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Multi-Label ECG Signal Classification Based on Ensemble Classifier

ZHANQUAN SUN, CHAOLI WANG, (Member, IEEE), YANGYANG ZHAO, AND CHAO YAN
Shanghai Key Laboratory of Modern Optical System, Engineering Research Center of Optical Instrument and System, Ministry of Education, School of Optical-electrical and Computer Engineering, University of Shanghai for Science and Technology, Shanghai 200093, China

Corresponding author: Zhanquan Sun (sunzhq@usst.edu.cn)

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ABSTRACT Electrocardiogram (ECG) has been proved to be the most common and effective approach to investigate the cardiovascular disease because that it is simple, non-invasive and low cost. ECG signal automatic classification is a popular research topic and some efficient research work has been done on it. Most of current research work focuses on single ECG label classification, i.e. one ECG signal record corresponds to one label. In practice, one ECG signal usually embraces several cardiovascular diseases at the same time. It is more important to study multi-label ECG signal classification. To our knowledge, few research works have been done on the research topic. To resolve the multi-label ECG signal classification problems, we propose a novel ensemble multi-label classification model in this paper. The model combines several multi-label classification methods to generate a high performance classifier. Mutual information is used to measure the weight of each classifier. At last the ensemble multi-label classification model is used to analyze a clinic ECG signal dataset. The analysis results show that the overall classification performance is improved. It provides a feasible analysis method for multi-label ECG signal automatic classification.

INDEX TERMS Electrocardiogram, multi-label classification, ensemble classification, mutual information.

I. INTRODUCTION

Electrocardiogram (ECG) can measure and record the electrical activities of the heart, which has been widely applied in the diagnosis of all kinds of cardiovascular diseases because that it is effective, simple, non-invasive and low cost [1]. A typical ECG signal is shown in Fig 1. It should be pointed out that it is hard to analyze massive ECG records and diagnose cardiovascular disease manually, which requires rich special knowledge and a lot of clinic experience. Furthermore, the diagnosis results are affected by many subjective factors. In order to solve the problems, automatic ECG classification methods have been proposed to improve the diagnosis efficiency and accuracy, and some pioneer works have been done [2]–[4]. Most current research focuses on single label classification. Support vector machines (SVM), k-nearest neighbor (kNN), decision tree, and random forest etc. classifiers are applied to ECG signal classification [5], [6]. But in practice, ECG signals usually embrace several cardiovascular diseases at the same time. Therefore, the only-one-label-per pattern restriction of the classic learning (single-label) is not satisfied. It is more important to study multi-label ECG signal classification than to study single label ECG signal classification. To our best knowledge, few research works related to multi-label ECG classification have been done. Currently many multi-label classification (MLC) methods have been proposed. MLC problems can be tackled from two points of view: problem transformation and algorithm adaptation. Many problem transformation methods consider the different combinations of labels in the dataset as a new class in the way as multiclass learning does. Binary Relevance (BR) is a representative approach of problem transformation, and it decomposes a multi-label learning problem into some independent binary classification problems without considering label correlation [6]. On the other hand, according to the type of label correlation being exploited, existing multi-label approaches can be generally grouped into three categories [7]. First-order approaches tackle multi-label learning without exploiting label correlation among labels [8]. Second-order approaches mine

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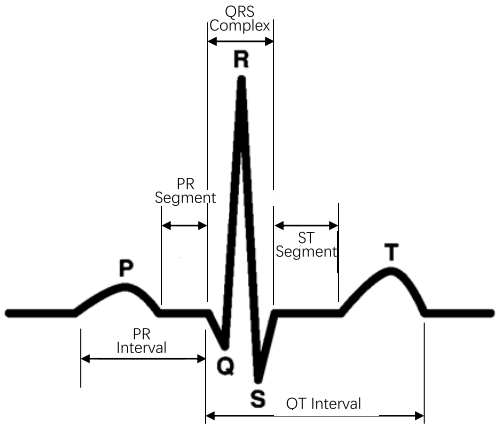


FIGURE 1. ECG signal wave.

pairwise relationship between label pairs [9]. And high-order approaches mine relationships among all the class labels or a subset of class labels [10]. Some efficient algorithm adoption methods have been proposed, such as multi-label kNN (MLkNN), multi-label SVM (ML-SVM) and so on. These approaches differ from one another in their capability to capture the intrinsic properties, such as label correlation, local invariance and so on.

ECG signal is a kind of weak electrical signal and it is easy to be affected by noise. Signal preprocessing is performed to filter signal noise and delete error signals of raw records to guarantee the signal quality. For eliminating these noises, many filter methods can be applied to ECG signal preprocessing, such as neural network, wavelet, empirical mode decomposition, recursive least square, least mean square based adaptive filtering technologies and so on [11], [12]. Feature extraction is mainly used to get the statistical, frequency and morphological features from ECG signal. All ECG information should be embraced in the features. Feature extraction is the most important issue in ECG auto identification. Many ECG feature extraction methods have been proposed to extract detailed ECG features, such as morphology, temporal information, wavelet transform, high-order statistics, Hermite basis function, and hidden Markov modeling and so on [13], [14]. Based on the extracted ECG features, different classifiers are adopted to perform ECG signal auto classification. In this paper, multi-label classifier is used to classify the ECG signal. Different multi-label classifier has its limitation. For improving the classification performance, an ensemble multi-label classifier is proposed to realize high performance ECG signal classification. In the method, several multi-label classifiers are taken as the basic classifier. The weight of each basic classifier is evaluated based on mutual information. The ensemble classification results are determined through comparing with the threshold values of each class. The optimum threshold values are calculated with genetic algorithm method and F1 score is taken as the object function. The efficiency of the proposed method is illustrated with a practical ECG dataset analysis.

