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Multi support vector machine and image processing for diagnosis of coronary artery disease

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Multi Support Vector Machine (MSVM);
Image processing.

Abstract

The optimal non-invasive test, Coronary Computed Tomography Angiography (CCTA), is to control Coronary Artery Disease (CAD). This paper proposes a developed algorithm called Multi Support Vector Machine (MSVM) applied in classification and diagnosing a common heart disease, CAD, utilizing the features extracted from the patients' CCTA images through two image-processing-based approaches. These image-processing-based approaches including the quantification of cardiovascular vessels and the Auto Encoder (AE) network are utilized for the extraction of the features from the CCTA images. Then, a novel MSVM algorithm is developed for diagnosing heart diseases. A dataset from the Tehran Heart Center is utilized in addition to a collection of datasets from the literature to evaluate the performance of the proposed algorithms based on accuracy, precision, and recall performance measures. The proposed MSVM algorithm is compared with a number of existing methods in the literature where the results show that the proposed MSVM algorithm outperforms all the competing methods in terms of all the performance measures. In addition, it is concluded that the proposed MSVM algorithm performs much better than the classical Support Vector Machine (SVM) method under all the scenarios.

1. Introduction

Cardiovascular Diseases (CVDs) are one of the main sources of mortality among people [1], which are growing due to different reasons such as high blood pressure and cholesterol, smoking, overweight and obesity, diabetes, family history of heart disease, psychological factors, high fasting glucose, physical inactivity, and diet of junk foods [2]. While CVDs cover various types of heart diseases, the most common type of heart disease is Coronary Artery Disease (CAD). CAD is a form of CVDs that results in the narrowing or occlusion of the major blood vessels (coronary arteries) and accordingly causes myocardial ischemia, oxygen deficiency, or necrosis, manifesting as chest pain, chest tightness, or myocardial infarction, oxygenation of the heart, and other symptoms [3]. According to the World Health Organization's (WHO) reports, CAD has been the most common cause of death worldwide in recent decades where, for example, 28.07% of total deaths in 2020 in Iran were due to CAD, as the first cause of death in Iran. In most cases, the lack of initial detection of heart disease in the patients leads to an increase in the death rate [4]. Accordingly, an early and accurate diagnosis of the disease and special medical care for the patients suffering from such diseases can reduce, considerably, the death rates [5]. Generally, the diagnosing approaches are categorized as invasive and non-invasive. In this regard, angiography is one of the widely used and accurate approaches while it is expensive and invasive, and

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has some risks such as heart attack and death [6,7]. Accordingly, proposing non-invasive and accurate diagnosis approaches which can provide an accurate prediction of heart diseases would be highly significant [8,9]. In this regard, data mining is a promising approach that can be applied to non-invasive diagnosis approaches, and provide an accurate prediction of disease, based on the acquired attributes.

Nowadays, various imaging methods, including Coronary Computed Tomography Angiography (CCTA) images, have been used by specialists for diagnosing heart diseases. On the other hand, a number of research studies have used data mining methods for diagnosing CVDs. However, the data mining approaches based on image processing have received less attention in the literature for processing and analyzing CCTA images. The CCTA images are important non-invasive tools for diagnosing CVDs where, in these images, different layers of the heart are imaged, and the heart is modeled in three dimensions. By observing the condition of the main vessels in the heart, heart diseases like CAD can be detected. The CCTA is often utilized to determine patients with suspected CAD as it allows non-invasive detection of coronary artery stenosis [10]. While there exist a huge number of these images in the hospitals, they are currently analyzed visually by doctors and based on their experience which can lead to some incorrect diagnoses of the diseases due to human error, the high workload of doctors and etc. Hence, it is essential to propose some robust and intelligent approaches for accurate diagnosis of heart diseases using the CCTA images, based on historical data and without the need for specialist doctors. On the other hand, as mentioned previously, an early and accurate detection of CAD is very important and vital for on-time administration of appropriate treatment, preventing patients from more damages and reducing the death rates. Accordingly, it is of high importance to improve the accuracy of approaches developed for diagnosing the CAD. Therefore, the main purpose of this paper is to develop an approach in order to both improve the diagnosis accuracy of the CAD and reduce the dependency of the diagnostic procedure on the doctors. In this regard, initially, two image-processing-based approaches are proposed to extract features from the patients' CCTA images. In the first approach, the quantification of cardiovascular vessels is applied to the CCTA images to extract the features while in the second approach, an Auto Encoder (AE) network [11-13] is developed as an unsupervised deep learning method for extracting the related features from the CCTA images. Then, considering Support Vector Machine (SVM) as one of the best methods for classification and diagnosis of CAD [14], a novel classifier entitled Multi Support Vector Machine (MSVM) algorithm, as an improved version of SVM, is proposed in this paper and is applied to the extracted features of both quantification of cardiovascular vessels and AE network methods to diagnose the CAD. To the best of the authors' knowledge, this research paper is novel in this subject where, a novel classification algorithm, entitled MSVM, is proposed for diagnosing the CAD based on the extracted features through two image processing algorithms.

The rest of the paper is organized as follows. The literature of the subject is reviewed in Section 2. In Section 3, the details of the proposed MSVM algorithm and the feature extraction methods are presented. The performance of the proposed MSVM algorithm, applied to the CCTA images of Tehran Heart Center Hospital and some benchmark datasets, is evaluated and compared to the competing methods in terms of accuracy, precision, and recall measures in Section 4. Finally, the concluding remarks and recommendations for future research are provided in Section 5.

