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Automated Detection and Localization of Myocardial Infarction With Staked Sparse Autoencoder and TreeBagger

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ABSTRACT Novel techniques in deep learning networks are proposed for the staked sparse autoencoder (SAE) and the bagged decision tree (TreeBagger), achieving significant improvement in detection and localization of myocardial infarction (MI) from single-lead electrocardiograph (ECG) signals. With our layer-wise training strategies, the SAE-based diagnostic feature extraction network can automatically and steadily extract the deep distinguishing diagnostic features of the single-lead ECG signals and avoid the vanishing gradient problem. This feature extraction network is formed by stacking shallow SAEs. In addition, to automatically learn the stable distinctive feature expression of the label-less input ECG signals, this feature extraction network adopts unsupervised learning. Moreover, TreeBagger classifier can optimize the results of multiple decision trees to more accurately detect and localize MI. The experiment and verification datasets include healthy controls, various types of MI with anterior, anterior lateral, anterior septal, anterior septal lateral, inferior, inferior lateral, inferior posterior, inferior posterior lateral, lateral, posterior, and posterior lateral, from PTB diagnostic ECG database. The evaluation results show that the new techniques can effectively and accurately detect and localize the MI pathologies. For MI detection, the accuracy, the sensitivity, and the specificity rates achieve as high as 99.90%, 99.98%, and 99.52%, respectively. For MI localization, we obtain consistent results with the accuracy of 98.88%, sensitivity 99.95%, and specificity 99.87%. The comparative studies are conducted with the state-of-the-art techniques, and significant improvements by our methods are presented in the context. Success in the development of the accurate and comprehensive tool greatly helps the cardiologists in detection and localization of the single-lead ECG signals of MI.

INDEX TERMS Electrocardiograph, myocardial infarction, sparse autoencoder, bagged decision tree, deep learning networks.

I. INTRODUCTION

Myocardial infarction (MI) is a persistent hypoxia and ischemia of the myocardium caused by acute occlusion of the coronary artery, which eventually leads to myocardial necrosis [1]. According to data from the American

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Heart Association, the estimated annual incidence of MI is 605000 new attacks and 200000 recurrent attacks, in other words, an American will have an MI in approximately every 40 seconds [2]. And about 110000 Americans died of MI in 2015. Thus, it is of great significance to investigate MI detection and localization. The waveform changes of electrocardiogram (ECG) can effectively characterize the location of myocardial ischemia or necrosis in real time, thereby locate

the occluded coronary artery for early diagnosis of MI [3]. Therefore, daily ECG monitoring and timely detection are the key factors to reduce the mortality of MI.

At present, the use of single-lead portable ECG monitors in daily monitoring is a trend due to its low instrumentation cost, highly efficient and comfort uses [4]. However, the time-varying dynamics and morphological characteristics of single-lead ECG signal show significant and complex variations for different patients with MI, under different area of MI and different degrees of myocardial damage. These make it quite challenging for doctors to visually interpret ECG signals. It is time consuming and may even result to missed diagnosis and misdiagnosis.

There have been several methods for generic and fully automatic MI detection and localization to assist physicians with single lead ECG, such as characteristic waves analysis method [5]–[8], time-frequency domain approach [9]–[16], and neural network method [17], [18], [20], [21].

The characteristic wave analysis methods extract the distinctive features of the ECG characteristic waves, such as ST-T complex, Q wave etc. This demands for an accurate detection of characteristic waves of heartbeats. But the ECG waveform of MI changes with complex patterns, which greatly limits the accuracy of the automatic detection of the characteristic waves.

Instead of using the characteristic waves, the time-frequency domain algorithms are based on entire heartbeat. These algorithms explore wavelet transform (WT) method in mapping signal lead ECG signal to multi-scale space, then use handcrafted feature extraction and reduce feature set using feature selection algorithms, finally use shallow classifier to realize the diagnosis of MI. However the handcrafted features can hardly be generalized for different patients due to the interpatient variations and complicity of the ECG signals.

The neural network methods train the model through supervised classification. Without requiring the handcrafted feature extraction stage, they usually use the experience of the trained model to extract ECG features to complete the identification of MI. In order to automatically extract valid features from heartbeats containing redundant information, these algorithms always design a multi-layer network with large computational complexity. However, as the layers increases, the vanishing gradient problem of the multi-layer network becomes more serious.

