validation and classification. Section 5 is about analysis of findings followed by discussions in Section 6. Section 7 presents the conclusions.

2. Literature survey

Currently development of automated techniques for disease detection based on different imaging modalities has received lot of attention. MRI based CAD systems are mainly for detection of abnormality and further for classification of abnormality into its possible progression stages or subtypes. Ayelet Akselrod et al. [1] proposed method which uses segmentation to obtain a hierarchical decomposition of a multichannel, anisotropic MR scans. The features describing the segments in terms of intensity, shape, location, neighborhood relations, and anatomical context fed into a decision forest classifier. Atiq Islam et al. [2] proposed a stochastic model for characterizing tumor texture in brain MR images. The paper is about patient-independent tumor segmentation scheme based on Ada-Boost algorithm. Ahmed Kharrat et al. [3] used Wavelets Transform (WT) as input to Genetic Algorithm (GA) and SVM. C. P. Loizou et al. [4] introduced the use of multi scale amplitude modulation–frequency modulation (AM–FM) texture analysis of MS. Their paper is about identifying potential associations between lesion texture and disease progression, and in relating texture features with relevant clinical indexes, such as the Expanded Disability Status scale (EDSS). The results listed shows SVM classifier succeeded in differentiating between patients that, two years after the initial MRI scan, acquired an $EDSS \leq 2$ from those with $EDSS > 2$ (correct classification rate = 86%).

C. Elliott et al. [5] proposed an approach where sequential scans are jointly segmented, to provide temporally consistent tissue segmentation while remaining sensitive to newly appearing lesions. The method uses a two-stage classification process: 1) a Bayesian classifier provides a probabilistic brain tissue classification at each voxel of reference and follow-up scans, and 2) a random-forest based lesion-level classification provides a final identification of new lesions. Pallab Roy et al. [6] proposed a method that adopts a robust intensity normalization technique and lesion contrast enhancement filter for enhancing the region of interest. They used a SVM to classify lesion pixels and level set based active contour and morphological filtering to achieve higher accuracy on lesion pixel identification.

Salim Lahmiri et al. [7] extracted features from the LH and HL sub-bands of wavelet decomposition using first order statistics and used SVM. The proposed approach shows higher performance than when using features extracted from the LL sub-band. It is concluded that the horizontal and vertical sub-bands of the wavelet transform can effectively encode the discriminating features of normal and pathological images. Zahra et al. [8] proposed a fully automatic probabilistic framework based on

conditional random fields (CRFs) for the problem of gad-enhancing lesion detection. The performance of the proposed algorithm is also compared to a logistic regression classifier, a support vector machine and a Markov random field approach. El-Dahshan et al. [9] proposed a hybrid intelligent machine learning technique for detection of brain tumor through MRI. The proposed technique is based on- the feedback pulse-coupled neural network for image segmentation, the discrete wavelet transform for features extraction, the principal component analysis for reducing the dimensionality of the wavelet coefficients, and the feed forward back-propagation neural network to classify inputs into normal or abnormal. Mina Nazari et al. [10] described the methodology of a Content Based Image Retrieval (CBIR) to discrimination between the normal and abnormal medical images based on features. The main indices are finding Normal, Abnormal and clustering the abnormal images to detect two certain abnormalities: Multiple Sclerosis and Tumor. Melika Maleki et al. [12], presented hybrid method based on convolution neural network (CNN) for features extraction and a multilayer neural network for classification into two classes normal and MS. The convolution neural network for recognition of Multiple sclerosis is considered in this paper showed that CNN has strong potential for detection of MS. Petronella et al. [14] presented algorithm based on the K-NN classification technique. The method uses voxel location and signal intensity information for determining the probability being a lesion per voxel, thus generating probabilistic segmentation images. High specificity and lower specificity has been observed in comparison with the combined segmentation.

Literature Survey can be summarized as: For MS/ Tumor detection and classification using Brain MRI supervised techniques such as K-NN [11, 14], artificial neural networks [9, 11, 12], Ada-boost [2] and SVM [3, 4, 7, 10]. However the classes considered greatly vary and the problem of classifying MS lesions from that of tumor with improved accuracy is still a challenge.

3. Classifiers Used

3.1. K-Nearest Neighbor (K-NN)

K-NN is one of the simplest classification techniques based on a distance function and a voting function. In this statistical pattern recognition method, a class is assigned to a sample by searching for samples in a learning set with similar values in a predefined feature space. A new image is classified by comparison with the K learning samples that are closest in terms of Euclidean distance. We also used the most common, Euclidean distance function for K-NN.

3.2. Support Vector Machine (SVM)

A SVM introduced by Vapnik, is a supervised, multivariate classification method that takes as input - labeled data from two classes and outputs - a class label for the test image into one of two classes by finding a hyper plane that maximizes the separating margin between the two classes.