2. Literature review

In this section, a brief review of the research efforts performed on the problem of diagnosing heart diseases by different approaches, in addition to the approaches applied to images for diagnosis purposes, is provided. It should be noted that various methods including data mining and machine learning algorithms, Artificial Neural Networks (ANNs), fuzzy clustering algorithms, and evolutionary algorithms have been developed in the literature to diagnose the various types of arrhythmias and heart diseases in different databases.

To name a few, Babaoğlu et al. [15] applied and evaluated the efficiency of Binary Particle Swarm Optimization (BPSO) and Genetic Algorithm (GA) as feature selection techniques on diagnosing CAD based on the dataset obtained from the patients who carried out Exercise Stress Testing (EST) and Coronary AngioGraphy (CAG). Ciecholewski [16] applied SVM and CLIP3 algorithms to the heart images obtained from Single-Photon Emission Computed Tomography (SPECT) to diagnose ischemic heart disease and showed that the SVM performs highly accurate. Giri et al. [17] utilized advanced SVM, Gaussian Mixture Model (GMM), Probabilistic Neural Network (PNN), and K-Nearest Neighbor (KNN) for diagnosis of cardiac health. They applied the Discrete Wavelet Transformation (DWT) to the heart rate signal extracted from Electrocardiogram (ECG) to provide suitable features. Vafaie et al. [18] proposed an algorithm for the automatic diagnosis of CVDs, which could classify an ECG signal with unknown characteristics according to the similarities between it and ECG signals with known properties. Krishnaiah et al. [19] proposed an approach based on fuzzy logic to remove the uncertainty of unstructured data and applied the fuzzified data for diagnosis of heart diseases. Venkatalakshmi and Shivsankar [20] introduced a predictive data-mining method for diagnosis of heart disease and applied their method to a UCI dataset with 294 records and 13 features for each record. Masethe and Masethe [21] applied the J48, Naïve Bayes (NB), Reduced Error Pruning Tree (REPTRee), Bayes Network, and Classification and Regression Tree (CART) for heart disease prediction on a dataset from the Medicine Centre of South Africa with 11 features for each sample. Based on the results, they concluded that the tree-based algorithms such as CART, REPTRee, and J48 have better performances than other methods. Chandna [22] proposed an Artificial Neuro-Fuzzy Inference System (ANFIS) for diagnosing heart diseases and obtained an accuracy of 98.24%. Xiong et al. [23] proposed a machine learning method for classification of patients with significant stenosis using myocardial features derived from a single CCTA scan. Ismaeel et al. [24] proposed an Extreme Learning Machine (ELM) algorithm as a warning system for the presence of heart diseases based on the factors such as age, sex, cholesterol, and blood glucose. Bahrami and Shirvani [25] proposed the J48, KNN, NB, and SMO methods for diagnosing heart disease. They used 209 records each containing 8 features from an Iranian hospital and, reducing the number of features to 4, showed that the J48 algorithm was the best classifier with an accuracy of 83.73%. Paul et al. [26] proposed a GA based on a fuzzy Decision Support System (DSS) in order to predict the risk level of heart disease. Patil and Kinariwala [27] proposed three algorithms including Classic Random Forest (CRF), Modified Random Forest (MRF), and Weighted Random Forest (WRF) for automatic diagnosis of heart disease. They used a UCI dataset with 303 samples and showed that the WRF outperforms the competing models. Dolatabadi et al. [28] proposed an SVM algorithm to diagnose CAD automatically based on heart rate variability signal extracted from ECG. Zreik et al. [29] presented a novel method to identify CAD in the CCTA images, where the convolutional AE network and SVM algorithm were used. Shahid and Singh [30] proposed an approach based on emotional neural network and Particle Swarm Optimization (PSO) for diagnosing CAD and applied some feature selection methods to enhance the performance of their proposed approach. Nasarian et al. [31] proposed a feature selection algorithm entitled heterogeneous hybrid feature selection (2HFS) for extracting the related features from CAD datasets. Then, they applied some classifiers to the features selected by 2HFS and evaluated the accuracy of CAD diagnosis. Alizadehsani et al. [32] proposed an approach based on traditional classification algorithms to deal with the uncertainty among CAD data for the prediction of stenosis in the different arteries. Zomorodi-Moghadam et al. [33] applied two methods to a real-world CAD dataset for feature selection and proposed a hybrid PSO for detection of CAD.

Considering all the references cited above, the data mining models based on image processing as non-invasive approaches have received less attention in the literature for processing and analyzing the CCTA images. In addition, considering the significance of early and accurate diagnosis of the CAD in preventing patients from more damages and reducing the death rates, any improvement in the accuracy of diagnosing approaches would be of great importance. Hence, in this paper, a novel classifier entitled MSVM algorithm is proposed for accurately diagnosing the CAD, based on the features extracted from the patients' CCTA images through two image-processing-based approaches. The details of the proposed method are described in the next section.

3. The proposed method

In this section, the details of the proposed MSVM algorithm, as a developed version of SVM, is provided to classify and diagnose the CAD. The general scheme of the classification and diagnosing the heart disease utilizing the features extracted from the patients' CCTA images through two image-processing-based approaches is presented in Figure 1.

In this paper, two feature extraction methods including the quantification of cardiovascular vessels and extraction of features using the AE network have been utilized. According to Xu et al. [34], the AE network dominates other feature extraction methods. Also, based on Phellan and Forkert [35], the Frangi filter [36] is one of the best nine vessel enhancement and robust algorithms for noise. Therefore, for the image processing stage, it is rational to utilize the Frangi filter and AE network in this paper.