Generally speaking, the existing methods still cannot satisfy clinical applications, because the handcrafted features are limited due to their fixed form and the poor generalization capability. And the depth features automatically extracted by the supervised learning to train the network are effective to realize the diagnosis of MI, but these algorithms need to design a multi-layer network. This makes them unreliable to be widely used in clinically or practice.

In deep neural networks, the Autoencoder has its advantage in extracting the effective features of the signal and reconstructing it. We explored with this method in the previous work to reduce the noise of the ECG signal and

achieved good results [22]–[24]. In this work, we proposes a more accurate and automatic algorithm based on Staked Sparse Autoencoder (SAE) and Bagged Decision Tree (TreeBagger) to assist in the early diagnosis of MI based on single-lead ECG signals. The SAEs-based diagnostic feature extraction network is proposed for extracting the distinguishing diagnostic features of the single-lead ECG signals. Among them, this feature extraction network is formed by stacking shallow SAEs, and it adopts a layer-wise learning strategy. So this feature extraction network steadily learns the optimal expression of the input signal and avoids the vanishing gradient problem brought by the design of multi-layer network. In addition, this feature extraction network automatically learns the stable deep feature expression of the input ECG signals without labels based on unsupervised training. And we design a shallow classifier TreeBagger to classify the ECG signals. The TreeBagger classifier avoids the loss of features due to it does not reprocess the extracted effective features. Moreover it weighs the results of multiple decision trees and optimize the final decision to achieve higher stability and accuracy.

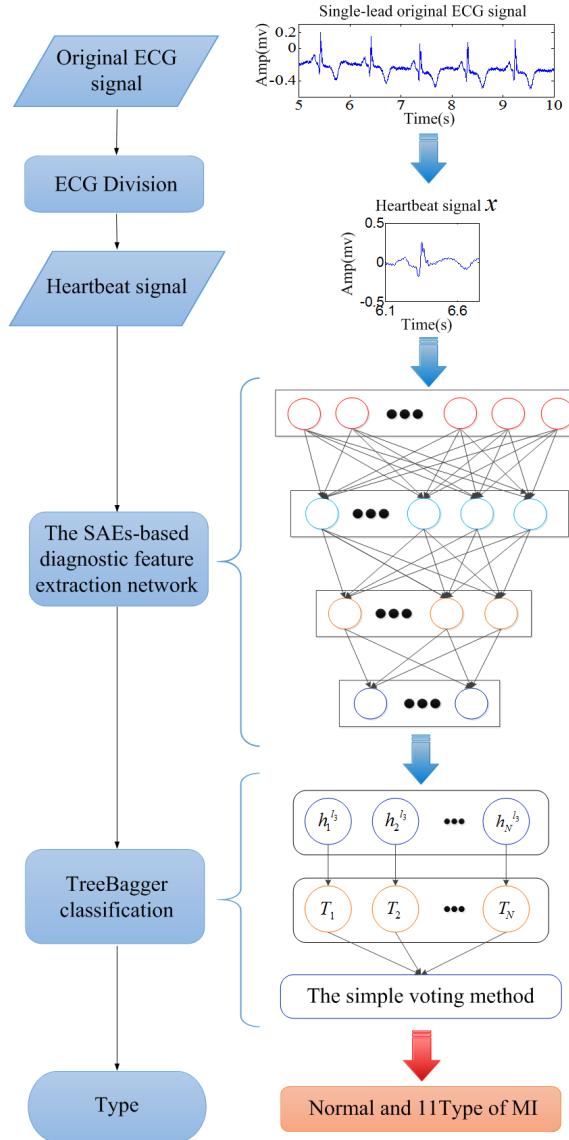
The remainder of this paper is organized as follows. Section II describes the benchmark ECG database used in this comparative study and details of the proposed method. Experimental results and discussion are presented in Section III. Conclusions and future work are given in Section IV.

