Nonlinear Feature Extraction Methods Based on Dual-Tree Complex Wavelet Transform Subimages of Brain Magnetic Resonance Imaging for the Classification of Multiple Diseases

Amir Bazdar[1,2],
Amir Hatamian[1],
Javad Ostadieh[1,3],
Javad Nourinia[1],
Changiz Ghobadi[1],
Ehsan Mostafapour[1]

[1]Department of Electrical and Computer Engineering, Urmia University, [2]Department of Electrical Engineering, Islamic Azad University, Urmia Brach, Urmia, [3]Department of Electrical Engineering, Islamic Azad University, Khoy Brach, Khoy, Iran

Abstract

It has been a long time since we use magnetic resonance imaging (MRI) to detect brain diseases and many useful techniques have been developed for this task. However, there is still a potential for further improvement of classification of brain diseases in order to be sure of the results. In this research we presented, for the first time, a non-linear feature extraction method from the MRI sub-images that are obtained from the three levels of the two-dimensional Dual tree complex wavelet transform (2D DT-CWT) in order to classify multiple brain disease. After extracting the non-linear features from the sub-images, we used the spectral regression discriminant analysis (SRDA) algorithm to reduce the classifying features. Instead of using the deep neural networks that are computationally expensive, we proposed the Hybrid RBF network that uses the k-means and recursive least squares (RLS) algorithm simultaneously in its structure for classification. To evaluate the performance of RBF networks with hybrid learning algorithms, we classify nine brain diseases based on MRI processing using these networks, and compare the results with the previously presented classifiers including, supporting vector machines (SVM) and K-nearest neighbour (KNN). Comprehensive comparisons are made with the recently proposed cases by extracting various types and numbers of features. Our aim in this paper is to reduce the complexity and improve the classifying results with the hybrid RBF classifier and the results showed 100 percent classification accuracy in both the two class and the multiple classification of brain diseases in 8 and 10 classes. In this paper, we provided a low computational and precise method for brain MRI disease classification. the results show that the proposed method is not only accurate but also computationally reasonable.

Keywords: *Brain magnetic resonance imaging classification, feature reduction, k-means algorithm, nonlinear features, radial basis function networks*

Submitted: 06-Aug-2021 **Revised:** 11-Mar-2022 **Accepted:** 19-Apr-2022 **Published:** 29-May-2023

Introduction

Brain magnetic resonance imaging (MRI) processing for diagnosing various brain diseases is a favorite topic of research.[1-12] It is used for rapid medical treatment because of the importance of correct diagnosis of brain disease.[13-16] In addition, as diagnosis becomes easier with image processing techniques, routine tests and checkups for patients can be performed more quickly and easily. There are a number of brain diseases that alter brain tissues in some areas. These diseases can be diagnosed by MRI of the brain. In this study, we consider nine types of brain diseases, and Figure 1 shows the disease and normal MRIs of the brain, selected from the MRI database of Harvard Medical School.[17] Recently, many methods have been introduced and many improvements have been made by various researchers on the subject of brain MRI processing.[1-3,19-23] A number of these improvements in feature extraction and reduction of parts that perform advanced signal processing and modeling techniques have been used to select the correct and salient features of each disease.[1-4,20-22] In a study by Zarei and Asl,[24] a nonlinear feature extraction method based on the wavelet coefficients has been proposed for the electrocardiogram (ECG) processing. Furthermore, in many papers,[25-27] the usage of the dual-tree complex wavelet

How to cite this article: Bazdar A, Hatamian A, Ostadieh J, Nourinia J, Ghobadi C, Mostafapour E. Nonlinear feature extraction methods based on dual-tree complex wavelet transform subimages of brain magnetic resonance imaging for the classification of multiple diseases. J Med Sign Sens 2023;13:165-72.

Address for correspondence:
Dr. Ehsan Mostafapour,
Department of Electrical and Computer Engineering,
Urmia University, Urmia, Iran.
E-mail: e.mostafapour@urmia.ac.ir

Access this article online
Website: www.jmssjournal.net
DOI: 10.4103/jmss.jmss_145_21
Quick Response Code:

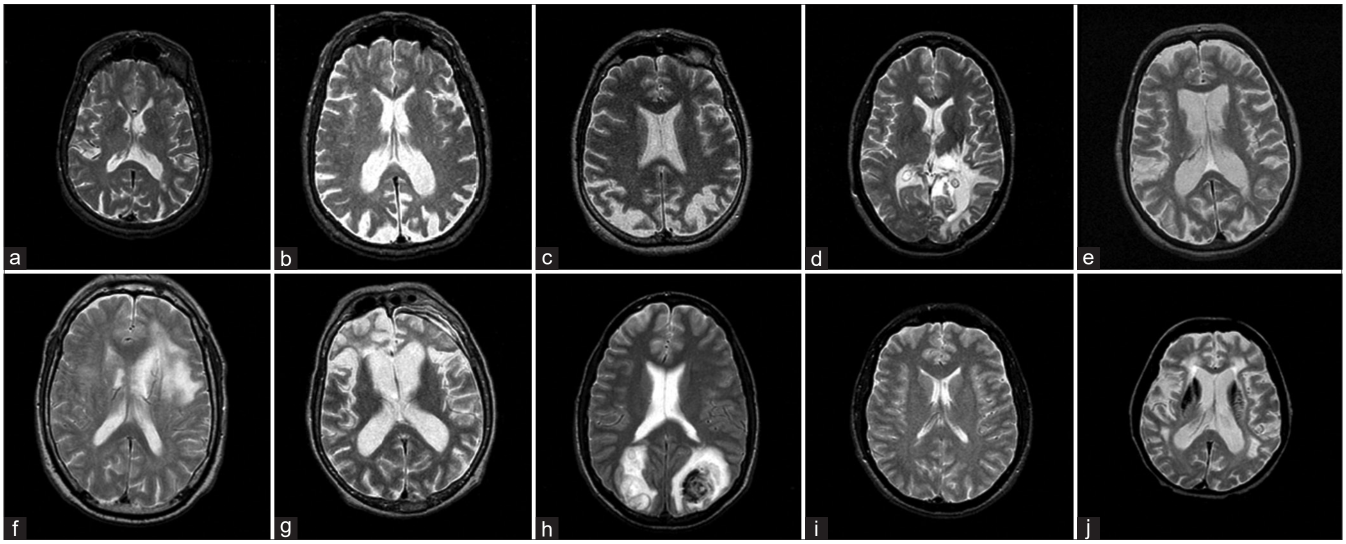

Figure 1: Diseased brain magnetic resonance imaging: (a) normal, (b) Alzheimer, (c) Alzheimer plus visual agnosia, (d) Glioma, (e) Huntington, (f) Meningioma, (g) Pick, (h) sarcoma, (i) AIDS dementia, (j) cerebral calcinosis

transform (DT-CWT) has been proposed for the brain disease detection based on MRIs. By considering these findings, we proposed a nonlinear feature extraction method from the DT-CWT subimages of MRIs to detect multiple diseases.

Other corrections have been made in the classification section.[5] Recently, a number of researchers have used hybrid classification,[10] and a number of others have used two separate classifications to compare their results.[1] In most articles, MRI processing has been the proposed supporting vector machines (SVMs) classification method or a variable of it. For example, in the study by Kalbkhani *et al*.,[3] SVM is used with kernel or in the study by Mohammad Jafarzadeh *et al*.,[4] SVM is used with radial basis function (RBF) kernels. Although the SVM classifier is very powerful and sophisticated, it is an expensive classifier in terms of computing, especially when we use multiple binary SVMs for multiple classifications. In this paper, we used the “K-means, recursive least square (RLS)” learning algorithm for RBF classifiers and show that they perform better than other proposed classifiers. Consequently, for applications where the computational difficulty is important, we recommend the “k-means, RLS” classifier. The aim of this paper is to introduce the neural network with the capacity to update learning algorithms at all levels. Among all the strong and reliable neural networks, hybrid “k-means, RLS” RBF network is the most accurate network compared to the networks presented for brain MRI classification. This superiority is most notable in multiple classification scenarios. Learning schematic of hybrid “k-means, RLS” learning has already been tried in the classification of two classes,[8] which has been compared with multilayer perceptron (MLP) neural networks and SVM classifiers and surpassed both. In the study by Haykin,[8] it is reminded that there is an urge for more substantial tests that use real-world datasets for getting definite results on the performance comparisons between the RBF networks based on RLS algorithm and the SVMs (not only in terms of efficiency but also in terms of convergence speed) as well as the complexity of computations. Here, in the MRI classification of the brain, there is a chance that this comparison will be made. It is important to remember that in the study by Zarei *et al*.[24] the SVM network is proposed for heart ECG classification, and in the study by Mohammad Jafarzadeh *et al*.[4] the SVM network is proposed for the MRI classification. In most articles on MRI classification, the same SVM classifier has been used many times. It takes a long time to introduce a powerful classifier that is updated with newly proposed algorithms. To be able to understand and use these classified hybrid networks, we need to get be familiar with the neural network structures of adaptive algorithms. The result is a robust classification scheme used in brain MRI classification. Our goal in this research is to compare the hybrid RBF network with SVM using the nonlinear features of the DT-CWT subimages in the MRI classification.