In linear SVM when the linear hyper plane could not be found to separate data, a non-linear function is used to map the input pattern into higher-dimensional space. Thus the data which is linearly separable may be analyzed with a hyper plane, and the linearly non separable data can be analyzed with kernel functions such as higher order polynomials, Gaussian RBF and tan sigmoid etc.

3.3. Ada-boost Algorithm

Freund and Schapire have proposed an adaptive Boosting algorithm, named Ada-Boost. Boosting combines the results of several weak classifiers in order to construct a strong classifier. Boosting develops a linear combination of the input set of weak classifiers, in order to develop a strong classifier [2]. Strong classification algorithms use the techniques such as ANN, SVM etc. Weak classification algorithms use the techniques such as Decision trees, Bayesian Networks, Random forests etc.

The misclassified samples will be assigned with larger weight before the next training iteration. In general, the samples closest to the decision-making boundary will be easily misclassified. Therefore, after several iterations, these samples assume the greatest weights. Ada-Boost generates a sequence of hypotheses and combines them with weights, which can be regarded as an additive weighted combination to make the final hypothesis about the class label which will be the prediction of the Strong Classifier.

4. Methodology

The MRI T2 slices of brain are used for experimentation. The classification with cross-validation is done using K-fold values (folding factors) 3, 5, 7, 9, 15. In the training phase, feature vectors and class labels (predefined in the database or labeled by the radiologist) of each image are used. The feature vectors are extracted for each image using GLCM calculated for distance $d = 1$ with angles $\theta = 0^\circ, 45^\circ, 90^\circ, 135^\circ$ and second order statistical parameters are calculated.

The features are selected which showed maximum similarity within the class and minimum between the classes. Table 1 describes the Haralick's [13] features used, which satisfied the criteria under consideration:

Table 1. Feature Set

Features	Formulae
Contrast	$C = \sum_{i,j} i - j ^2 p(i, j)$
Correlation	$C_r = \sum_{i,j} \frac{(i - \mu_i)(j - \mu_j)p(i, j)}{\sigma_i \sigma_j}$
Energy	$E = \sum_{i=1}^{m-1} \sum_{j=1}^{n-1} (p(i, j))^2$
Homogeneity	$H = \sum_i \sum_j \frac{1}{1 + i - j } p(i, j)$

Where i and j are the horizontal and vertical cell coordinates and $p(i, j)$ is the cell value in a normalized GLCM. The μ_i, μ_j, σ_i and σ_j denote the mean and standard deviation.

In next step, classification is done using K-NN, SVM and Ada-boost classifiers. The work is done for 3 models: i. MS and Normal ii. MS and Tumor and iii. Benign and Malignant Tumor. The performance for all models with 3 classifiers for different K-fold values is evaluated and compared using different parameters like accuracy, error rate, specificity, sensitivity; TP, FP, TN and FN (Section 4.1). Section 4.2 describes the database used for experimentation.

4.1. Performance measures

TP: True Positive, the classification result is positive in presence of clinical abnormality.

TN: True Negative; the classification result is negative in absence of clinical abnormality.

FN: False Negative, the classification result is negative in presence of clinical abnormality.

FP: False Positive, the classification result is positive in absence of clinical abnormality.

Sensitivity (Se): Correctly Classified Positive samples/True Positive samples i.e. True positive fraction

$$Se = \frac{TP}{TP + FN}$$

Specificity (Sp): Correctly Classified Negative samples/True Negative samples i.e. True negative fraction

$$Sp = \frac{TN}{TN + FP}$$

Accuracy (Ac): Correctly Classified samples/classified samples

$$Ac = \frac{TN + TP}{TN + TP + FN + FP}$$

4.2. Database

The Multiple Sclerosis data provided by NITRC: 2008 MICCAI MS Lesion Segmentation Challenge [15] which has been acquired at the Children's Hospital Boston (CHB) and the University Of North Carolina (UNC) is used.

The UNC cases were acquired on a Siemens 3T Allegra MRI scanner with slice thickness of 1 mm and in-plane resolution of 0.5 mm. No scanner information was provided about the CHB cases. The complete set of images of one patient consisted of a T1-weighted (T1), a T2-weighted (T2), and fluid attenuated inversion recovery (FLAIR) image.

The Tumor images consists of images from Harvard Medical School website [16], MICCAI BraTS (Brain Tumor Segmentation) challenge 2012 database [18] and clinical datasets from different hospitals in India. Normal image database consists of images from 'Information eXtraction from Images' (IXI) dataset [17] and Harvard Medical School website.