II. MATERIALS AND METHODS

With reference to Fig. 1, the framework of our proposed algorithm for the problem of early MI diagnosis from single-lead ECG signals can be outlined as follows. Firstly, the original single-lead ECG signals are denoised and divided to obtain the clean heartbeats. Then the shallow SAEs is trained in unsupervised learning, and the hidden layers of the shallow SAEs is designed to structure the SAEs-based diagnostic feature extraction network for directly and automatically extract the distinguishing features of the input heartbeats, so avoiding the high computational complexity brought by the design of multi-layer network. Finally, the features are fed to the TreeBagger classifier to classify normal ECG signals and 11 different types of MI, namely anterior, anterior lateral, anterior septal, anterior septal lateral, inferior, inferior lateral, inferior posterior, inferior posterior lateral, lateral, posterior, and posterior lateral.

A. ECG DATA DIVISION

In this study, the single-lead ECG signals from the PTB (Physikalisch-Technische Bundesanstalt) diagnostic ECG database [25] are used for the performance evaluation of the proposed method. The PTB diagnostic ECG database is an open source publically available and used as a benchmark for evaluating the early diagnosis of MI and related algorithms. The PTB consists of 368 records from 148 patients with MI, and 80 records from 52 healthy subjects known as healthy controls. Each record comprises 12 conventional leads and

**FIGURE 1.** Block diagram of the proposed method.

3 Frank leads, and sampled at 1000Hz. Each record usually lasts for 2 minutes, and all signals last at least 30 seconds. The total of 148 MI patients included 11 types of MI in the followings:

- Anterior Myocardial Infarction (AMI),
- Anterior Lateral Myocardial Infarction (ALMI),
- Anterior Septal Myocardial Infarction (ASMI),
- Anterior Septal Lateral Myocardial Infarction (ASLMI),
- Inferior Myocardial Infarction (IMI),
- Inferior Lateral Myocardial Infarction (ILMI),
- Inferior Posterior Myocardial Infarction (IPMI),
- Inferior Posterior Lateral Myocardial Infarction (IPLMI),
- Lateral Myocardial Infarction (LMI),
- Posterior Myocardial Infarction (PMI), and
- Posterior Lateral Myocardial Infarction (PLMI).

Because the ECG signal of lead II is coaxial with cardiac conduction, which makes the forward wave amplitude of ECG signal of lead II the largest and the waveform amplitude the clearest, hence doctors in daily monitoring mostly choose lead II as the analysis signal. In our present work, we have used only lead II ECG signals to assist doctors in accurately completing the early diagnosis of MI in clinically or practice based on the proposed method.

The lead II ECG signals are pre-processed to remove noise by using Daubechies 6 (DB6) wavelet basis function base the Discrete Wavelet Transform (DWT) [26]. Then, the ECG heartbeat segmentation of the denoised ECG signals is subjected to the R-peak detection using the Pan-Tompkins technique [27], and the segmentation of the ECG heartbeat is automated by taking 250 and 400 samples before and after the R-peak respectively. Finally, the II lead ECG signals are divided into a set of ECG heartbeat signals with a length of 651. The number of heartbeats of each type of MI and normal subjects is given in Table 1.

TABLE 1. Number of beats for normal and 11 types of MI.

MI type	Number of 12-lead-single beats
Anterior	6429
Anterior Lateral	6718
Anterior Septal	11523
Anterior Septal Lateral	274
Inferior	12752
Inferior Lateral	8168
Inferior Posterior	49
Inferior Posterior Lateral	2715
Lateral	461
Posterior	466
Posterior Lateral	781
Normal	10588
Total	60924

B. DERIVING FOR THE CHARACTERISTIC MATRIX

In this work, the shallow SAE based on a hidden layer achieves the diagnostic feature of input heartbeat in unsupervised learning while keeping the input and output consistent [23], [24], as shown in Fig. 3. We take the normalized heartbeat signal $x \in [0, 1]^n$ as the input signal, and use the Sigmoid function as the activation function of the hidden layer, then the output of the hidden layer is also an encoder, which is formulated as follows

$$h^l = f_\theta(x) = s(Wx + b). \quad (1)$$

Thus the deep eigenvector $h^l \in [0, 1]^{d_1}$ with the dimension d_1 are extracted, and $\theta = \{W, b\}$ are parameters for the encoder of SAE, where $W \in R^{d_1 \times n}$ is the weight matrix, b is the offset vector. The reconstruction heartbeat is the output of the shallow SAE, and the output layer is a decoder, which is formulated as follows