The remainder of this article is structured accordingly: In the Section “Feature Refinement,” we studied feature extraction and selection methods for MRI. The explanation of nonlinear feature extraction from the transformed MRI subimages is presented in this section. Furthermore, we show in this section that spectral regression discriminant analysis (SRDA)[29] is somewhat the most trusted and least calculated algorithm for feature selection. In the Section “K-Means, RLS’ Hybrid Classifying for Radial Basis Function,” we explained the hybrid learning methods for RBF classifier and introduced the hybrid “K-means, RLS” algorithm for classification in this section. In the Section “Simulation and Classification Results”, we presented the simulation results and compared the SVM and “k-means, RLS” classifiers in terms of computational difficulty and accuracy. Finally, in the Section “Conclusion,” the conclusion and the ultimate goal of this article are given.

Feature Refinement

Feature refinement is the core part in the disease detection using computer vision.[1] We provided the explanation of our disease detection scheme in three parts as follows:

The two-dimensional dual-tree complex wavelet transform

In the study by Zarei and Asl,[24] the use of DT-CWT in ECG feature extraction is suggested. The principal disadvantage of 2D discrete wavelet transform (DWT) in 2D image analysis is the lack of variance shift and poor directional selectivity.[18,26] This indicates that the value of the wavelet coefficients changes considerably when the input image rotates or moves slightly. Moreover, this occurs to the down sampling at every step. To obtain the variance shift is to use the undecimated shape of the dynamic filter tree, although this scheme requires complex calculations and a lot of hassle at its output. The 2D DT-CWT solves this issue with the hash factor which is basically less than undecimated DWT. In previous studies,[25-27] the authors have described the shift invariance characteristics of the DT-CWT. The 2D DT-CWT uses two trees of real filters (tree A and tree B) as depicted in Figure 2. In a study,[30] the formulation for the quadratic mirror filters is given. The two trees belong to the real and imaginary parts of the imaginary wavelet transmission. The DT-CWT transforms the MRI image using two discrete wavelet transforms (DWTs) sampled in parallel for the identical information. Filters are selected to interpret upper DWT subcategory signals as the real part of mixed wavelet transmission and lower DWT subcategory signals as the imaginary part. By designing the transmission like this, the 2D DT-DWT shifts steadily. The selected transformed subimages are $LL_{1a,}.LL_{2a,}.LH_{2a,}.LL_{3a,}.LH_{1b,}.HL_{2b,}.LL_{2b,}.and.HL_{3b}$.

The MRI input of the brain in this study is 256 × 256 pixels. After three stages of 2D DT-CWT, LL_3 subgroup has a size of 32 × 32 pixels. By selecting the coefficients of this subgroup as features, we have the initial features 32 × 32 = 1024.[3,4] In this case, the resulting primary feature vector has 1024 inputs. The large-scale classification of such a vector has unacceptable computational complexity, and there are features related to the photograph background that do not provide any useful information for classification. Therefore, feature selection and reduction are necessary. We want to reduce these features to 7 or less. Here, we describe a method for selecting the appropriate feature and its benefits.

Extraction of nonlinear features from two-dimensional dual-tree complex wavelet transform coefficients

Following the extraction of the 2D DT-CWT subimages from the MRIs, we derive the nonlinear features. We used the approximate entropy (ApEn), fuzzy entropy (FE) and interquartile range (IQR), nonlinear features[24,28] for the