The rest of this paper is organized as follows. Section 2 present the related research works. An ensemble multi-label ECG classification method is proposed in detail in section 3. A practical example is analyzed with the proposed method in section 4. Concluding remarks are described in Section 5.

II. RELATED WORKS

Large scale ECG database with labels is the precondition for investigating the automatic classification model. Most of current ECG researches are based on MIT-BIH, ST-T and AHA databases [15]. All the ECG signs are labeled with a single class. In practice, lots of ECG signals embrace multiple cardiac disease types at the same time. For developing more implementable training datasets, Dong etc. built a Chinese Cardiovascular Disease Database (CCDD) database that includes about 200,000 clinical ECG records with complete diagnosis results, i.e. each ECG signal embraces several abnormal types [16], [17]. It is one of the best open ECG datasets for research, which can be downloaded from the website http://ecgdb.com. The research work of the paper is based on a subset of the CCDD.

Signal preprocessing is the basic work to improve the ECG signal quality and ECG analysis performance. Some efficient research work has been done on this topic [18], [19]. Some machine learning methods are proposed to evaluate the quality of an ECG signal, and most of them are based on the features of ECG signals, such as RR intervals, P-wave and T-wave shapes and so on [20]. Low-quality ECG signals are picked out and processed with some filtering methods. Some research work is published on the Physionet website [21]. The WFDB software package is a powerful ECG signal processing tool, which can be used to filter many kinds of ECG noises [22]. Feature extraction is the most important research content and lots of research work has been done on this topic. Saurabh *et al.* used a multi-resolution wavelet to extract the wave and the complex boundaries of an ECG signal [23]. The Gabor wavelet multi-linear discriminant analysis was used to extract P and T waves and the QRS complex from ECG signals, and it obtained a highly accurate result [24]. Different wavelet methods have been applied to ECG signals. Based on the available wavelet methods, higher order hand-engineered features of ECG signals were extracted [25], [26]. Fernando *et al.* combined different ECG features together to generate 169 ECG features [27]. Many methodologies have been adopted to classify these extracted features, such as SVM [28], kNN rules [29], artificial neural networks [30], Bayesian network [31], wavelet transform and so on [32]. Little research work about multi-label ECG signal classification has been done. Many multi-label classification methods have been proposed [33]. A binary relevance method for multi-label classification is proposed in reference [6]. It converts multi-label learning into l independent binary classification problems. A classifier chain for multi-label classification problem is proposed in reference [34]. It transforms multi-label learning problem into l binary

classification problems which encode the label correlations into feature space and constructs the models according to a chaining order specified over the class labels. Label powerset (LP) transforms problems to multi-class classification which regards the subsets of the label space as new labels [35]. It makes use of ensemble learning to improve the LP algorithm by randomly selecting k labels each time and using the ensemble learning technique to get the final results. Algorithm adaption approaches are to adapt the existing single-label learning algorithm to directly tackle multi-label learning problems. MLkNN identifies the set of labels to be associated using the maximum a priori (MAP) principle based on prior and posterior probabilities from the frequency of each label within the neighborhood [36]. Rank-SVM is based on SVM and defines both a linear model that minimizes the ranking loss and a size predictor to obtain the set of relevant labels from the ranking [37]. Multi-label decision tree adapts decision tree to solve multi-label learning problems [38]. Each multi-label classification method has its limitation. To further improve the classification performance, ensemble learning is taken as the most perspective method. Ensemble classifiers' performance is usually better than single classifiers. An ensemble of *n* class chains, each with a random chain and a random sample with replacement from the training dataset, is proposed in reference [10]. But the method only takes advantage of one kind of multi-label classifier. The improvement of the classification performance is limited. A random k-labelsets for multilabel classification is proposed in reference [39]. The labelset is sampled into small scale labelsets randomly. Each sub-labelset is used to build a multi-label classifier based on LP method. The final classification result is the argumentation of each sub-classifier through prescribing a threshold value. The threshold is prescribed subjectively. An ensemble multi-label classification model of Bayesian networks is proposed in reference [40]. In the ensemble model, each classifier can only identify one class. An ensemble multi-label classification model based on random k-lablesets is proposed in reference [41]. Different measures can be used to evaluate the performance of multi-label classifier. Accuracy usually is taken as the object function in current research. F1 score is the synthetical indictor of precision and recall rate, which is suitable to be taken as the object function. But no research work has been done on it. F1 score is taken as the object function to get the optimum threshold value and genetic algorithm method is use to solve the optimization problem. The proposed method is used to classify ECG signals.

III. MULTI-LABEL ECG CLASSIFICATION METHODS BASED ON ENSEMBLE METHOD

ECG signal reflects the electrical activity of the heart muscles. It is mainly formed by P wave, QRS complex, and T wave etc. Each wave corresponds to a different activity part of the heartbeat. P wave records the electrical activity of the upper heart chambers. QRS wave is the largest one and it records the electrical activity of the ventricles. T wave reflects the heart's return to the resting state between two beats. Any irregularity in P wave, QRS complex, T wave components and R-R interval indicates illness of heart. Doctors can diagnose cardiac diseases manually according to the change of waves. The object of the study is to classify the ECG abnormal type based on the ECG signals automatically. The architecture of the auto recognition procedure is as follows. Original ECG signals are collected with several leads, such as 3-lead, 8-lead, and 12-lead and so on. The 12-lead ECG are commonly used in clinic.