$$z^l = g_{\tilde{\theta}}(h^l) = s(\tilde{W}h^l + \tilde{b}), \quad (2)$$

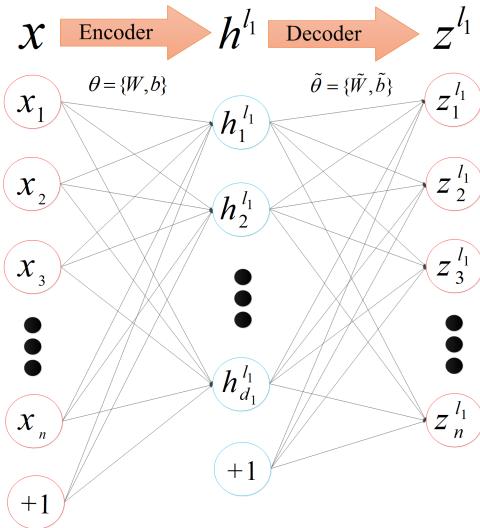


FIGURE 2. The shallow SAE based on a hidden layer.

where $\tilde{\theta} = \{\tilde{W}, \tilde{b}\}$ are parameters for the decoder of SAE, $\tilde{W} \in R^{n \times d_1}$ is weight matrix, and $\tilde{W} = W^T$. The parameters are optimized by minimizing the reconstruction error, which is formulated as follows

$$\min_{\theta} J(\theta) = \frac{1}{m} \sum_{i=1}^m \left[L(x^{(i)}, g_{\tilde{\theta}}(f_{\theta}(x^{(i)}))) + \gamma \sum_{j=1}^{d_1} KL(\rho \parallel \hat{\rho}_j) \right], \quad (3)$$

where γ is the weight of sparse regular terms, and m is the number of training samples. $L(\cdot)$ is the loss function, which characterizes the distance between the reconstructed heartbeat and the input heartbeat, it now follows that

$$L(x, z) = - \sum_{k=1}^n [x_k \log z_k + (1 - x_k) \log (1 - z_k)]. \quad (4)$$

And $KL(\rho \parallel \hat{\rho}_j)$ is the sparse regular term, which is introduced to enable SAE to adapt to the complex and individual differences of ECG signals. The sparse regular term constructed using the KL distance is expressed as the cross-entropy between two Bernoulli random variables, and it is given as

$$KL(\rho \parallel \hat{\rho}_j) = \rho \log \frac{\rho}{\hat{\rho}_j} + (1 - \rho) \log \frac{1 - \rho}{1 - \hat{\rho}_j}, \quad (5)$$

where the sparsity parameter ρ represents the average response values of the hidden layer node in the trained SAE, and $\hat{\rho}_j$ is the average response values of the j th node of the hidden layer and it is expressed as

$$\hat{\rho}_j = \frac{1}{m} \sum_{i=1}^m h_j = \frac{1}{m} \sum_{i=1}^m f_{\theta_j}(x^i). \quad (6)$$

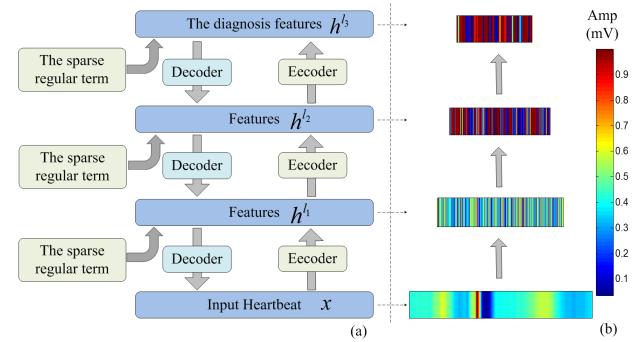


FIGURE 3. The shallow SAE is based on the SAEs-based diagnostic feature extraction network. (a) The SAEs-based diagnostic feature extraction network. (b) Amplitude plot of the output signal of each layer.

The SAE is trained with a gradient descent to minimize the loss function and find the optimal parameters. When the value of the loss function is small enough, the output of the hidden layer h^l_1 is considered to be the effective low-dimensional feature representation of the input heartbeat signal. The shallow SAE learn the optimal expression of the input signal and obtains effective parameters of the hidden layer.