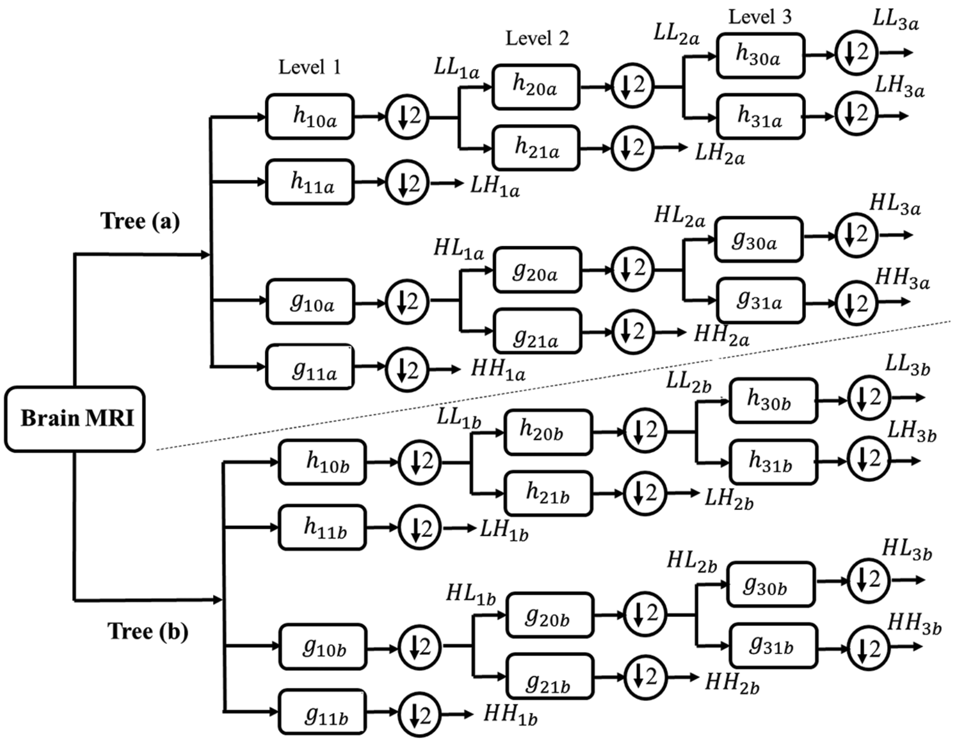

Figure 2: Three levels of the two-dimensional dual-tree complex wavelet transform applied to preprocessed brain MRI. MRI – Magnetic resonance imaging

Table 1: The nonlinear features types drawn from the two dimensional dual-tree complex wavelet transform subimages

Feature	Explanation
FE	Fuzzy entropy
ApEn	Approximate entropy
IQR	Interquartile range

first time for the MRI classification in this paper. These features are integrated in Table 1 and described in the study by Zarei and Asl.[24] We have not included its calculations in this section.

It is important to mention that for drawing the nonlinear features from the 2D DT-CWT subimages, we first turned the 32 × 32 subimage matrix to a vector of 1 × 1024 length and then applied the nonlinear feature extraction formulation in the studies by Zarei and Asl[24] and Ostadieh *et al*.[28] to it. By utilizing these three feature extraction schemes and with the eight selected DT-CWT subimages described in the Section "K-Means, RLS' Hybrid Classifying for Radial Basis Function," we have 24 features for each MRI inserted into the classifier. Here, we have feature reduction.

The spectral regression discriminant analysis for feature reduction

SDRA[29] is a dominant feature reduction algorithm, and for this reason, we utilized it here. For SDRA, we have a set of $x_1,\ldots x_m \in R^N$ data which belong to Nc various classes and m_k is assigned to a number of samples from kth class $\left(\sum_{k=1}^{Nc} m_k = m\right)$. The SDRA steps are summarized as follows:[4]

1. First we have:

$$\boldsymbol{y}_k = \begin{bmatrix} \underbrace{0,\ldots,0}_{\sum_{i=1}^{k-1} m_i}, \underbrace{1,\ldots 1}_{m_k}, \underbrace{0,\ldots,0}_{\sum_{i=k+1}^{Nc} m_i} \end{bmatrix}^T \qquad k = 1,\ldots,Nc \tag{1}$$

and $y_0 = [1,1,\ldots,1]^T$ represents the vector of ones. Since y_0 in the subspace is described as, $\{y_k\}$ the Nc-1 vectors are obtained as follows:

$$\left\{\underline{y_k}\right\}_{(k=1)}^{Nc}, (\underline{y_i^T} y_0 = 0 \text{ where } \underline{y_i^T}\ \underline{y_j} = 0, i \neq j) \tag{2}$$

2. At this point, new input "l" is appended to each x_i which is still assigned as x_i. Hence, Nc-1 vectors $\{a_k\}_{k=1}^{Nc-1} \in R^{N+1}$ are made that a_k as a solution to the the regularized least squares problem as below:

$$\alpha_k = \left(\sum_{i=1}^{m} \left(\alpha^T x_i - \underline{y}_i^k\right)^2 + \alpha \| \alpha \|^2\right) \tag{3}$$

Here, $\underline{y}_i^k$ is the ith member of $\underline{y}_k$ and $\alpha \geq 0$ is used for feature reduction control.

3. The Nc-1 vectors $\{a_k\}$ are the essential vectors of SRDA. Let $A = [\alpha_1,\ldots,\alpha_{Nc-1}]$, which is a $(N+1)\times(Nc-1)$ transformation matrix. The x can be embedded into **z** in the $(Nc-1)$ dimension subspace by:

$$z = A^T [x\ 1] \tag{4}$$

Using the SRDA, we reduce the features of each MRI to 1 and 7 according to the number of the classes.

"K-means, RLS" Hybrid Classifying for Radial Basis Function

The RBF network with hybrid learning scheme is presented in Figure 3. The reason for the learning method to be hybrid is that it comprises two stages:[28]

1 Stage 1: The proposed classifying scheme uses unsupervised algorithms (here the k-means clustering) for the hidden layer
2 Stage 2: Uses the regularized least squares (RLS) algorithm to calculate the linear outer layer weight vector. This two-step design method has a favorite feature pair called simplicity of calculations and accelerated convergence.