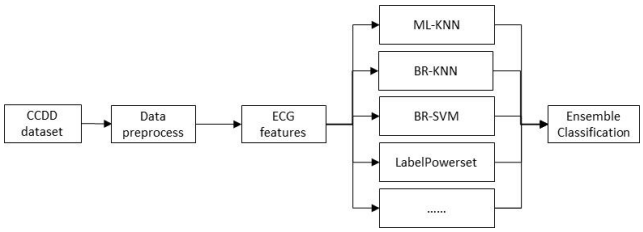


FIGURE 2. Multi-label ECG signal classification procedure.

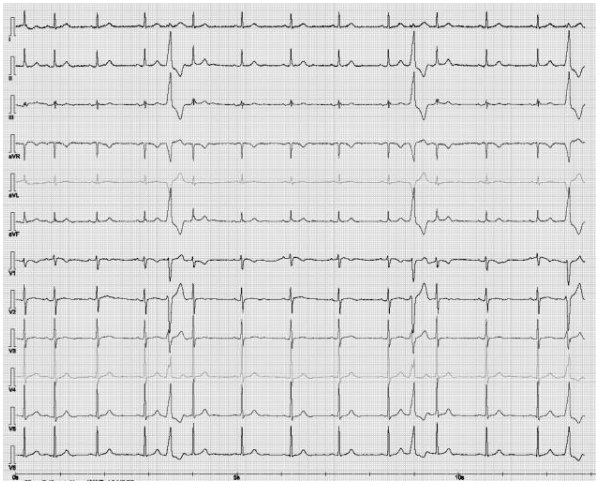
The procedure of multi-label ECG classification is shown in Fig 2. Some ECG leads' records contain noises and some leads' records are fault caused by incorrect manipulation. The noises and fault data must be processed to get high quality ECG signal data. After data preprocessing, manual designed ECG feature extraction methods and automatic ECG feature extraction methods are combined to extract ECG features. Feature selection is proposed to find the most informative feature combination. At last, an ensemble classifier is designed to identify cardiac diseases.

A. ECG SIGNAL PREPROCESS

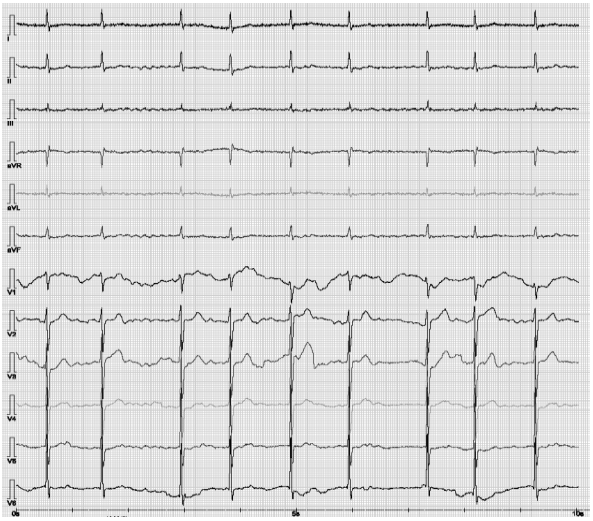
This research mainly focuses on 12-lead ECG signal analysis. The data source is a subset of the CCDD dataset. All records in the CCDD dataset were collected with 12-lead ECG devices from different hospitals. Different signal noises are embraced in these records. To obtain high quality ECG signals, we used data preprocessing methods to filter noise and remove the contaminated data. Based on the WFDB toolbox, the median filter is used to remove impulse noise and baseline drift from signals. A high pass filter with threshold frequency value 0.5Hz is used to filter muscle interference. A low pass filter with threshold frequency value 50Hz is used to filter power interferences. 10th order bandpass Butterworth filters with cut-off frequencies of 5Hz and 45Hz (narrow band) and 1Hz to 100 Hz (wide band) are used to filter other signal noises. Preprocessed ECG signals are analyzed with the following steps.

B. ECG FEATURE EXTRACTION

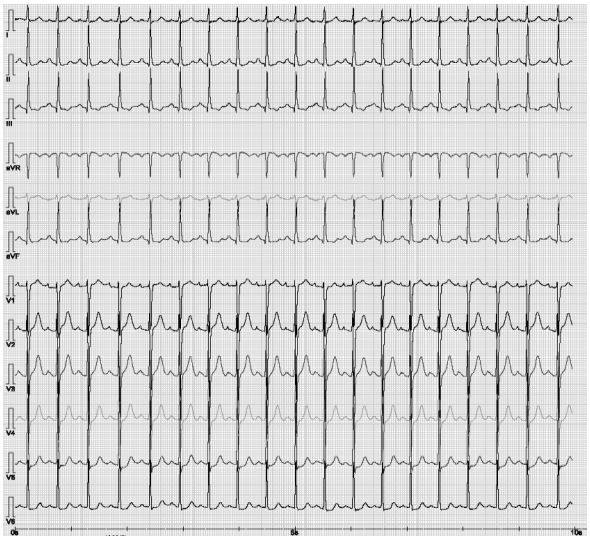
After preprocessing, different feature extraction methods are used to extract distinguishable features. Based on the experience of experts, a lot of hand-engineered features have been extracted and some efficient toolboxes have been developed, which can be used to extract hand-engineered features.