In this work, $\rho = 1$, so the average response values of the hidden layer node is as close as possible to 0.1. If the activity of a node is over high, the sparse regular term will inhibit the node. Thereby, the number of activated nodes in the hidden layer is reduced, which is beneficial to obtaining the stable distinctive diagnostic features of the input heartbeat.

According to the above algorithm, the output of the first hidden layer is used as the input of the second shallow SAE. Repeat the entire procedure until three shallow SAEs are constructed, as shown in Fig. 3. The SAEs-based diagnostic feature extraction network for MI is formed by stacking the hidden layer of three SAE-based feature extraction, and the hidden layer of third shallow SAE is taken as the output layer of the SAEs-based diagnostic feature extraction network for MI, thereby completing the diagnostic feature extraction of the input heart beat signal $x^{(i)}$.

Based on the layer-wise learning strategy, the SAEs-based diagnostic feature extraction network avoids the vanishing gradient problem with the deepening layers. In addition, based on unsupervised learning training, this feature extraction network automatically learns the feature expression of the input heartbeat without labels, and it can extracting more stable distinctive deep features of the input heartbeat under the constraints of sparse regular terms.

C. CONSTRUCTING A TREE BAGGER FOR MI CLASSIFICATION

A TreeBagger classifier is constructed for detection and classification of MI. Our TreeBagger classifier utilizes the decision tree classifiers as the base learners, then applies Bagging algorithm to integrate the output of multiple decision trees as the final output.

TABLE 2. Confusion matrix of MI detection.

Original/Predicted	MI	Normal	ACC(%)	SE(%)	SP(%)
MI	50328	8	99.90	99.98	99.52
Normal	51	10537			

First, we use the random self-sampling method to extract the training set and obtain N sub-training sets of the same size as the original training set, where N corresponds to the maximum number of trees that can be constructed.

Then the decision tree classifier is constructed by the Gini index based on each sub-training set, until the number of trees being constructed reaches the maximum N . In this classification process, the TreeBagger classifier does not reprocess the diagnostic features that have been obtained using the SAEs-based diagnostic feature extraction network to avoid the loss of effective features. Finally, we adopt the simple voting method [29] to integrate the results of all decision trees as the final result and it is given as

$$H(x) = \arg \max_{y \in Y} \sum_{n=1}^N \text{TRUE}\left(T_n\left(h_n^{l_3}\right) = y\right) \quad (7)$$

where $\text{TRUE}(\bullet)$ is the indication function. If \bullet is true, the value is 1; otherwise the value is 0. $T_n(\bullet)$ corresponds to the output of n th decision tree classifier. $h_n^{l_3}$ is sub-dataset of the diagnosis feature h^{l_3} extracted by the SAEs-based diagnostic feature extraction network.

The single decision tree classifier is susceptible to sample interference and tends to overfit when the sample is unbalanced in practice. Our constructed TreeBagger classifier can integrate the results of multiple decision trees with a simple voting method, thereby reducing the influence of overfitting and improving the generality of the classifier.

III. EXPERIMENTAL RESULTS

The performance analysis of the proposed method is based on sensitivity (SE), specificity (SP), and accuracy (ACC) represented in the form of confusion matrix. These parameters are estimated by comparing the actual test output and the predicted output. A confusion matrix visualize the number of true positives (TP), false positives (FP), false negatives (FN), and true negatives (TN) for a classifier. The sensitivity relates to the ability of trained model to identify positive results of MI, and it is defined as

$$Se = \frac{TP}{TP + FN}. \quad (8)$$

The specificity is related to the ability of identifying the negative outcomes (healthy control or non-infarcted), and it is defined as

$$SP = \frac{TN}{TP + FN}. \quad (9)$$

The classification accuracy of a measurement system is the degree of closeness of measurements of a quantity to that of

TABLE 3. Comparision of MI detection performance with other methods.

