RESEARCH

A multi-label classification system for anomaly classification in electrocardiogram

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Abstract

Automatic classification of ECG signals has become a research hotspot, and most of the research work in this field is currently aimed at single-label classification. However, a segment of ECG signal may contain more than two cardiac diseases, and single-label classification cannot accurately judge all possibilities. Besides, single-label classification performs classification in units of segmented beats, which destroys the contextual relevance of signal data. Therefore, studying the multi-label classification of ECG signals becomes more critical. This study proposes a method based on the multi-label question transformation method-binary correlation and classifies ECG signals by constructing a deep sequence model. Binary correlation simplifies the learning difficulty of deep learning models and converts multi-label problems into multiple binary classification problems. The experimental results are as follows: F1 score is 0.767, Hamming Loss is 0.073, Coverage is 3.4, and Ranking Loss is 0.262. It performs better than existing work.

Keywords: Multi-label classification, Electrocardiogram, Classification of arrhythmia, Disease detection

Introduction

Human physiological signals contain human health information. Take the ECG signal as an example. It is widely used in diagnosing heart diseases and is currently the most commonly used tool for diagnosing heart diseases [1]. However, it is challenging to record and analyze a large number of physiological signals and manual diagnosis [2, 3], which requires rich professional knowledge and clinical experience. In addition, the diagnosis result is also affected by many subjective factors. In order to solve these problems, people have proposed automatic classification of physiological signals to improve the efficiency and accuracy of diagnosis [4, 5].

Research on the automatic classification of human physiological information has been ongoing. In the case of ECG signals, early researchers generally chose some traditional machine learning classifiers to process, and analyze physiological signal data, such as random forests, and support vector machines. However, the feature extraction of machine learning methods is mainly done manually [6, 7]. The main advantage of a deep neural network compared to machine learning is that it can automatically fit data features [8], without the need to use human experts to perform explicit feature extraction steps. In this way, the automatic classification of physiological signals is more efficient. In addition, due to its flexible structure and powerful learning capabilities [9], deep network models tend to perform better than classic machine learning classifiers [10].

At present, most of the current research work is to segment the heartbeat and then perform single-label classification. However, single-label classification can no longer meet the needs of automatic classification and diagnosis. In practice, an ECG signal usually contains multiple cardiovascular diseases simultaneously, so the study of multi-label ECG signal classification is necessary [11].

Multi-label problems are common in clinical ECG databases. In the multi-label problems, the relationship between patients and labels is one-to-many. The method of multi-label problems can be thought of from two angles. The first is the problem conversion method, that is, the method of transforming the data to adapt to the existing algorithm. This method mainly deals with the multi-label training data sample to convert the

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multi-label learning problem into other known learning problems for a solution; the second is the Algorithm adaptation method is to transform existing algorithms to adapt to data samples. This method expands or improves traditional machine learning methods to adapt to multi-labeled data learning problems. Huang et al. [12] used multiple random forest classifiers to construct a classifier chain in line with the clinical diagnosis process for multi-label classification of ECG signals. Subsequent single classifiers in the classifier chain are built on previous predictions. This algorithm brings massive computational consumption [13].

Multi-label human physiological signal data is not easy to obtain because the manual labeling cost of multi-label data is too large. It is not realistic to label a large number of physiological signals by human experts [14]. When only a limited amount of data is available, it is difficult for the deep learning algorithm to effectively learn the characteristics of a small number of signal data. The imbalance of physiological signal data exists widely, affecting the model's classification results [15, 16].

In this work, we combine Bi-LSTM with the binary correlation method and propose a method to solve the multi-label classification of ECG signals. Its advantage is that the network structure is relatively simple, and the number of training iterations is small. The rest of this paper is set as follows: Section "Related work" introduces the related work. Section "Our methods" gives the details of our methods. In section "Experiment", we compared the proposed approach to other methods. Section "Discussion" and section "Conclusion" concludes and presents future research directions.

Related work

Arrhythmia detection has always been the focus of human attention in medicine. Many researchers have done a lot of work in automatic classification. Most of the work done is the single-label classification of the heartbeat. The multi-label classification of physiological signals is relatively rare, and the difficulty of multi-label classification is greater than that of single-label classification.