(a) ECG signal with sinus arrhythmia, sinus bradycardia, and atrial premature beats

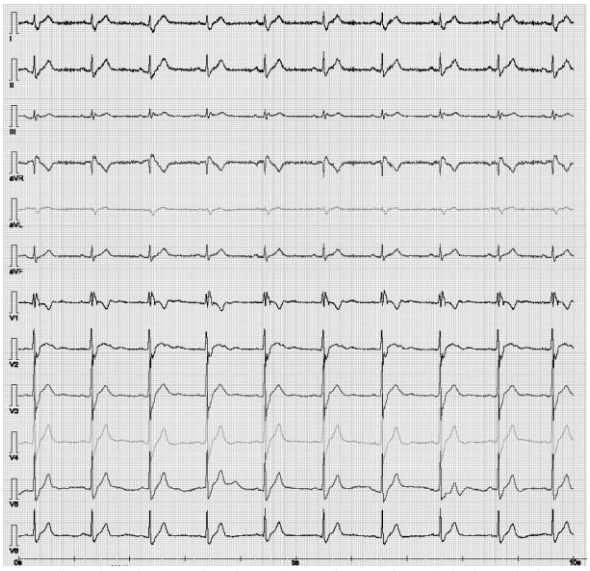


(b) ECG signal with atrial fibrillation and left ventricular high voltage



(c) ECG signal with atrioventricular heart-block and left ventricular high voltage

FIGURE 3. Several multi-label ECG signal samples.



(d) ECG signal with sinus bradycardia and complete right bundle branch block

FIGURE 3. *(Continued.)* Several multi-label ECG signal samples.

WFDB is one of the most efficient ECG signal analysis toolboxes. Based on WFDB, 169 features were extracted in reference [27]. The features include 22 morphological features (QT-interval, QRS-interval, P-power, etc.), 36 signal quality indices (the degree of agreement between beat detection on different leads (bSQI), the degree of agreement between beat detection on different leads (iSQI), the kurtosis SQI (kSQI), the skewness SQI (rSQI)), 95 non-linear features (sample entropy, approximate entropy, Poincaré plot, and recurrence quantification analysis etc.), 8 time domain features (the standard deviation of R-peak intervals (SDNN), the square root of the mean squared difference of successive R-peaks (RMSSD), the number of pairs of successive R-peaks that differ by more than x ms (NNx)), and 8 frequency domain features (low frequency (LF) power, high frequency (HF) power).

C. MULTI-LABEL CLASSIFIER

Multi-label classification is the supervised learning problem where an instance may be associated with multiple labels. It is opposed to the traditional task of single-label classification where each instance is only associated with a single class label. Let $X \in R^m$ denote the m-dimensional input space and $y = \{y_1, y_2, \cdots, y_l$ denote the label space with l classes. The task of multi-label learning is to learn a mapping function. Multi-label classifier $H : x \rightarrow 2^y$ which assigns each instance $x \in X$ with a set of possible class label $H(x) \subseteq y$. Some efficient multi-label classification methods have been proposed. But each method has its own limitation. For improving the performance of multi-label ECG signal classification, several multi-label classification methods,

such as BR, ML-kNN, multi-label hierarchical adaptive resonance associative map (HARAM), multi-label twin support vector machine (MLTSVM), classifier chain, label powerset, sklearn embedder, and embedding classifier, are combined together to generate an ensemble classifier. The composed multi-label classifiers are introduced briefly as follows.

1) BINARY RELEVANCE

BR multi-label classifier comes from the idea of one-vs-all for multi-class classification. It transforms a multi-label classification problem with l labels into l single-label separate binary classification problems using the same base classifier, such as SVM, kNN, decision tree and so on. The prediction output is the union of all per label classifiers.

2) MULTI-LABEL HARAM [42]

MLHARAM aims at increasing the classification speed by adding an extra adaptive resonance theory layer for clustering learned prototypes into large clusters. The activation of all prototypes can be replaced by the activation of a small fraction of them, leading to a significant reduction of the classification time. HARAM is to find the highest activation function.

$$T_k^c\left(W_j^a\right) = \frac{\left|W_j^a \wedge W_k^c\right|}{\alpha + \left|W_k^c\right|} \tag{1}$$

where T_k is the activation function, W is the weight vector, $\wedge$ denotes the fuzzy AND operator. In the MLHARAM, the lowest activation value is estimated in the preparation step and its identifier is saved as an additional attribute of the prototype used as input.

3) MLTSVM

For l possible multi-label classification, MLTSVM is to seek l proximal hyper planes

$$f_k(x) : w_k' x_i + b_k = 0, \quad k = 1, \cdots, l \tag{2}$$

such that the kth hyper plane is closer to the instances with the label k, and is as far as possible from the others, where w_k and b_k are the normal vector and the bias term, respectively, of the kth proximal hyper plane. The primal problem of MLTSVM for the kth hyper plane can be expressed as

$$\begin{aligned} &\frac{1}{2}\sum \left\|w_k' x_i + b_k\right\|^2 + c_k \sum_{j\in \bar{I}_k} \xi_j + \frac{1}{2}\lambda_k(\|w_k\|^2 + b_k^2) \\ &s.t. -\left(w_k' x_i + b_k\right) \geq 1 - \xi_j, \quad \xi_j \geq 0, \ \ j \in \bar{I}_k \end{aligned} \tag{3}$$

Detail information can be found in reference [43].

4) MLkNN

MLkNN is an algorithm adoption method based on kNN. It uses kNN to find the nearest examples to a test class and uses Bayesian inference to select assigned labels. Given an instance x and its associated label vector y, the number of nearest neighbors is set k. Based on the labelsets of nearest neighbors, the membership counting vector is denoted by

$$\bar{C}_x(p) = \sum\nolimits_{a\in N(x)} y_a(p) \tag{4}$$

where $N(x)$ denotes the set of k nearest neighbors of x identified in the training set.

Based on Bayesian inference, the MLkNN determines the final labels according to the posteriori principle.

$$\bar{y}_t(p) = \arg max_{b\in\{0,1\}} P(H_b^p | E_{C_t(p)}^p) \tag{5}$$

Detail information can be referenced in [36].