3.1. Feature extraction method with quantification of cardiovascular vessels

The most important determinative symptom of heart diseases is the stenosis of the blood vessel in some areas along the vessel. Hence, the feature vector must be extracted in such a way that it contains information for the stenosis of the vessel. For this purpose, the image containing the vessel is divided into 16×16 blocks where a number is assigned to each block that indicates the value of the stenosis or dilation of the vessel. First, it is examined whether each block contains any part of the vessel; otherwise, the corresponding value for that block is considered zero. As an example, the steps in the feature extraction are illustrated in Figure 2 where, Figure 2(a) shows the original CCTA image and finally, Figure 2(f) shows the blocked extracted image of the blood vessel. In this regard, the Frangi filter [36] is first used to extract the vessel boundaries from CCTA images. The extracted images by Frangi filter contain both light and dark-colored vessels (Figure 2(b)) where the light-colored vessels are the interested ones in this paper. Hence, the Fuzzy C-Means (FCM) clustering method [37-39] is applied to these images, and considering the three colors of black as the background, light-gray as interested vessels, and the dark-gray as other vessels, the number of the clusters is chosen as three. Accordingly, three clusters are obtained by FCM and the light intensity of the pixels in the cluster of light-gray vessels is set as 255 (white) and the light intensity of other clusters is set as 0 (black). However, the output of the FCM method contains a lot of extra white pixels where the window search is used to determine and remove these extra white pixels. In the window search, some square windows in different sizes and directions are applied to the image, and the light intensity of the windows is set as 0, if all the four borders of those windows are black (Figure 2(d)).

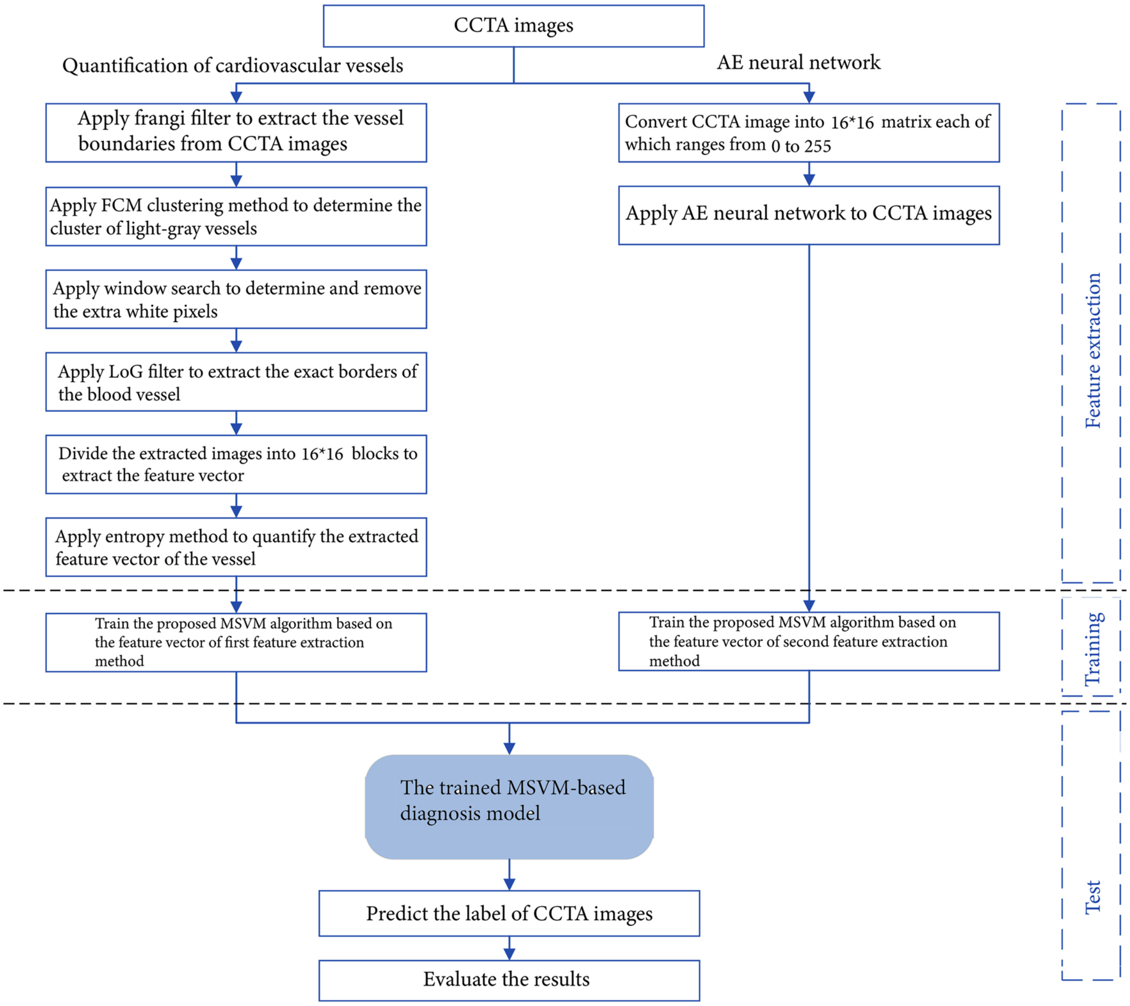

Figure 1. The flowchart of the proposed method.