Here, we explain the function of RBF layers separately:

1. The input layer comprises the source neurones connecting the RBF network to environment. Network inlets are for classifying features
2. The hidden layer consists of hidden sections that use the hidden transition from the input space to the hidden space. The number of neurons in the hidden layer is high, and it is the only part of the network that uses unsupervised algorithms for clustering. The main task of this layer is to compute the following RBF:[8]

$$\varphi_j(x) = \varphi\left(\| x - x_j \|\right) \qquad j = 1,2,\ldots,N \tag{5}$$

The x_j defines the center of the RBF. In addition, x is the input feature vector. Hence, unlike a multilayer perceptron, links that connect source nodes to hidden parts are weightless direct connections. Our assumed basis function in this paper is Gaussian.

3. The algorithm for the output layer is the adaptive linear RLS algorithm The amount of neurons in the output layer is lower than the hidden layer.

The hybrid learning steps for the RBF is explained here.

K-means algorithm for clustering

The algorithm that we use for clustering in the hidden layer is the K-means and it has two parts:[8]

1. Part 1: To reduce the variance of the clusters based on

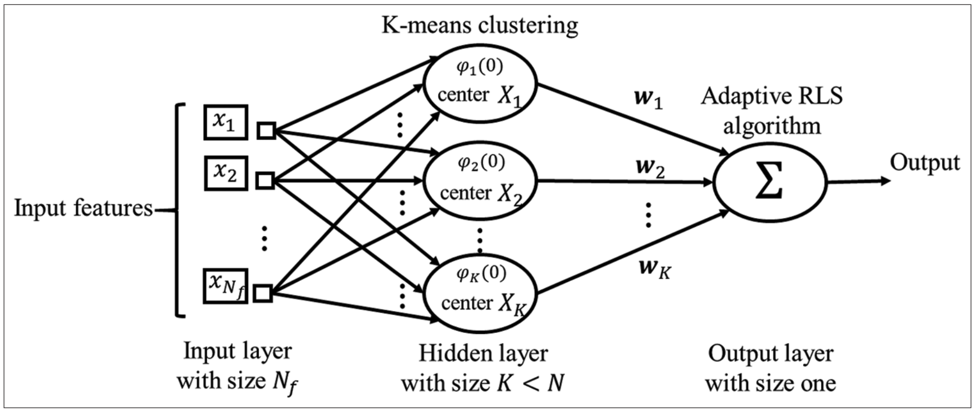

Figure 3: The proposed hybrid "k-means, RLS" RBF classifier. RBF – Radial basis function

the cluster means ($\{\hat{E}\}_{j=1}^{K}$), we must do the following optimization:

$$\min_{\{\mu\}_{j=1}^{K}} \sum_{j=1}^{K} \sum_{C(i)=j} \| x_i - \mu_j \|^2 \quad \text{for a given } C \tag{6}$$

2. Part 2: For optimizing the cluster means ($\{\hat{E}\}_{j=1}^{K}$), we must minimize the following cost function:

$$C(i) = \arg\min_{1\le j\le K} \| x_i - \mu_j \|^2 \tag{7}$$

The RLS adaptive algorithm part

The algorithm for the output layer is RLS as we mentioned earlier. Assume that the following $K \times 1$ vector denotes the output of the K neurons in the hidden layer of RBF:

$$\phi(x_i) = \begin{bmatrix} \varphi(x_i, \mu_1) \\ \varphi(x_i, \mu_2) \\ \vdots \\ \varphi(x_i, \mu_K) \end{bmatrix} \tag{8}$$

This vector is produced in response to the inputs x_i, $i = 1,2,...,N$. Therefore, for the training to be supervised, we have the training sample $\{\phi(i), d(i)\}_{i=1}^{N}$. Here, d_i is the desired output of the RBF classifier for the stimulus x_i and is achieved using the RLS algorithm that comprises the following command lines:[8]

By assuming the training sample $\{\phi(i), d(i)\}_{i=1}^{N}$, compute the next quantities for iteration numbers n=1 to N:[8]

$$P(n) = P(n-1) - \frac{P(n-1)\phi(n)\phi^T(n)P(n-1)}{1+\phi^T(n)P(n-1)\phi(n)} \tag{9}$$

$$g(n) = P(n)\phi(n) \tag{10}$$

$$\acute{a}(n) = d(n) - \hat{w}^T(n-1)\phi(n) \tag{11}$$

$$\hat{w}(n) = \hat{w}(n-1) + g(n)\alpha(n) \tag{12}$$

To commence the method, we take $\hat{w}(0) = 0$ and, $P(0) = \lambda^{-1} I$ in which λ is the forgetting factor of the RLS algorithm.[8]

In the study by Rifkin,[9] a full comparison analysis was made between the SVMs and the hybrid RBF classifiers. In the simulation part, we compare the performance of the hybrid RBF network with the performance of SVM and K-nearest neighbor classifiers in the brain disease classification.