5) CLASSIFIER CHAIN

Classifier chain provides implementation of Jesse Read's problem transformation method. For l labels, classifier chain will train l classifiers ordered in a chain according to the Bayesian chain rule. The first classifier is trained just on the input space, and then each next classifier is trained on the input space and all previous classifiers in the chain. Detail information is referenced in [34].

6) LABEL POWERSET

Label powerset is a problem transformation approach to multi-label classification that transforms a multi-label problem to a multi-class problem with one multi-class classifier trained on all unique label combinations found in the training data. The method maps each combination to a unique combination id number, and performs multi-class classification using the classifier as a multi-class classifier and combination ids as classes. Detail information is referenced in [35].

7) LABEL SPACE PARTITIONING CLASSIFIER (LSPC)

LSPC method partitions the label space into separate and small multi-label sub problems with a label space cluster. The multi-label classifier is trained in each label space subset. The final prediction result is the sum of each sub classifier. Detail information is referenced in [44].

D. ENSEMBLE MULTI-LABEL CLASSIFIER

The ECG signals are classified with each multi-label classifier individually. The classification results based on different multi-label classifier are combined according to the following ensemble method to generate the final classification result.

1) ENSEMBLE CLASSIFIER

Let $x_i = (x_{i1}, x_{i2}, \cdots, x_{im})$ be an instance, $y_i^j = \left(y_{i1}^j, \cdots, y_{iq}^j, \cdots, y_{il}^j\right), y_{iq} \in \{0, 1\}$ be the multi-label classification result of classifier $j, j \in \{0, 1, \cdots, k$ and k is the number of single classifiers. The final classification result is calculated as follows.

$$\bar{y}_{iq} = sign\left(\sum\nolimits_{j=1}^{k} w_{jq} y_{iq}^j - \theta_q\right), \quad q \in \{0, 1, \cdots, l\} \tag{6}$$

where w_{jq} denotes the weight of the jth classifier corresponding to the qth label, i.e. the weight of each label is

different. θ_q is the threshold value of label y_q. The weight w_{jq} is determined based on mutual information between the classification results and ground truth labels. The probability distribution of label q of classifier j is denoted by $p(y_q^j)$. The probability distribution of label q of ground truth is denoted by $p(y_q)$. The joint probability distribution of classifier j and ground truth label is denoted by $p(y_q, y_q^j)$. The mutual information between classification result of multi label classifier j and the ground truth label is

$$I\left(y_q; y_q^j\right) = -\sum_{y_q^j=0}^{1} p\left(y_q^j\right) \log p\left(y_q^j\right) - \sum\nolimits_{y_q=0}^{1} p\left(y_q\right) \log p\left(y_q\right) + \sum\nolimits_{y_q^j=0}^{1} \sum\nolimits_{y_q=0}^{1} p(y_q, y_q^j) \log p(y_q, y_q^j) \quad (7)$$

Through normalization, the weight w_{jq} can be calculated as follows.

$$w_{jq} = I\left(y_q; y_q^j\right) / \sum\nolimits_{i=1}^{k} I\left(y_q; y_q^i\right) \quad (8)$$

The threshold value θ_q is usually prescribed 0.5. It cannot assure the best ensemble classification performance. For obtaining the optimum threshold value, the following optimization procedure is introduced

$$\theta_q^* = \max_{0<\theta_q<1} f\left(\theta_q\right) \quad (9)$$

where $f(\cdot)$ is the evaluation function, such as accuracy, precision, recall, and F1 score and so on. For example, when accuracy is taken as the evaluation function, the cost function is

$$f\left(\theta_q\right) = \frac{1}{|X|} \sum\nolimits_{x \in X} \left[\bar{y}_{iq} = y_{iq}\right] \quad (10)$$

where $|X|$ denotes the cardinality of X. $\left[\bar{y}_{iq} = y_{iq}\right]$ denotes a sign function, i.e. $\left[\bar{y}_{iq} = y_{iq}\right] = 1$ when the prediction value $\bar{y}_{iq}$ equal the ground truth y_{iq} or else $\left[\bar{y}_{iq} = y_{iq}\right] = 0$.

The above function is not derivable and Eq.(9) has no analytic solutions. For improving the calculation speed, we use generatic algorithm to solve the optimum equation. The method is as follows.

2) THRESHOLD VALUE OPTIMIZATION BASED ON GENETIC ALGORITHM

From the expression of Eq. (6) and (10), we can find that the optimization problem is difficult to get an analytical solution. Genetic algorithm is a search technique used in computing to find exact or approximate solutions to optimization and search problems. It is an efficient method to solve complicated optimization problems. It is used to solve the threshold optimization problem. The procedure can be summarized as follows.

a: REPRESENTATION

The threshold value $\theta_q, q \in \{0, 1, \cdots, l$, is denoted by a binary vector, i.e. chromosome. The vector length depends on the required precision. Initial n population of potential solutions should be created.

b: EVALUATION FUNCTION

The evaluation function plays the role of environment, rating potential solutions in terms of their fitness. $f\left(\theta_q\right)$ is taken as the evaluation function.

c: CROSSOVER

After prescribing probability of crossover, chromosomes are selected to cross in terms of their fitness. The chance to be chosen is bigger if the fitness value is bigger. Commonly used method is one-point crossover, two-point crossover and multi-point crossover through roulette wheel method. One-point crossover is adopted in this paper.

d: MUTATION

Mutation rate is prescribed firstly. In each mutation, one or more genes are mutated between 0 and 1 according to the mutation rate. Random point mutation is adopted as the mutation method

e: SELECTION

Enlarged solution space is composed of chromosomes generated through crossover, mutation, and current generation chromosomes. After competition, n best chromosomes are selected as the parent generation of the next iteration.

f: STOPPING CRITERION

The iteration will stop when iteration epoch reaches prescribed threshold value T. The chromosome corresponds to the maximum fitness value is taken as the optimum resolution. Corresponding θ_q^* value is taken as the best threshold value.