The IXI data has been collected at three different hospitals in London: Hammersmith Hospital using a Philips 3T system, Guy's Hospital using a Philips 1.5T system and Institute of Psychiatry using a GE 1.5T system. Table 2 describes the detail database considered for each model.

Table 2. Databases used in the implemented system

Model	Total number of images
i	516 (MS: 258 and Normal: 258)
ii	88 (MS: 44 and Tumor: 44)
iii	70 (Benign: 20 and Malignant: 50)

With K-NN, Euclidean distance function and value of K (no. of nearest neighbors considered) =1, 3, 5, 7, 9 are used for experimentation. The results are taken for SVM with kernels: linear, polynomial of order 5 and 9, Radial basis function of sigma- 1 and 2.

For Ada-boost classifier we used decision stump as a weak classifier and the number of iterations are set till the training error reduces to zero.

5. Analysis of Findings

Model i. MS and Normal (see Table 3):

Table 3. Results for MS and Normal MRI Classification

Classifier details	TP	FP	FN	TN	Acc (%)	Se	Sp
K-fold =3							
K-NN	K= 9	80	4	6	82	94.2	0.93
SVM	Linear	86	0	0	86	100	1
Ada-boost	T = 25	86	1	0	85	99.4	1
K-fold=9							
K-NN	K= 9	29	1	0	27	98.3	1
SVM	Linear	29	0	0	29	100	1
Ada-boost	T = 27	29	0	0	29	100	1

Model ii. MS and Tumor (See Table 4):

Table 4. Results for MS and Tumor MRI Classification

Classifier Details	TP	FP	FN	TN	Acc (%)	Se	Sp
K- fold = 3							
K-NN	K= 5	13	3	2	11	82.7	0.86
SVM	Polynomial= 5	15	2	0	13	93.3	1
Ada-boost	T = 37	14	3	0	11	89.2	1
K-fold = 9							
K-NN	K= 5	5	0	0	5	100	1
SVM	Polynomial= 5	5	0	0	5	100	1
Ada-boost	T = 48	5	0	0	5	100	1

Model iii. Benign and Malignant (See Table 5):

Table 5. Results for Benign and Malignant Tumor Classification

Classifier details	TP	FP	FN	TN	Acc (%)	Se	Sp
K-fold = 3							
K-NN	K= 1	15	2	1	5	86.9	0.93
SVM	Linear	14	0	2	7	91.3	0.87
Ada-boost	T = 20	16	3	1	4	83.3	0.94
K-fold = 9							
K-NN	K= 1	6	0	0	2	100	1
SVM	Linear	5	0	0	2	100	1
Ada-boost	T = 33	6	0	0	2	100	1

Table 6 shows the comparison of our CAD system with previous work done on the basis of type of classes considered, classifiers, databases, type of MRI images, performance measures used to detect MS lesion and brain tumor. Following abbreviations are used in this table: DSC- Dice Similarity Index,

TPF- True Positive Factor, FPF- False Positive Factor, FD- False Detection, PPV - Positive Predictive Value and EDSS- Expanded Disability Status Scale.