Simulation and Classification Results

In the simulation section, to build our classifier, we used the MATLAB program of the two-class hybrid RBF classifier (described by Haykin[8]) and converted it to a 10-class and 8-class classifier. We also added the RLS algorithm and the result is a powerful classifier. The RBF network with hybrid k-means and RLS is considerably quicker and requires less convergence time and computation than SVM. This advantage is important in multiple classification scenarios. The results of Rifkin[9] show a 30% reduction in time, and as the number of photographs increases, this time difference becomes more apparent. In the studies by Kalbkhani *et al*.[1] and Mohammad Jafarzadeh *et al*.,[4] a one-against-one approach is used for multiple SVM classifications. In the study by Ayachi and Amor,[14] it is proven that this method is the best for binary SVM expansion. However, in this paper for our RBF network, we used the one-against-all approach which in the study by Haykin[8] proved to be the best method for extending this classification. We present the final diagram of the classification method we have presented in Figure 4.

Database Description and the Two-Class Classification

The database we used in this article includes T2-weighted brain MRIs with 256 × 256 pixels. These photographs were taken from the Harvard School Database.[17] We have selected 10 photographs for each of the previously mentioned diseases. Because of this, the brain data set has 100 images with 10 normal numbers and 90 brain images with the diseases. Based on these photos, we performed our classification. The cross-validation is considered of course due to the limited amount of images in Harvard data set. Since the amount of images belonging to each class is low, i.e., ten images per class, three-fold cross-validation approach is used to obtain the performance. Therefore, database is randomly partitioned into three nonoverlapping parts. Two parts have three images from each class and one part contains four images from each class. The classifier training and testing is performed three folds. In each fold, two parts are utilized for training phase and one part is utilized for testing the accuracy of the classifier. Then, the results are averaged. We now compare the classification efficiency of our proposed method and the results of other sources for the two-class scheme. These results are given in Table 2. Results are given based on the correct classification rate (CCR) which is given as follows:[8]

$$CCR\ \% = \frac{\sum_{i=1}^{N_c} correct\ classification\ in\ class\ i}{total\ number\ of\ Sample\ MRIs} \times 100 \qquad (13)$$

In Table 2, it can be seen that only the results comparable to our proposed method are the results of reference[1,4], but the classifiers of these two sources are SVM, and we explained that this classifier has more computational complexity than the RBF classifier. The only standard data set that is used in our comparing references is the MRI data set of the Harvard Medical School.[17] And also, our work is the advanced and developing version of Kalbkhani[1] and is mainly based on this data set.

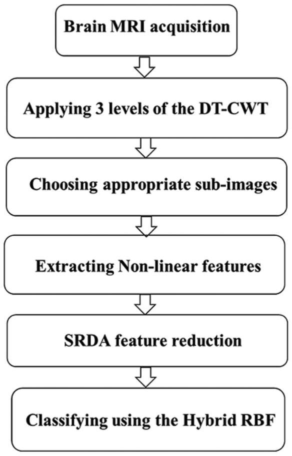

Figure 4: The overall diagram of presented method for classification. RBF – Radial basis function; MRI – Magnetic resonance imaging; DT-CWT – Dual-tree complex wavelet transform; SRDA – Spectral regression discriminant analysis

Eight- and ten-class cases

For the eight-class case, we select eight classes out of ten. In a number of simulations, however, we obtain 99% CCR for the

Table: 2 Comparison of various classification methods in two-class brain disease scenario

References	Used method	Number of features	CCR (%)
Chaplot *et al*.[5]	DWT+SVM	4761	98
Dahshan *et.al*.[6]	DWT+PCA+KNN	7	98.6
Kalbkhani *et al*.[2]	One-level 2D DWT+cumulant+LDA+SVM	1	100
Das *et al*.[7]	RT+PCA+SVM	9	100
Kalbkhani *et al*.[1]	DWT+GARCH+PCA+SVM	1	100
Mohammad Jafarzadeh *et al*.[4]	DWT+SRDA+SVM	1	100
Proposed method	Nonlinear features+2D DT-CWT+SRDA+hybrid RBF	1	100

CCR – Correct classification rate; SVM – Supporting vector machines; PCA – Principal component analysis; KNN – K-nearest neighbor; DWT – Discrete wavelet transform; 2D DWT – Two-dimensional DWT; LDA – Linear discriminant analysis; SRDA – Spectral regression discriminant analysis; 2D DT-CWT – Two-dimensional dual-tree complex wavelet transform; RBF – Radial basis function; GARCH – Generalized auto-regressive conditional heterosedasticity; RT – Ripplet transform