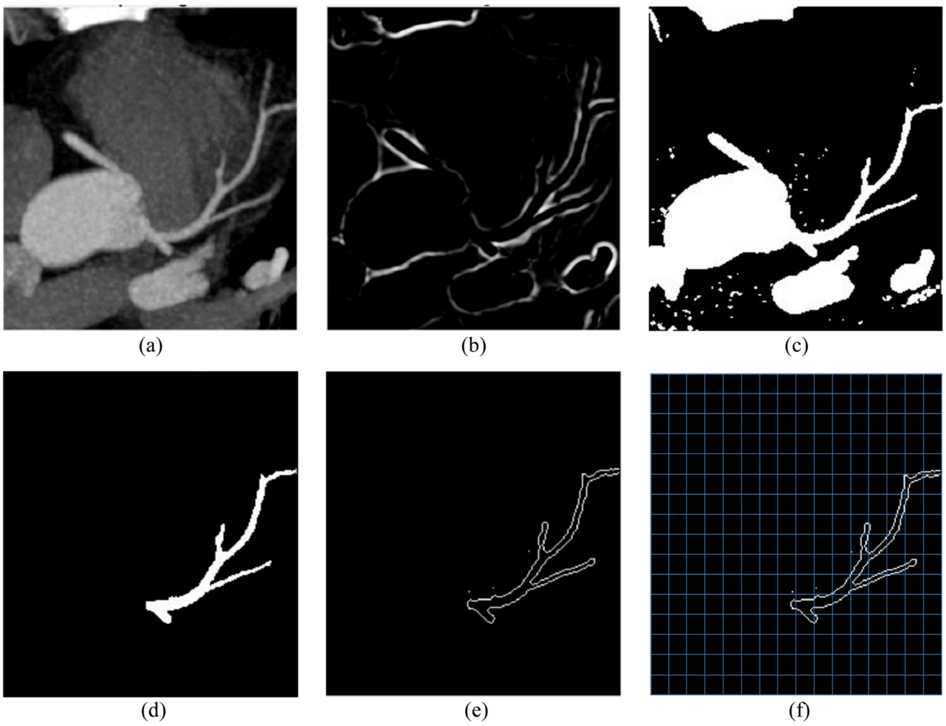

Figure 2. The steps in the extraction and blocking the image of the vein (a) the original CCTA image, (b) after Frangi filter, (c) after FCM clustering, (d) after window search, (e) after LoG filter, and (f) after 16 × 16 blocking.

In the next step, the Laplacian of Gaussian (LoG) filter [40] is used to extract the exact borders of the blood vessel and finally, the extracted image is divided into 16×16 blocks, as described above. As it is obvious from Figure 2(f), the corresponding value for a number of the blocks would be zero.

Then, to quantify the extracted image of the vessel and assign a value to each of the blocks, the entropy method is used in which, the score of each block is determined based on the entropy value of that block. In a data-mining sense, entropy is a measure of the randomness in the data being processed where, the higher the entropy, the harder it is to draw any conclusions from that data. Accordingly, the entropy of each block represents its degree of disorder and if the twist of the vessel in a block is high or equivalently if the vessel is stenotic or dilated, the entropy of that block would be high. In the same manner, if the disorder of a block is small, the entropy of that block would be low. Consequently, the entropy of the blocks that are completely black would be zero. The entropy of the blocks [41] is calculated based on the following equation:

$$\text{Entropy} = -\sum_i p_i \log_2 p_i, \tag{1}$$

where p_i is the probability of a pixel of a block having gray level i, and $i = 0,1,\ldots,255$ is the number of gray levels.

3.2. *Feature extraction with AE network*

The main idea of the AE network is to transform the collection of data into a lower dimension vector (encoding), and then to re-transform that vector into the first state (decoding). Thus, the AE network has two main parts: encoder and decoder. Considering the usual architecture of AE networks, in the encoder part, the input vector $\boldsymbol{x}$ is converted to a lower dimension vector $\boldsymbol{z}$ using a weight matrix $\boldsymbol{W}$ where, generally, the transpose of $\boldsymbol{W}$ is used in the decoder part, too. However, in this paper, only the encoding section of the network is used to transform the CCTA images into the feature vectors of lower dimensions.

The architecture of the AE network is shown in Figure 3. The AE networks are unsupervised learning algorithms because they do not require any data labels to adjust the weights, and only the similarity of the input vectors with decoded vectors is considered. Therefore, without the need for labeling the images, a smaller-dimensional vector is extracted from the input images, which is used in the MSVM training step. The AE network contains 4096 (64×64) nodes in the input layer, one hidden layer containing 400 nodes, and 4096 nodes in the output layer. It should be noted that one hidden layer is considered for simplicity while the number of the nodes in the hidden layer is obtained based on try-and-error.

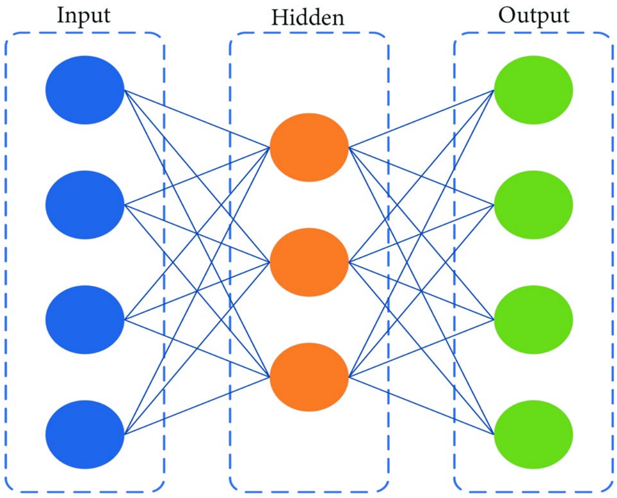

Figure 3. The AE network architecture.