Author	ACC(%)	SE(%)	SP(%)
Arif et al., 2010 [7]	-	99.70	99.90
Sun et al., 2012 [8]	-	91.00	-
Safdarian et al., 2014 [5]	94.00	-	-
Liu et al., 2015 [30]	94.40	-	-
Sharma et al., 2015 [10]	96.00	93.00	99.00
Acharya et al., 2016 [9]	98.80	99.45	96.27
Padhy et al., 2017 [31]	95.30	96.00	94.60
Kumar et al., 2017 [12]	99.31	99.62	98.12
Acharya et al., 2017 [18]	95.22(with noise) 93.53(without noise)	95.49 93.71	94.19 92.83
Liu et al., 2017 [19]	96.00	95.40	97.37
Kora et al., 2017 [32]	99.30	99.97	98.70
Dohare et al., 2018 [6]	96.60	96.60	96.60
Costa et al., 2018 [33]	94.00	96.00	92.00
Liu et al., 2018 [17]	98.79	98.73	99.35
Sharma et al., 2018 [14]	99.62(with noise) 99.74(without noise)	99.76 99.84	99.12 99.35
Sadhukhan et al., 2018 [15]	95.60	96.50	92.70
Tripathy et al., 2019 [16]	99.74	99.87	99.60
Proposed method	99.90	99.98	99.52

its actual value and it is defined as

$$ACC = \frac{TP + TN}{TP + TN + FP + FN}. \quad (10)$$

In this work, the 10-fold cross-validation is used to select the number of instances for training and testing the proposed method. The pretreated heartbeats are randomly divided into 10 subsets, each subset is tested once and the rest subsets are used for training, thus 10 models are obtained. Finally, the average validation performance of 10 models is used as the performance index of the proposed method. The SAEs-based diagnostic feature extraction network is structured as 651-300-150-60, and the maximum number of trees that can be constructed N was set to 200 in terms of experimental precision and operational efficiency.

A. RESULTS FOR MI DETECTION

The distinguishing feature vector is extracted from each of the single-lead heartbeats extracted by the SAEs-based diagnostic feature extraction network. Each feature vector corresponds to a heartbeat. This feature vector is used as input for the TreeBagger classifier. Table 2 shows the confusion matrix of MI detection, which includes the number of TP, TN, FN, FP, and three classification performance parameters (ACC, SE, SP). It is observed that the TreeBagger classifier has an accuracy of 99.90%, sensitivity of 99.98% and specificity of 99.52%. In the 50328 ECG heartbeat of MI, the proposed method only missed 8 ECG heartbeats. The higher accuracy values obtained using the proposed method is due to the high separability of features extracted by the stacked SAEs. Therefore, omission diagnostic rate of MI by the proposed method is only 0.015%.

TABLE 4. Confusion matrix of MI localization.

Original /Predicted	AMI	ALMI	ASMI	ASLMI	IMI	ILMI	IPMI	IPLMI	LMI	PMI	PLMI	Normal	ACC(%)	SE(%)	SP(%)
AMI	6366	29	8	0	13	1	0	0	1	0	2	9	99.84	99.02	99.94
ALMI	21	6581	48	0	31	20	0	5	0	4	1	7	99.67	97.96	99.89
ASMI	3	8	11485	0	16	5	0	2	0	0	0	4	99.80	99.67	99.83
ASLMI	0	0	0	274	0	0	0	0	0	0	0	0	100.00	100.00	100.00
IMI	6	7	11	0	12574	4	0	135	0	0	14	1	99.53	98.60	99.77
ILMI	0	10	3	0	11	8140	0	2	0	0	0	2	99.90	99.66	99.94
IPMI	0	0	1	0	0	0	48	0	0	0	0	0	100.00	97.96	100.00
IPLMI	0	1	2	0	21	1	0	2679	0	0	11	0	99.45	98.67	99.49
LMI	0	4	0	0	0	0	0	0	455	0	0	2	99.99	98.70	100.00
PMI	0	0	0	0	0	0	0	0	0	466	0	0	99.99	100.00	99.99
PLMI	0	0	5	0	17	2	0	155	0	0	602	0	99.66	77.08	99.95
Normal	3	3	5	0	2	1	0	0	0	0	0	10574	99.94	99.87	99.95

Fair comparisons of the MI detection algorithms are conducted based on the PTB database. The experimental results of the proposed method are compared with the state-of-the-art methods reported in literature, as shown in Table 3. The sensitivity value is 99.52% which is slightly less than some methods. However the accuracy value is 99.90% and the sensitivity value is 99.98%, which are significantly higher than that of other methods. Compared with other methods using 12-leads ECG signals, the proposed method only uses single-lead ECG signals to obtain higher accuracy, which proves that this method can extract more valuable and distinguish diagnostic information by the SAEs-based diagnostic feature extraction network in unsupervised learning.