Table 3: Comparison of various classification methods in eight and ten class brain disease scenarios

References	Used method	Number of classes	Number of features	Number of images	CCR (%)
Kalbkhani *et al*.[1]	2D DWT+GARCH+PCA+SVM	8	7	80	98.21
Kalbkhani *et al*.[3]	2D DWT+MCFS+KNN	8	41	80	98.75
Mohammad Jafarzadeh *et al*.[4]	2D DWT+SRDA+SVM	8	7	100	100
Mohammad Jafarzadeh *et al*.[4]	2D DWT+SRDA+SVM	10	9	100	98
Kalbkhani *et al*.[2]	One-level 2D DWT+cumulant+LDA+SVM	8	7	80	99.89
Proposed method	Nonlinear features+2D DT-CWT+SRDA+hybrid RBF	8	7	80	100
Proposed method	Nonlinear features+2D DT-CWT+SRDA+hybrid RBF	8	7	80	100
Proposed method	Nonlinear features+2D DT-CWT+SRDA+hybrid RBF	10	7	100	100

CCR – Correct classification rate; SVM – Supporting vector machines; PCA – Principal component analysis; KNN – K-nearest neighbor; DWT – Discrete wavelet transform; 2D DWT – Two-dimensional DWT; LDA – Linear discriminant analysis; SRDA – Spectral regression discriminant analysis; 2D DT-CWT – Two-dimensional dual-tree complex wavelet transform; RBF – Radial basis function; GARCH – Generalized auto-regressive conditional heterosedasticity; RT – Ripplet transform; MCFS – Multi-cluster feature selection proposed method in ten classes. This percentage was 100% in most simulations. This classification percentage is the first hybrid “K-means, RLS” RBF network using the nonlinear features of the 2D DT-CWT coefficients and is obtained with less computation and processing time than SVM.

To compare the classification results in this case, we prepared Table 3. In Table 3, the results are given based on the number of features and images used for each method. It can be seen that the hybrid RBF classifier works as well as the SVM classifier in our proposed method, surpassing all other methods with 100% CCR in 10 classes.

Conclusion

In this paper, an effective algorithm for brain MRI disease classification is proposed based on the nonlinear feature extraction. Our feature vector was obtained from three levels of the 2D DT-CWT and then given to SRDA feature reduction algorithm. The SRDA reduced feature vector dimensions from 24 to 1 and 7 features for 2-, 8-, and 10-class cases, respectively. RBF classifier with “K-means, RLS” learning was used for classification and the results were obtained. The CCRs equal to 100% for all cases that are better than the recently introduced algorithms. In addition, the proposed method has less computational complexity. Hybrid RBF network has 30% less computing time and computing time compared to multiclass SVM. Finally, in comparison with the deep neural networks, the proposed classifier works with much less computational complexity and processing time. In future works, we will replace the RLS algorithm with newer and more advanced adaptation algorithms to improve the proposed classifier. This will open a new way of research to improve this method with newly emerged adaptive algorithms.

Financial support and sponsorship

None.

Conflicts of interest

There are no conflicts of interest.