IV. MULTI-LABEL CLASSIFICATION EVALUATION MEASURES

Commonly used measures for evaluating multi-label classification include Hamming loss, subset accuracy, Jaccard similarity, precision, recall and F1 value. The metrics are as follows.

A. HAMMING LOSS

It is a label-wise measure that counts the proportion of the labels that were misclassified in all instances, i.e.

$$\text{HammingLoss}\,(h) = \frac{1}{|X|} \sum\nolimits_{x \in X} \frac{1}{l} \sum\nolimits_{j=1}^{l} \left[\left(L_j \in h\left(x\right)\right) \otimes \left(L_j \in y\right)\right] \quad (11)$$

where $\otimes$ is the logical exclusive-OR, $h\left(x\right)$ denotes the classification function, and L_j denotes the jth label.

TABLE 1. Selected CCDD data information.

No.	Disease types	Sample number	Binary code
0x020201	Sinus arrhythmia	11501	1000000
0x020401	Sinus bradycardia	11103	0100000
0x030201	Atrial premature beats	4133	0010000
0x030701	Atrial fibrillation	5018	0001000
0x060201	Atrioventricular heart-block	3843	0000100
0x060305	Complete right bundle branch block	5090	0000010
0x080205	Left ventricular high voltage	10872	0000001

B. SUBSET ACCURACY

It is an instance-wise measure that measures the proportion of exactly correct classification result, i.e.

$$\text{Subset Accuracy (h)} = \frac{1}{|X|}\sum\nolimits_{x\in X}\left[h\left(\tilde{x}\right) = y\right] \quad (12)$$

C. JACCARD SIMILARITY

It is a measure of distance between the prediction and the ground truth, i.e.

$$\text{Jaccard}\,(h) = \frac{1}{|X|}\sum\nolimits_{x\in X}\frac{h(x)\cap y}{h(x)\cup y} \quad (13)$$

where $h(x) \cap y$ is the cardinality of the intersection of vector $h(x)$ and vector y, and $h(x) \cup y$ is the cardinality of the union of vector $h(x)$ and vector y.

D. PRECISION

It is the measure of how many classified positive labels are correctly, i.e.

$$\text{precision (h)} = \frac{\sum_{j=1}^{l} t_{p_j}}{\sum_{j=1}^{l}\left(t_{p_j} + f_{p_j}\right)} \quad (14)$$

where t_p denotes true positive, f_p denotes false positive.

E. RECALL

It is the measure of how many positive labels have been classified correct, i.e.

$$\text{recall (h)} = \frac{\sum_{j=1}^{l} t_{p_j}}{\sum_{j=1}^{l}\left(t_{p_j} + f_{n_j}\right)} \quad (15)$$

where t_p denotes true positive and f_n denotes false negative

F. F1 SCORE

F1 score is the harmonic mean of precision and recall, i.e.

$$F_1 = \frac{2(precision\,(h) * recall(h))}{precision\,(h) + recall(h)} \quad (16)$$

V. EXPERIMENT AND ANALYSIS

A. DATA SOURCE

The example is based on the CCDD [16]. CCDD consists of approximately 200,000 short-term ECG records, and each record has its own diagnostic results. The records of the CCDD are all 12-lead ECGs with approximately 10 $\sim$ 30s in duration, and each is digitized at 500 Hz. The 200,000 records correspond to 270 ECG labels in total. The sample number of each label is unbalanced. The number of normal ECG records is about 100000 with the most quantity. The label number with least quantity is less than 10. Without loss of generality, we select 7 labels to study. They are sinus arrhythmia (SA), sinus bradycardia (SB), atrial premature beats (APB), atrial fibrillation (AF), atrioventricular heart-block (AHB), complete right bundle branch block (CRBBB), left ventricular high voltage (LVHV) etc. There are 46729 records in total. The data information of the selected ECG labels is listed in Table 1. The data is analyzed in GPU workstation. It uses 1 GPU computational node with 4 Titan X GPU cards. Some typical ECG signal curves are shown in Fig 3.

B. DATA PREPROCESSING

The original ECG dataset is collected from clinic original records and they are not processed. Some signal noises are embraced in the data records. For assuring the quality and improving the identification performance, data preprocessing methods introduced in section 3 are applied to the original ECG records. WFDB toolbox is used to filter the baseline wandering, power line interference and EMG noise. Threshold value method and regression method are used to get rid of wrong records caused by lead falling off or wrong operation. Then the data are normalized to range value [0, 1]. After preprocessing, the processed data are used to extract ECG signal features and train the multi-label ECG classifier.

C. FEATURE EXTRACTION

Firstly, we use WFDB toolbox to extract classic ECG features, such as RR rate, signal quality indices, heart rate variability metrics, QRS features, morphological features, P-wave power and QT-interval and so on. We extract 169 ECG signal features with the WFDB toolbox.

D. MULTI-LABEL ECG SIGNAL CLASSIFICATION

Based on the ECG features, we train the multi-label ECG signal classifiers individually. The classification results are combined together to generate the final classification results. For comparison, commonly used ensemble classification methods are compared.