Considering the above-mentioned explanations, in the encoding stage, the AE network takes an input $\boldsymbol{x} \in R^d$ and maps it to $\boldsymbol{z} \in R^p$, based on the following equation:

$$\boldsymbol{z} = \sigma(\boldsymbol{W}\boldsymbol{x} + \boldsymbol{b}), \tag{2}$$

where the vector $\boldsymbol{z}$ is known as the encoded vector or hidden information, the function σ is an activating function such as sigmoid, the matrix $\boldsymbol{W}$ is the weight matrix, and $\boldsymbol{b}$ is the bias vector. After the encoding stage, the decoding stage maps the vector $\boldsymbol{z}$ to vector $\boldsymbol{x}'$, which its dimension is similar to $\boldsymbol{x}$, based on Eq. (3):

$$\boldsymbol{x}' = \sigma'(\boldsymbol{W}'\boldsymbol{z} + \boldsymbol{b}'). \tag{3}$$

In the training step, the AE network is trained in such a way that the reconstruction error is minimized in which, the reconstruction error is defined as follows:

$$\left\|\boldsymbol{x} - \boldsymbol{x}'\right\|^2 = \left\|\boldsymbol{x} - \left(\sigma'\left(\boldsymbol{W}'\left(\sigma\left(\boldsymbol{W}\boldsymbol{x} + \boldsymbol{b}\right)\right) + \boldsymbol{b}'\right)\right)\right\|^2. \tag{4}$$

3.3. *Multi Support Vector Machine (MSVM)*

A novel classification algorithm entitled MSVM, as an improved and generalized version of SVM, is introduced to classify and determine the patients with CAD. In the proposed MSVM, the space of the observations is divided into several subspaces and then, the SVM is performed separately in each of the subspaces. The steps for implementation of this algorithm are as follows:

- The distribution of the observations of each class is obtained in each dimension of the data. If the data is *N*-dimensional then, 2*N* distribution functions are obtained, considering the fact that the class-label attribute is a binary variable;
- The average of each distribution function is obtained in each of the dimensions;

- In each dimension, the difference between the averages is calculated and the dimension which has the smallest difference is chosen as the cut-off dimension;
- The data space is split into three subspaces by cutting the space on the average values. Note that if the data space is two-dimensional, the cutoffs are linear; if it is three-dimensional, the cutoffs are planes; and if it is n-dimensional, the cutoffs are hyper-planes;
- In each of the subspaces, the SVM algorithm is executed separately and support vectors are obtained;
- At the testing stage, it is first examined that the test sample is located in which of the subspaces and then, the support vector of that subspace is used to label the test sample.

In the following, the above-mentioned method is illustrated by an example including two attributes and a binary class-label attribute. In this regard, the average of the distribution function of each of the classes in each dimension is obtained and then, the difference of the averages is calculated and is displayed in Figure 4(a).

Based on Figure 4(a), the average difference for the horizontal lines is the smallest value and therefore, the dimension y is chosen as the cut-off dimension and the entire data set is divided into three subspaces as shown in Figure 4(b). Then, for each subspace, the SVM method is implemented separately and the related separator lines and support vectors are specified as shown in Figure 4(c).

Based on the fact that, in this method, the data space is split into three subspaces and the SVM has been implemented separately for each of the subspaces, the proposed method performs better than the typical SVM in distinguishing between different classes of observations. In the proposed MSVM, among different kernels, two well-known and widely-used kernels including the linear kernel and the RBP kernel, as a nonlinear kernel, [42-44] are considered where their performances are evaluated and compared in the next section.

It should be considered that the proposed MSVM is different from the multi-class SVM where the multi-class SVM was proposed in the literature to expand the application of SVM from a two-class problem to a multi-class problem while in the MSVM, it has been proposed to split the space into multiple subspaces and then apply the SVM in each subspace separately. In this regard, one can consider a multi-class MSVM approach for the classification of multi-class problems by MSVM which is recommended for future research.

4. Experimental results

The performance of the proposed MSVM algorithm is evaluated and compared to the existing algorithms in the literature. The proposed MSVM has been implemented in MATLAB R2018b software.