Table 6. Comparison of Our CAD system with previous work done

Author	Classes	MRI images	Method	Measures	Result	Database
A. A. Ballin et al. [1]	lesion & non lesion (MS)	PD, T1, T2, FLAIR	Decision Forest	Accuracy	0.98 ± 0.01	Scientific Institute Ospedale San Raffaele
				Sensitivity	0.57 ± 0.14	
				Specificity	0.99 ± 0.01	
				DSC	0.55 ± 0.09	
				FPF	0.39	
C. P. Loizou et al. [4]	EDSS ≤ 2 and EDSS > 2 (MS)	T2	SVM	correct rate	0.86	Ayios Therissos Medical Diagnostic Center
				Sensitivity	0.79	
				Specificity	0.90	
C.Elliot et al.[5]	lesion and non- lesion (MS)	T1, T2, FLAIR, T1	Bayesian classifier	Sensitivity at FD rate=0.1	0.83 ± 0.08	NA
				Sensitivity at FD rate=0.2	0.89 ± 0.05	
P. K. Roy et al.[6]	lesion and non- lesion (MS)	T1, T2, FLAIR	SVM (linear kernel)	mean F1 score	0.5	MS Lesion Segmentation Challenge 2008 dataset
				No. of win, drawn and loss (W;D;L)	20;0;4	
Zahra K. et al. [8]	Lesion and non- lesion (MS)	PD, T1, T2, FLAIR	Conditional Random Fields (CRF)	Sensitivity	0.98	multicenter clinical data set
				Average FP No.	2.43	
M. Nazari et al. [10]	Normal, Tumor and MS class	T2	Support Vector Machine (SVM)	Accuracy for Normal	95%	Harvard Medical School website
				Accuracy for Tumor	84%	
				Accuracy for MS	100%	
Sahar Jafarpour et al. [11]	Normal, Tumor and MS class	T2	MNN and K-Nearest Neighbor	Accuracy for MS	92.86%	Laboratory of Neuro Imaging (LONI)and Harvard Medical School
				Accuracy for Normal and tumor	100%	
M. Maleki et al. [12]	Normal and MS MRI	FLAIR	multilayer neural network (MNN)	Accuracy	92.6%	-
				Sensitivity	92.13%	
				Specificity	84.12%	
Petronella Anbeek [14]	MS lesion and non-lesion	T1 and FLAIR	K-Nearest Neighbor		All Average	MS Lesion Segmentation Challenge 2008
				Sensitivity	50.92%	
				Specificity	97.39%	
				PPV	67.26%	
Our CAD system	MS and Normal	T2	K-NN	Accuracy (K = 9)	98.25%	MS Lesion Segmentation Challenge 2008 dataset [15] + Harvard Medical School data + data from hospitals in India
			SVM	Accuracy (Linear Kernel)	100%	
			Ada-Boost	Accuracy (T=27)	100%	
	MS and Tumor		K-NN	Accuracy (K = 5)	100%	
			SVM	Accuracy (Polynomial order =5)	100%	
			Ada-Boost	Accuracy (T=48)	100%	
	Benign and Malignant		K-NN	Accuracy (K = 1)	100%	
			SVM	Accuracy (Linear Kernel)	100%	
	Ada-Boost	Accuracy (T=33)	100%			

Table 7 presents the performance of each classifier for all 3 models for set of test images collected from the different hospitals in India (True

Labels are in “Blue” Color and misclassification labels are in “Red” color):

Table 7. Test Image results

Model			Images									
			1	2	3	4	5	6	7	8	9	10
MS and Normal	True Labels >>		MS	MS	MS	MS	MS	N	N	N	N	N
	K-NN	k=1	MS	MS	MS	MS	MS	N	N	N	N	N
	SVM	Poly-5	MS	MS	MS	MS	MS	N	N	N	MS	MS
	Ada-Boost	T= 8	MS	MS	MS	MS	MS	N	N	N	N	N
MS and Tumor	True Labels >>		MS	MS	MS	MS	MS	T	T	T	T	T
	K-NN	k=1	MS	MS	MS	MS	MS	T	T	T	T	MS
	SVM	Poly-5	MS	MS	MS	MS	MS	T	T	T	T	T
	Ada-Boost	T= 66	MS	MS	MS	MS	MS	T	T	T	T	MS
Benign and Malignant	True Labels >>		B	B	B	B	B	M	M	M	M	M
	K-NN	k=1	M	M	B	B	B	B	M	M	M	M
	SVM	Linear	B	B	B	B	B	B	M	M	B	M
	Ada-Boost	T= 46	B	M	B	B	M	B	M	M	B	M

Figure 1. Comparison of Test results and radiologist feedback

6. Discussions

As can be seen Table 3 SVM gives better performance than K-NN and Ada-boost for classification of MS and Normal images. Table 4 shows that all 3 classifiers gives 100% accuracy with K-fold = 9. However SVM classifier with

polynomial of order = 5 and RBF at sigma = 1 gives better

performance than K-NN and Ada-boost for classification of MS and tumor images. Also, from Table 5, SVM classifier with linear kernel gives better performance than K-NN and Ada-boost for classification of Benign and Malignant Tumor images. Table 6 shows that the CAD system implemented in this work outperforms the previous

systems implemented. As can be seen in Table 7, K-NN classifier with $K=1$ and Ada-boost with 8 number of iterations gives best performance than SVM for 'MS and Normal' model in terms of comparing the assigned label to the test image by the specified classifier with respect to the truth label. SVM gives better performance than K-NN and Ada-boost classifiers for model ii and iii. The above test scans are also shown to radiologist and the comparison is presented in Figure 1; which shows the performance of CAD system using SVM is better for all 3 models under consideration as compared to K-NN and Ada-boost.

7. Conclusion

The CAD system for efficient classification of the human brain MR images into MS and Normal, MS and Tumor or Benign and Malignant has been implemented with the three learning algorithms with minimum number of features.

For all 3 models the classification accuracy is 100% as compared to previous work in this field. For test images the developed CAD system has done equally well as that of the radiologist. SVM proved to be best among three classifiers used in this automated diagnosis system.

This work presents significant contribution in the field of automatic classification of brain MRI using different models proposed. Such system can be proved to be helpful to radiologist and particularly to trainee or new reader to identify MS or tumor lesions with improved accuracy.

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