1) MULTI-LABEL CLASSIFICATION RESULTS

The extracted features are used to train the multi-label ECG classifiers respectively. 60 percent samples are chosen randomly for training and the left 40 percent samples are used for test. The training samples are chosen with 10 class validation. The average classification results based on each multi-label

TABLE 2. Classification results based on different multi-label classification methods.

methods	accuracy score	Hamming Loss	Jaccard similarity	precision	recall	F1
BRSVM[6]	0.412	0.101	0.443	0.505	0.347	0.356
MLkNN[36]	0.556	0.093	0.591	0.719	0.501	0.563
MLHARAM[42]	0.479	0.134	0.614	0.552	0.625	0.554
MLTSVM[43]	0.254	0.137	0.311	0.573	0.351	0.432
Label Powerset[35]	0.702	0.125	0.743	0.856	0.662	0.707
Classifer Chain[34]	0.651	0.067	0.682	**0.894**	0.582	0.675
LSPC[44]	0.031	0.268	0.362	0.364	**0.741**	0.478
Proposed Ensemble method	**0.752**	**0.062**	**0.789**	0.808	0.716	**0.752**

TABLE 3. Weight values of each classifier corresponding to different class.

	SA	SB	APB	AF	AHB	CRBBB	LVHV
BRSVM	0.154	0.170	0.481	0.149	0.449	0.425	0.302
MLkNN	0.159	0.148	0.088	0.149	0.043	0.044	0.103
MLARAM	0.145	0.122	0.102	0.153	0.031	0.048	0.098
MLTSVM	0.063	0.082	0.038	0.078	0.076	0.041	0.003
Label Powerset	0.211	0.191	0.081	0.171	0.125	0.174	0.233
Classifier Chain	0.233	0.196	0.135	0.184	0.213	0.218	0.246
LSPC	0.035	0.091	0.074	0.115	0.063	0.051	0.015

TABLE 4. Threshold values corresponding to each class.

	SA	SB	APB	AF	AHB	CRBBB	LVHV
Threshold value	0.501	0.512	0.245	0.576	0.223	0.225	0.328

TABLE 5. Weight values calculated based on correlation coefficient measure.

	SA	SB	APB	AF	AHB	CRBBB	LVHV
BRSVM	0.130	0.138	0.151	0.135	0.141	0.109	0.120
MLkNN	0.143	0.144	0.000	0.146	0.000	0.041	0.000
MLARAM	0.152	0.151	0.174	0.144	0.179	0.162	0.170
MLTSVM	0.210	0.188	0.215	0.166	0.207	0.250	0.276
Label Powerset	0.074	0.094	0.141	0.119	0.162	0.150	0.064
Classifier Chain	0.140	0.143	0.133	0.139	0.128	0.133	0.190
LSPC	0.151	0.143	0.187	0.150	0.183	0.154	0.180

TABLE 6. Weight values calculated based on Euclid distance measure.

	SA	SB	APB	AF	AHB	CRBBB	LVHV
BRSVM	0.171	0.165	0.177	0.207	0.195	0.171	0.170
MLkNN	0.101	0.067	0.099	0.150	0.126	0.070	0.072
MLARAM	0.114	0.131	0.109	0.082	0.113	0.147	0.136
MLTSVM	0.048	0.052	0.058	0.052	0.070	0.056	0.063
Label Powerset	0.111	0.110	0.116	0.087	0.086	0.122	0.108
Classifier Chain	0.161	0.146	0.152	0.113	0.132	0.149	0.151
LSPC	0.295	0.328	0.288	0.309	0.278	0.284	0.300

classifier, i.e. BRSVM, MLKNN, MLHARAM, MLSVM, Label Powerset, Class Chain and LSPC et. al. are listed in Table 2.

Based on the classification results of each multi-label classifier, ensemble method introduced in section 3 is used to generate the final ECG signal classifier. 60 percent of the test samples are selected to train the ensemble classifier and the left are used to evaluate the performance of the ensemble classifier. In the ensemble classifier, the weight of each multi-label classifier is calculated according to Eq. (8) and the calculation results are listed in Table 3.

In the optimization process of determining the threshold θ_q, the F1 value is chosen as the cost function $f\left(\theta_q\right)$ of Eq. (9). The precision is set 0.001. The length of the chromosome in the genetic algorithm is set 70, i.e. each $\theta_1, 1 \in \{1, \cdots, 7\}$

TABLE 7. Ensemble classification results based on different correlation measure.

methods	accuracy score	Hamming Loss	Jaccard similarity	precision	recall	f1
Euclid distance	0.678	0.066	0.713	**0.861**	0.609	0.682
Coefficient	0.608	0.076	0.648	0.825	0.542	0.607
Proposed ensemble method	**0.752**	**0.062**	**0.789**	0.808	**0.716**	**0.752**

TABLE 8. Ensemble classification results based on different ensemble method.

methods	accuracy score	Hamming Loss	Jaccard similarity	precision	recall	F1
ECC [10]	0.561	0.121	0.687	**0.827**	0.565	0.683
Random k-labelsets[39]	0.727	0.105	0.723	0.763	0.702	0.725
Ensemble Bayesian Network [40]	0.746	0.072	0.759	0.789	0.734	0.713
RAKEL++[41]	0.737	0.065	0.778	0.795	**0.796**	0.740
Proposed ensemble method	**0.752**	**0.062**	**0.789**	0.808	0.716	**0.752**

corresponds to 10 binary codes the equation can be derived, as shown at the bottom of the page, where θ_1 denotes threshold value of SA, θ_2 denotes threshold value of SB, θ_3 denotes threshold value of APB, θ_4 denotes threshold value of AF, θ_5 denotes threshold value of AHB, θ_6 denotes threshold value of CRBBB, and θ_7 denotes threshold value of LVHV. The initial population size is set 10 and they are initialized randomly. The crossover rate is set 0.5, the mutation rate is set 0.2, and the iteration threshold value is set 10000. The threshold values are listed in Table 4. The final average classification results predicted with the ensemble classifier are listed in Table 1 also.