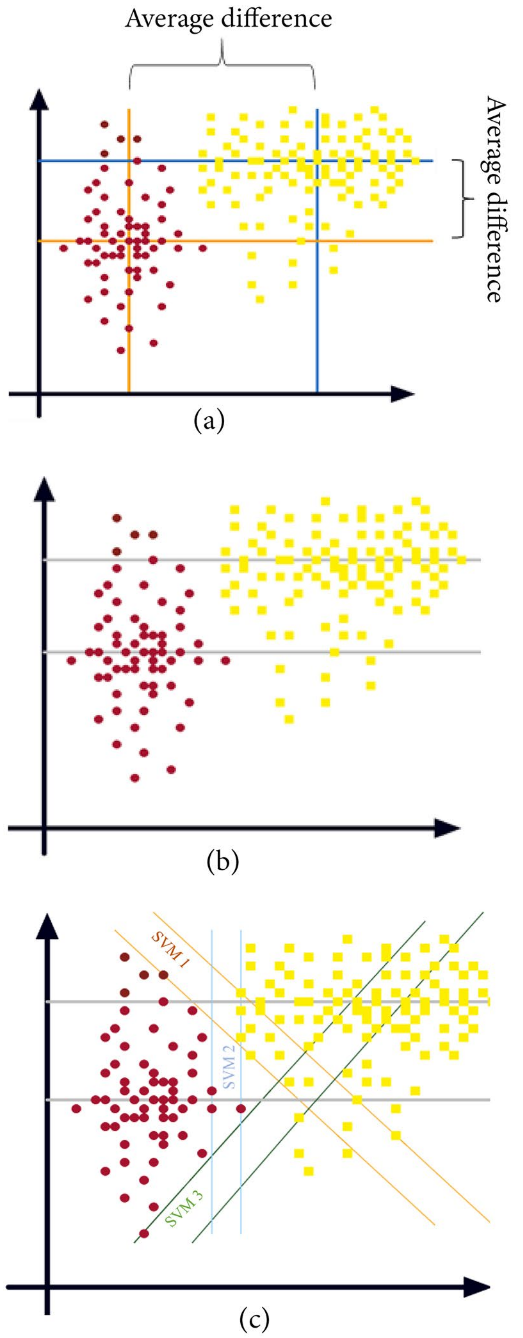

Figure 4. The illustration of MSVM classification algorithm: (a) The average of distributions and the difference of the averages, (b) splitting the datasets into three subspaces, and (c) execution of MSVM.

4.1. *Evaluation measures*

A 10-fold cross-validation is used to evaluate the performance of the proposed MSVM. In the MSVM algorithm, the data are partitioned into 10 folds and at each iteration, a partition containing 10% of the data is reserved for testing and the remaining partitions containing 90% of the data are used for training.

To evaluate the performance of the MSVM algorithm, three performance measures of accuracy, precision, and recall [45] are used. These performance measures are given in Eq.s (5)-(7):

Table 1. The confusion matrix (class 1: The existence of heart disease, class 0: Non-existence of heart disease).

Predicted\Actual	Class 1	Class 0
Class 1	TP	FP
Class 0	FN	TN

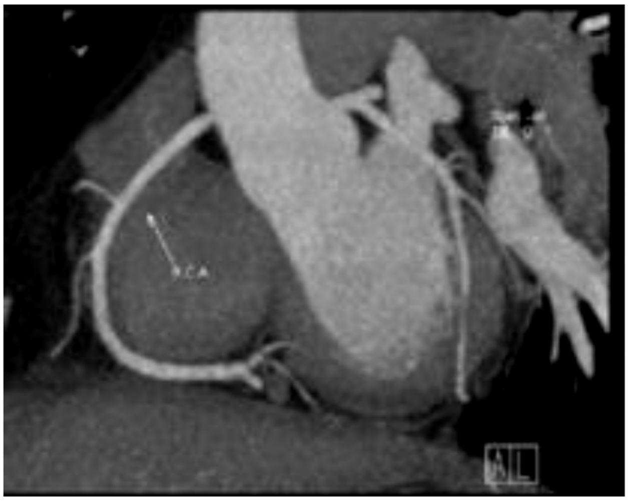

Figure 5. The side-view CCTA image of heart.

$$\text{Accuracy}=\frac{TP+TN}{TP+FP+FN+TN}, \tag{5}$$

$$\text{Precision}=\frac{TP}{TP+FP}, \tag{6}$$

$$\text{Recall}=\frac{TP}{TP+FN}, \tag{7}$$

where TP is the True Positive and TN the True Negative show the number of positive and negative observations that are classified correctly, respectively. In addition, FP present False Positive and FN the False Negative show the number of positive and negative observations that are classified incorrectly as negative and positive, respectively (see Table 1).

4.2. *Performance evaluation*

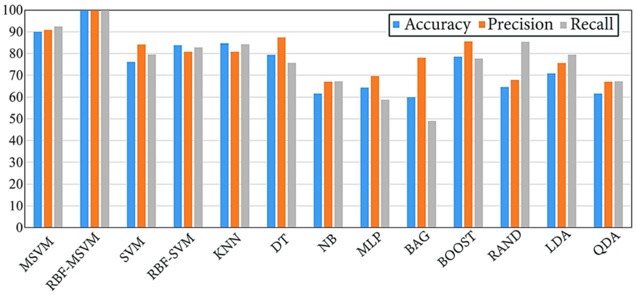

Figure 6. The accuracy, precision, and recall of the proposed MSVM algorithm under the first feature extraction method compared to other algorithms.

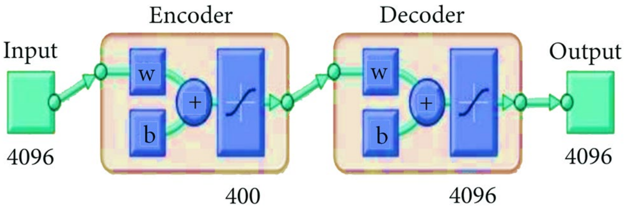

Figure 7. Architecture of the AE network to extract the features.

In this section, the performance of the proposed MSVM algorithm is evaluated and compared with other existing algorithms in the literature including SVM, Radial Basis Function Support Vector Machine (RBF-SVM), KNN, DT, NB, Multi-layer Perceptron (MLP) neural network, Bagging (BAG), Boosting (BOOST), Random Subspace (RAND), LDA and Quadratic Discriminant Analysis (QDA) [46] in terms of accuracy, precision and recall criteria. For this purpose, the CCTA images of 50 patients are collected from the *Tehran Heart Center Hospital* where the target variable is to determine whether or not the patients have CAD. Tehran Heart Center is a specialized heart hospital affiliated with the Tehran University of Medical Sciences. This dataset consists of the side-view CCTA images of the patients where an example is shown in Figure 5. After data pre-processing, the training dataset contains 138 samples where 83 samples belong to class 1 and 55 samples belong to class 0. In this hospital, the gender and age of the patients are also recorded, and therefore, in the experiments, these two attributes are also appended to the extracted vector of the images' attributes.