Many algorithms extract the handcrafted extracted characteristics of MI in frequency domain manually as indicators of MI. Sharmaa *et al.* [14] decompose the single-lead heartbeat into six subbands based on the wavelet of the two-band optimal biorthogonal filter bank. Then the fuzzy entropy, signal-fractal-dimensions, and renyi entropy are extracted from each subband, and the effective features filtered by t-test to form feature set for MI detection. Tripathy *et al.* [16] decompose 12-lead ECG signals using Fourier-Bessel series expansion based empirical wavelet transform (FBSE-EWT), then extract statistical features such as kurtosis, skewness and entropy from sub-band signals of each lead as the features of MI detection. However, with the different degree of myocardial ischemia or the different location of occluded vessels, the ECG waveform of MI is complex and changeable. In addition, there are interpatient variations not only in the ECG signals of patients, but also in the ECG signals of normal people. The design of handcrafted extracted features relies on the prior knowledge of designer, hence their fixed form and the complicity and variety of ECG signals results in poor generalization of manual features. Our proposed method extract the distinguishing features of the single-lead ECG signals directly and automatically without the handcrafted feature extraction stage.

TABLE 5. Classification results of 10-fold cross validation MI localization.

Classes	ACC(%)	SE(%)	SP(%)			
AMI	99.84	± 0.09	99.02	± 0.89	99.94	± 0.04
ALMI	99.67	± 0.18	97.96	± 1.15	99.89	± 0.09
ASMI	99.80	± 0.20	99.67	± 0.62	99.83	± 0.10
ASLMI	100.00	± 0.00	100.00	± 0.00	100.00	± 0.00
IMI	99.53	± 0.12	98.60	± 0.61	99.77	± 0.14
ILMI	99.90	± 0.06	99.66	± 0.22	99.94	± 0.06
IPMI	100.00	± 0.01	98.00	± 18.00	100.00	± 0.00
IPLMI	99.45	± 0.22	98.67	± 1.63	99.49	± 0.20
LMI	99.99	± 0.02	98.70	± 3.04	100.00	± 0.01
PMI	99.99	± 0.03	100.00	± 0.00	99.99	± 0.03
PLMI	99.66	± 0.14	77.07	± 7.84	99.95	± 0.07
Normal	99.94	± 0.10	99.87	± 0.25	99.95	± 0.07

Based on the above comparisons, it can be concluded that the proposed method is more effective to detect MI using the diagnosis feature of MI extracted from single-lead ECG signals by the SAEs-based diagnostic feature extraction network. In the case of unsupervised learning and limited by sparse regular terms, the diagnosis feature of MI extracted automatically from the SAEs-based diagnostic feature extraction method can be adapted to the dynamic changes of ECG signals of MI patients, and thus has a wider adaptability.

B. RESULTS FOR MI LOCALIZATION

MI detection is evaluated as a two-class problem. Localization of MI is a multilabel classification task. The PTB database is used for fair comparisons with the state-of-the-art MI diagnostic methods. The normal ECG and 11 classes of MI pathologies, AMI, ALMI, ASMI, ASLMI, IMI, ILMI, IPMI, IPLMI, LMI, PMI and PLMI, are used for evaluation of the proposed MI localization method.

Table 4 shows the confusion matrix for the 11 types of MI and the normal ECG based the TreeBagger classifier. From this table, 50331 heartbeats of the 50336 heartbeats of MI are correctly detected with an accuracy of 99.99%, thus the missed diagnosis rate of MI is 0.01%. And 49670 heartbeats

TABLE 6. Comparision of MI localization performance with other methods.