References

1. Kalbkhani H, Shayesteh M, Zali B. Robust algorithm for brain magnetic resonance image (MRI) classification based on GARCH variance series. J Biomed Signal Process Control 2013;8:909-19.
2. Kalbkhani H, Shayesteh M, Rashidi A. “Brain Tumor Classification from MRI Images Based on Cumulant Features”. 2019 27th Iranian Conference on Electrical Engineering (ICEE). IEEE; 2019.
3. Kalbkhani H, Salimi A, Shayesteh M. “Classification of Brain MRI Using Multi-cluster Feature Selection and KNN Classifier”, 23rd IEEE Iranian Conference on Electrical Engineering; 2015. p. 93-8.
4. Mohammad Jafarzadeh B, Kalbkhani H, Shayesteh M. “Spectral Regression Discriminant Analysis for Brain MRI Classification”, 23rd IEEE Iranian Conference on Electrical Engineering; 2015. p. 353-7.
5. Chaplot S, Patnaik L, Jagannathan N. Classification of magnetic resonance brain images using wavelets as input to support vector machine and neural network. Biomed Signal Process Control 2006;1:86-92.
6. El-Dahshan ES, Hosny T, Salem AB. Hybrid intelligent techniques for MRI brain images classification. Digit Signal Process 2010;20:433-41.
7. Das S, Chowdhury M, Kundu M. Brain MR image classification using multisclae geometric analysis of ripplet. J Progress Electromagnetics Res 2013;137:1-17.
8. Haykin S. Neural Networks and Learning Machines. Upper saddle river, New Jersey: Prentice Hall; 2008. p. 230-63.
9. Rifkin RM. “Everything Old is New Again: A Fresh Look at Historical Approaches in Machine Learning”, Ph.D. Thesis, MIT; 2002.
10. Golamreza D, Masoumi S. “Introducing Hybrid k-Means, RLS Learning Algorithm in RBF Network for Low Computational Brain MRI Multi-Classification,” 4th National Conference on Applied Research in Electrical, Mechanical and Mechatronic, Tehran; February, 2016.
11. Cai D, Zhang C, He X. Unsupervised Feature Selection for Multi-cluster Data”, in Proceedings of the 16th ACM SIGKDD International Conference on Knowledge Discovery and Data Mining; 2010. p. 333-42.
12. Nowak RD. Wavelet-based Rician noise removal for magnetic resonance imaging. IEEE Trans Image Process 1999;8:1408-19.
13. Zhang J, Ma K, Meng Hwa Er, Chong V. “Tumor Segmentation from Magnetic Resonance Imaging by Learning via One-class Support Vector Machine”, In International Workshop on Advanced Image Technology; 2004. p. 207-11.
14. Ayachi R, Amor N. “Brain Tumor Segmentation Using Support Vector Machines”, In Proceedings of European Conference on Symbolic and Quantitative Approaches to Reasoning with Uncertainty; 2009. p. 736-47.
15. Batista J, Kitney R. “Extraction of Tumors from MR Images of the Brain by Texture and Clustering”, In Proceedings of the International Conference on Image Analysis and Processing; 1995. p. 235-40.
16. Wu M, Lin C, Chang C. “Brain Tumor Detection Using Color-Based k-Means Clustering Segmentation”, In International Conference on Intelligent Information Hiding and Multimedia Signal Processing; 2007. p. 245-50.
17. MRI Brain Data Base of “Harvard Medical School”, Data. Available from: http://www.med.harvard.edu/AANLIB/. [Last accessed on 2022 Jan 01].
18. Hackmack K, Paul F, Weygandt M, Allefeld C, Haynes JD, Alzheimer’s Disease Neuroimaging Initiative. Multi-scale classification of disease using structural MRI and wavelet transform. Neuroimage 2012;62:48-58.
19. Latifi-Navid M, Bilen M, Konukseven EI, DOĞAN M, Altun A. Fast and accurate semi-automatic haptic segmentation of brain tumor in 3D MRI images. Turk J Electr Eng Comput Sci 2014;24:1397-411.
20. Varuna Shree N, Kumar TN. Identification and classification of brain tumor MRI images with feature extraction using DWT and probabilistic neural network. Brain Inform 2018;5:23-30.
21. Mohsen H, El-Dahshan A, El-Horbaty M, Salem A. Classification of brain MRI for Alzheimer’s disease based on linear discriminate analysis. Egypt Comput Sci J 2017;41:44-52.
22. Xiao Z, Ding Y, Lan T, Zhang C, Luo C, Qin Z. Brain MR image classification for Alzheimer’s disease diagnosis based on multifeature fusion. Comput Math Methods Med 2017;2017:1952373.

23. Najafi S, Amirani MC, Sedghi Z. "A New Approach to MRI Brain Images Classification", Proceedings of 19th IEEE Iranian Conference on Electrical Engineering; 2011. p. 100-4.
24. Zarei A, Asl BM. Automatic detection of obstructive sleep apnea using wavelet transform and entropy-based features from single-lead ECG signal. IEEE J Biomed Health Inform 2019;23:1011-21.
25. Basukala D, Jha D, Kwon GR. Brain image segmentation based on dual-tree complex wavelet transform and fuzzy C-means clustering algorithm. J Med Imaging Health Informatics 2018;8:1776-81.
26. Jha D, Kim JI, Kwon GR. Diagnosis of Alzheimer's disease using dual-tree complex wavelet transform, PCA, and feed-forward neural network. J Healthc Eng 2017;2017:9060124.
27. Wang S, Lu S, Dong Z, Yang J, Yang M, Zhang Y. Dual-tree complex wavelet transform and twin support vector machine for pathological brain detection. Appl Sci 2016;6:169.
28. Ostadieh J, Amirani MC, Valizadeh M. Enhancing obstructive apnea disease detection using dual-tree complex wavelet transform-based features and the hybrid "K-means, recursive least-squares" learning for the radial basis function network. J Med Signals Sens 2020;10:219-27.
29. Cai D, He X, Han Z. SRDA: An efficient algorithm for large-scale discriminant analysis. IEEE Trans Knowl Data Eng 2008;20:1-12.
30. Vermaak H, Nsengiyumva P, Luwes N. Using the dual-tree complex wavelet transform for improved fabric defect detection. J Sens 2016;2016:1-8.