In the first feature extraction method, applying the quantification of cardiovascular vessels, the CCTA images are first converted from 512×512 to 64×64 pixel images for improvement in the image processing time and then, the images are divided into 16×16 blocks. Hence, the dimension of the feature vector is 18 $(=16+2)$ where 2 dimensions are related to the attributes of the age and gender of the patients. Finally, the proposed MSVM algorithm is applied to the extracted features and the results are summarized in Figure 6. Based on the results, the accuracy, precision, and recall measures of the proposed MSVM algorithm with the linear kernel are, respectively, 90%, 90.88%, and 92.38% while the accuracy, precision, and recall measures of the proposed MSVM algorithm with RBF kernel are all three 100% and it can be concluded that the proposed MSVM algorithm outperforms all other existing algorithms. In addition, the proposed MSVM algorithm performs much better than the classical SVM method under both linear and RBF kernels.

In the second feature extraction method, the number of neurons in the hidden layer is considered 400 neurons and as a result, the CCTA images are first converted into 64×64 pixel images and then, they are converted to vectors with 400 features. Finally, the age and gender attributes are appended to the converted feature vector and consequently, a feature vector of length 402 is obtained. The architecture of the AE network for extracting the feature vector is represented in Figure 7.

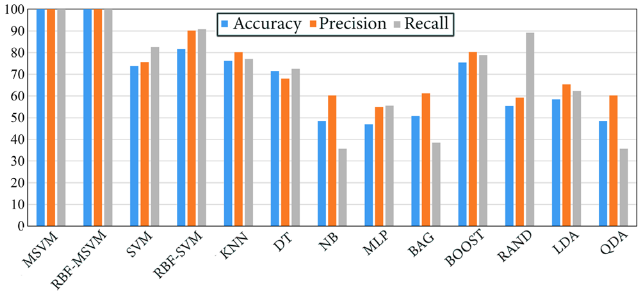

Figure 8. The accuracy, precision, and recall of the proposed MSVM algorithm under the second feature extraction method compared to other algorithms.

As shown in Figure 7, this network takes 4096 ($= 64 \times 64$) entries as input and initially converts them to a feature vector of length 400 by the encoder. Then, the extracted vector is fed into the decoder and, again, a vector of length 4096 is obtained, which is highly similar to the input vector. Applying the encoder of this network, the CCTA images are encoded and transformed to the vectors of length 400 and, after adding the patients' attributes of age and gender, the attribute vectors of length 402 are used in the proposed MSVM algorithm and other existing algorithms to classify the samples. In the next step, after feature extraction, the MSVM algorithm and other competing algorithms are applied to the extracted features, and the accuracy, precision, and recall measures of the algorithms are obtained and reported in Figure 8.

The results show that applying the proposed MSVM algorithm in the second feature extraction method with both linear and RBF kernels resulted in the accuracy, precision, and recall of 100%. Accordingly, the proposed MSVM algorithm utilizing the features, extracted through the second feature extraction method, provided the best performance in comparison with the proposed MSVM algorithm utilizing the features, extracted through the first feature extraction method, in terms of all the performance measures and both linear and RBF kernels. In addition, the proposed MSVM algorithm utilizing the features, extracted through both feature extraction methods, provides better performance compared to the classical SVM under both linear and RBF kernels.

Considering the much better performance of the proposed MSVM algorithm compared to a number of competing algorithms, the CAD is diagnosed, accurately and precisely, using extracted features from the CCTA images of the patients and without the need for specialist doctors. In other words, it can be determined accurately whether or not a patient has CAD by applying a machine-learning-based algorithm entitled MSVM on the features extracted from the patients' CCTA images and their characteristics such as gender and age where, in this procedure, the necessity for attendance, analysis, and intervention of the doctors in the diagnosis of the disease is minimal.

4.2.1. Comparision of image processing methods

Feature extraction through the AE network is an unsupervised method that merely may extract fundamental features from data. An AE network can convert input data to a z vector, containing fewer dimensions including all the information drawn from primary data, and restore the z vector to origin data again. The AE network algorithm consists of less complexity than the quantification of the cardiovascular vessel method which is an advantage.

However, the feature extracted from the AE network algorithm cannot be tangible and understandable. In other words, one cannot be sure that the features derived from primary data to what alluding to. Thus, these ambiguous features are disadvantages of this method.

Unlike the AE network algorithm, the quantification of the cardiovascular vessel method is more complex and time-consuming which is a disadvantage of this method. On the contrary, the segmentation of vessels in the quantification of cardiovascular vessel method from the images is more tangible and understandable, especially for cardiologists which is an advantage of this method. Although the training of the AE network is time-consuming, the AE network algorithm can be performed faster than the other one in terms of diagnosing time.

4.3. Performance comparison of MSVM under benchmark datasets

In this section, five benchmark datasets including Pima [47], Heart Statlog, Sonar Banknote authentication Ionosphere are used to evaluate and compare the performance of the proposed MSVM algorithm with other competing algorithms. The first dataset consists of 768 samples with 8 predictor variables and one target variable that shows whether a patient has diabetes or not. The second dataset consists of 270 samples of patients containing 13 predictor variables and one binary target variable that represents whether a patient has heart disease or not. The Sonar dataset stores different signal patterns collected from mines and rocks using different aspect angles and consists of 208 samples with 60 predictors and one binary target variable for rocks and mines. The fourth dataset consists of 1372 samples containing 4 predictor variables and one binary classifier to determine whether the banknotes are genuine or not. The last dataset contains 351 samples with 34 predictor variables and one target variable that determines the good or bad categories of the radar signals. The performance of the proposed MSVM algorithm with the linear kernel (MSVM) and RBF kernel (RBF-MSVM) is compared to the competing algorithms in terms of accuracy, precision, and recall performance measures.