Author	No. of classes	ACC(%)	SE(%)	SP(%)
Arif <i>et al.</i> , 2010 [7]	2	93.70(the maximum value)	-	-
Sun <i>et al.</i> , 2012 [8]	5	-	>85.00	-
Le <i>et al.</i> , 2013 [20]	6	-	>88.00	>92.00
Safdarian <i>et al.</i> , 2014 [5]	4	76.00	-	-
Sharma <i>et al.</i> , 2015 [10]	6	99.58	-	-
Noorian <i>et al.</i> , 2015 [13]	10	95.35	99.09	94.23
Acharya <i>et al.</i> , 2016 [9]	11	98.74	99.55	99.16
Padhy <i>et al.</i> , 2017 [31]	5	98.1	-	-
Costa <i>et al.</i> , 2018 [33]	2	95.83(the maximum value)	-	-
Liu <i>et al.</i> , 2018 [19]	6	94.82	-	-
Baloglu <i>et al.</i> 2019 [21]	11	99.78	-	-
Proposed method	12	98.88	99.95	99.87

of the 50336 heartbeats of MI were correctly located with an accuracy of 98.68%, thus the misdiagnosis rate of MI is 1.32%. It can be seen that this proposed method has a high accuracy rate for the diagnosis of MI. Table 5 shows the validation results obtained for localization of normal ECG and 11 types of MI. The classification accuracy values of 12 types of ECG signals are more than 99%. The diagnostic features extracted by the SAEs-based diagnostic feature extraction network can effectively characterize the pathological changes of single-lead ECG signals with different locations of the occluded coronary artery. And the TreeBagger classifier can achieve high precision in the classification of 12 types of ECG signals, which verifies the effectiveness of the proposed method.

The proposed method for MI localization is compared with the state-of-the-art methods and the results are shown in Table 6. Results reported in this paper are generally better than those of MI detection in the literature, with its accuracy value only less than the two by Sharma *et al.* [10] and Baloglu *et al.* [21]. Sharma *et al.* [10] extract multiscale wavelet energies and eigenvalues of multiscale covariance matrices from multiple heartbeats as the feature of one patient, and they allocate six types of MI. However, the proposed method only need the diagnostic features from one heartbeat to realize the diagnosis of MI, and the proposed method can directly and automatically extract the diagnostic features without the handcrafted feature extraction stage. Baloglu *et al.* [21] train the 10-layer deep convolutional neural network (CNN) in supervised classification, then use the trained model to complete the identification 11 classes of MI selected from the PTB database, in which ASLMI with larger necrotic area is ignored. The CNN structure is complex, and the 11 types of MI do not meet the clinical needs. However, the SAEs-based diagnostic feature extraction network of the proposed method consisting of the hidden layers of three shallow SAEs is used to implement feature extraction. And we designed the TreeBagger classifier to locate the 12 types of ECG signals.

In this work, for effectively calibrating the location of cardiovascular artery branch injury in clinical applications,

our proposed method extracts the diagnostic features from single-lead ECG signals. And we designed a shallow classifier TreeBagger to classify the 12 types of ECG signals. The TreeBagger classifier avoids the loss of features due to it does not reprocess the extracted effective features. Moreover it combines the results of multiple decision trees as the final decision to achieve higher stability and accuracy in the MI localization.

IV. CONCLUSION

We have presented an accurate and automatic algorithm based on SAE and TreeBagger for detection and localization of MI from single-lead ECG signals. The SAEs-based diagnostic feature extraction network avoids the vanishing gradient problem by the layer-wise training strategies, and learns the optimal feature expression of the label-less input heartbeat. Therefore this method extracts the deep distinctive features of the single-lead ECG signals. The TreeBagger classifier is constructed to realize MI diagnosis by combining the results of multiple decision trees and optimizing the diagnostic features.

The PTB database is used for fair comparisons with the state-of-the-art MI diagnostic methods. For MI detection, our method achieves better performances than other algorithms, and the accuracy, sensitivity and specificity are 99.90%, 99.98% and 99.52% respectively. Furthermore, for localization of 11 types of MI and normal ECG signals, this proposed method obtained the consistent results with the accuracy 98.88%, sensitivity 99.95%, and specificity 99.87%.

The experimental results confirm the effectiveness of the proposed method compared to other methods of MI diagnosis. The proposed method can effectively realize the diagnosis of 11 types of MI by using the TreeBagger classifier and the diagnostic features extracted from single-lead ECG signals by SAEs-based diagnostic feature extraction network, which has not been reported in the previous works. Success in the development of the accurate and comprehensive tool greatly helps the cardiologists in efficiently completing the early diagnosis of MI based on single-lead ECG signals.

Nevertheless, We still have some limitations in the coronary localization of multivessel disease such as IPLMI in this paper. In the future research, we will focus on the challenge of locating of the complex type of MI.

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