E. RESULTS COMPARISON

For illustrating the efficiency of the proposed method, several commonly used ensemble classifiers based on weights are adopted to analyze the dataset. Different correlation measure will produce different weight w_{jq} in Eq. (6). Correlation coefficient and Euclid distance are used to calculate the weight of each multi-label classifier.

1) ENSEMBLE CLASSIFIER BASED ON CORRELATION COEFFICIENT MEASURE

The ensemble weights based on correlation coefficients are calculated according to the following equation.

$$\mathrm{Corr}\left(y_q; y_q^j\right) = \frac{Cov(y_q; y_q^j)}{\sqrt{Var\left(y_q\right) Var(y_q^j)}}$$

where $Cov(y_q; y_q^j)$ is the covariance and $Var\left(y_q\right)$ is the variance of y_q. The weight values calculated based on correlation coefficients are listed in Table 5. The threshold value usually is set 0.5 in the commonly used ensemble classifier. The final ensemble classification results based on the weight values are listed in Table 7.

2) ENSEMBLE CLASSIFIER BASED ON EUCLID DISTANCE MEASURE

The ensemble weights based on Euclid distances are calculated according to the following equation.

$$d\left(y_q; y_q^j\right) = \sqrt{\sum_{i=1}^{n} (y_{iq} - y_{iq}^j)^2}$$

The weight values calculated based on the Euclid distances are listed in Table 6. The threshold value of ensemble classifier is set 0.5. The final ensemble classification results based on the weight values are list in Table 7 also.

3) COMPARISON WITH OTHER ENSEMBLE CLASSIFICATION METHODS

For illustrating the efficiency of the proposed ensemble multi-label cassifier, commonly used ensemble classifiers are used to analyze the dataset. Ensemble classifier chain (ECC) [10], ensemble classifier based on random k-labelsets [39], ensemble Bayesian network [40], and enemble classifier RAKEL++ [41] are used to classify the ECG signals. The analysis results are lised in Table 8.

F. RESULTS ANALYSIS

From Table 2 we can find that the multilabel classification results based on the proposed ensemble classfication method is better than that of each individual classifier in many evaluation factors. The factors accuracy score, Hamming loss, Jaccard similariy and F1 score are all improved markedly.

$$\left\{ \underbrace{\theta_1, 0,\cdots,1'}_{10} \underbrace{\theta_2, 0,\cdots,1'}_{10} \underbrace{\theta_3, 0,\cdots,1'}_{10} \underbrace{\theta_4, 0,\cdots,1'}_{10} \underbrace{\theta_5, 0,\cdots,1'}_{10} \underbrace{\theta_6, 0,\cdots,1'}_{10} \underbrace{\theta_7 0,\cdots,1'}_{10} \right\}$$

Especially, F1 score is improved markedly because it is taken as the cost function of the optimization.

From Table 7 we can find that the multilabel classification results based on the proposed ensemble classfication method is better than that base on other correlation measures with prescribed threshold value. It shows that correlation measure place an important role in the ensemble classifier. Mutual information can reflect arbitrary statitical relationship between variables. The ensemble classifier based on mutual information can measure the real complicate relationship between each classifer and the real label. It is more suitable than other measures.

From Table 8 we can find that the ensemble multi-label classification method proposed in this paper is better than commonly used ensemble methods in general. All the current ensemble multi-label classification methods assign the same weight to each classifier and the differences between different label are not considered. From the results we can find that the precision of classifier chain and ensemble chasslifier chain are better than other method. They are based on classifier chain. The recall rate of LSPC and RAKEL++ are better than other methods. They are based on label powerset method.

VI. CONCLUSIONS

Cardiac diseases auto identification based on ECG signals has been widely studied. Current research mainly focuses on single disease identification. In practice, most ECG signals embrace multi-label at the same time. For resolving the practical multi-label ECG classification problems, an ensemble classifier is proposed in this paper. The main contribution can be summarized following two aspects.

(1) Mutual information is adopted to calculate the relationship between each classifier and real ECG label. It can measure arbitrary statistical relationship between variables. Practical example analysis results show that mutual information is better than other measures. Classic ensemble classification methods usually assign only one weight to an individual classifier. It cannot reflect the impact of different classifiers on different labels. We propose a weight assignment method based on the individual mutual information between each label. It assigns different weight values to the same classifier in different labels.

(2) Classic ensemble classification method will prescribe a threshold value to determine the final classification result. The threshold values affect the final results markedly. For obtaining an objective threshold value, we propose an optimization model based on genetic algorithm. The method can find the optimum threshold value corresponding to each label. Practical example analysis results show that the proposed method can improve the classification result.

Based on the research, we find a suitable way to resolve multi-label ECG signal classification problems. More research work can be done in our future research work on the topic.

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ZHANQUAN SUN is currently pursuing the Ph.D. degree with the University of Shanghai for Science and Technology. He is also an Associate Professor with the University of Shanghai for Science and Technology. He has presided and attended 20 research projects. He has published about 60 academic articles. His major research interests include big data, data mining, and artificial intelligence.

CHAOLI WANG (Member, IEEE) is currently pursuing the Ph.D. degree with the University of Shanghai for Science and Technology. He is also a Professor with the University of Shanghai for Science and Technology. He has presided and attended ten research projects. He has published about 80 academic articles. His major research interests include nonlinear control, robot control, fuzzy control, and image identification.

YANGYANG ZHAO is currently pursuing the degree with the University of Shanghai for Science and Technology. His research interest includes artificial intelligence on medicine.

CHAO YAN is currently pursuing the degree with the University of Shanghai for Science and Technology. His research interest includes medical image analysis.