The results are summarized in Table 2. Again, the results show that the proposed RBF-MSVM outperforms all the competing algorithms under different datasets. In addition, the results show that the proposed MSVM algorithm under both linear and RBF kernels performs better than the classical SVM algorithm under both linear and RBF kernels, in all the cases. The classical RBF-SVM, KNN, LDA, and QDA algorithms perform the same as the proposed MSVM and RBF-MSVM, only, in the case of the Banknote dataset.

Table 2. Performace comparision of the proposed MSVM algorithm with the competing algorithms.

		Method												
Dataset	**Performance measures**	**MSVM**	**RBF-MSVM**	**SVM**	**RBF-SVM**	**KNN**	**DT**	**NB**	**MLP**	**BAG**	**BOOST**	**RAND**	**LDA**	**QDA**
Pima	Accuracy	79.08	**99.74**	76.97	73.28	67.10	69.60	75.26	76.05	69.68	74.70	61.97	77.37	75.26
	Precision	75.38	**99.31**	72.51	68.08	52.60	56.95	66.64	69.41	61,12	64.53	48.25	72.78	66.65
	Recall	60.32	**99.17**	56.42	45.74	53.65	55.45	69.45	72.26	31.60	58.21	51.98	57.14	60.45
Heart	Accuracy	86.67	**100**	83.33	63.70	57.78	74.44	84.07	76.14	75.56	82.59	52.59	82.33	84.07
	Precision	87.08	**100**	83.45	62.16	54.84	73.90	84.71	76.70	85.51	82.27	49.76	84.59	84.71
	Recall	82.55	**100**	78.59	50.89	48.53	65.08	78.33	71.33	55.18	78.96	88.02	77.76	78.33
Sonar	Accuracy	95.50	**100**	75.50	87.50	82.50	73.00	69.00	75.44	66.00	74.00	59.50	71.00	70.50
	Precision	95.89	**100**	77.89	87.19	83.24	70.52	67.21	74.29	71.73	70.35	66.00	68.67	77.33
	Recall	92.88	**100**	70.59	87.95	78.62	69.31	79.87	69.75	50.00	76.02	42.90	70.47	58.70
Banknote	Accuracy	**100**	**100**	98.25	99.27	99.20	94.31	83.72	98.32	94.09	91.61	68.32	97.01	98.32
	Precision	**100**	**100**	98.21	98.41	98.26	96.72	83.92	97.87	96.40	88.61	77.62	94.16	96.66
	Recall	**100**	**100**	98.48	**100**	**100**	89.78	79.35	98.95	90.31	92.11	47.87	**100**	**100**
Ionosphere	Accuracy	99.14	**99.71**	83.43	94.86	84.85	85.71	78.57	81.74	84.00	86.57	86.86	82.86	87.71
	Precision	79.47	**80.03**	75.04	78.32	75.50	67.03	60.75	74.78	74.56	74.59	73.75	74.79	65.36
	Recall	77.74	**78.82**	50.69	71.99	53.04	65.13	70.16	57.26	51.99	58.82	58.38	49.70	73.79

5. Concluding remarks

Coronary Artery Disease (CAD), a common heart disease resulting in the narrowing or occlusion of the major blood vessels, has been the most common cause of death worldwide in recent decades. Angiography is one of the widely used and accurate approaches for diagnosing the CAD while it is expensive and invasive, and has some risks such as heart attack and death. On the other hand, there exist some non-invasive imaging methods such as Coronary Computed Tomography Angiography (CCTA) images for diagnosing heart diseases while these methods are currently analyzed visually by doctors which can lead to some incorrect diagnoses of the diseases due to human error, the high workload of doctors, and etc. Accordingly, it is essential to propose an accurate and non-invasive approach for diagnosing CAD based on CCTA images and without the need for specialist doctors. For this purpose, in this paper, a novel algorithm called Multi Support Vector Machine (MSVM), as an improved and generalized version of SVM, is introduced and applied for classification and diagnosing the CAD, based on the features extracted from the patients' CCTA images through two feature extraction methods including the quantification of cardiovascular vessels and Auto Encoder (AE) network algorithm. Then, the performance of the proposed MSVM in combination with the two feature extraction methods is evaluated and compared separately with the Support Vector Machine (SVM) and other competing algorithms in terms of accuracy, precision, and recall measures. Based on the results, the proposed MSVM algorithm outperformed all other competing methods in terms of all the accuracy, precision, and recall measures, and under both feature extraction methods. Moreover, in all the cases, the MSVM and Radial Basis Function Multi- Support Vector Machine (RBF-MSVM) performed better than the classical SVM and RBF-SVM methods in terms of all the performance measures. Considering the superiority of the proposed method over competing algorithms, it also led to reduction in the dependency of the diagnosis of CAD on doctors and accordingly, the heart disease is diagnosed accurately and precisely based on a data-mining-based algorithm.

It should be noted that the proposed algorithm can be applied only on the datasets with two classes for target variable. Accordingly, extending the MSVM method for multiclass target variables would be an interesting subject that is suggested for future research.

Conflict of interests

The authors declare that they have no conflict of interests.

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Authors contribution statement

Mohammad Sadegh Hasuni Shahrbabak: Conceptualization, methodology, formal analysis, data curation, writing-original draft preparation, visualization.

Majid Khedmati: Supervision, project administration, writing, review and editing.

Mahdi Fathi: Methodology review, validation, writing-review and editing.

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