Classical machine learning methods

Tithi et al. [17] compared six machine learning algorithms: logical regression, decision tree, nearest neighbor, naive Bayes, support vector machine, and artificial neural network. Different classifiers have different classification effects on different diseases. For example, Bayes classification is the best way to classify coronary artery disease. Nevertheless, the model is very complex. Subramanian et al. [18] focused on Feature Engineering. By denoising ECG signals and extracting R–R interval feature peaks

and PQRS peaks, they adopted support vector machine for classification and achieved good classification results. However, manually extracting features will affect the efficiency of the entire work. Singh et al. [19] extracted three features and compared the classification performance of five algorithms: support vector machine, decision tree, random forest, Bayesian classification, and artificial neural network. Under different features, the performance of the classifier has its advantages and disadvantages. A good classifier should adapt more to different features.

Bulbul et al. [20] compared the classification effect of the Backpropagation algorithm and the Kernel–Adatron algorithm on ECG using a multilayer perceptron and support vector machine and proposed a method to improve the calculation time and standard classification performance of MLP and SVM. Nonetheless, they don't provide experimental data support. Chakraborty et al. [21] compared the methods of centralized machine learning to classify ECG and proposed a deep learning method based on an autoencoder. However, they did not complete the experimental proof as well. Dohare et al. [22] used the method of principal component analysis to reduce 220 features to 14 and used support vector machines for classification. The sensitivity was 96.66%, and the specificity was 96.66%. Except, it is heavily dependent on Feature Engineering. Celin et al. [23] used a variety of machine learning classifiers to classify ECG signals and concluded that Bayesian classifiers have higher classification accuracy through comparison.

Deep neural network based methods

Li et al. [24] proposed a multi-label classification algorithm based on ECG signal characteristics to analyze and screen the specific characteristics of each disease to make the characteristics interpretable. Jiang et al. [25] combined the convolutional neural network with the GRU gating unit, proposed a graph-based convolutional network, and trained a three-layer graph network to study the correlation between multiple labels. Cai et al. [26] proposed a multimodule multi-label ECG classification model, which combines one-dimensional convolution, squeeze blocks, etc. It is worth mentioning that the article is classified into 55 categories. Li et al. [27] proposed selecting ECG signals based on kernelized fuzzy rough set and multi-label classification of CPSC2018 data set by selecting the optimal subset. Nejedly et al. [28] proposed a convolutional neural network with residual blocks, a two-way gated recurrent unit, and an attention mechanism. However, their model is overfitted.

Jia et al. [29] proposed a residual convolutional network with squeeze blocks called SE-ResNet34. The generalization performance and stability of this model need further experimental proof. Cai et al. [30] proposed two deep

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models, one combining the convolutional network and the recurrent network, and the other using a deep residual network. The authors preprocessing is to record premature beats by manually positioning the ECG. Bodini et al. [31] designed an integrated model composed of four neural networks and a threshold-based classifier to classify different characteristic heart rate abnormalities. The method uses 27 categories of signal data. This method is suitable for multi-class ECG classification with limited number of samples. Sun et al. [32] proposed a deep learning classification framework for the problems of unbalanced heartbeat types, similar heartbeat characteristics, and difficult classification, which is composed of Bi LSTM and Generic Advantageous Networks (GAN). The performance of the model is better than the best baseline method. Wang et al. [33] proposed an arrhythmia classification method based on the GAN model, which focuses on improving the classification accuracy of small samples. Sun et al. [34] proposed a medical sensor disease prediction framework based on cloud service, which not only ensures the quality of cloud service but also realizes the anomaly detection of medical data flow.

Other methods

Sun et al. [35] proposed a multi-label integrated classification model, which estimates the weight of multiple classifiers based on mutual information, and determines the classification results through a threshold. Alexander et al. [36] developed an autoencoder to make an ECG embedding for classification. Baydoun et al. [37] proposed a method that converts the ECG into digitized data to train by machine learning. Salem et al. [38] transferred the method from some image fields to ECG fields for classification. Satija et al. [39] developed an auto-classification method for diagnosing unsupervised conditions.

Data privacy protection

For medical data, privacy protection is vital. There has been some work to protect privacy. Liu et al. [40] first proposed an ETC method suitable for processing ECG data. This method can provide reconstructed signals of the same quality on the premise of protecting data privacy. Han et al. [41] proposed a scheme for selectively encrypting ECG data in an untrusted body sensor environment. That is, select part of the content for encryption so as to protect the data. However, this is under the assumption that the amount of data is huge, and encryption is very time-consuming. Ayman et al. [42] proposed a lossless ECG compression model based on privacy protection. Their approach is to use shallow neural networks to learn the characteristics of ECG. And they used a privacy protection protocol to reduce the external access

to data. Nisha et al. [43] implemented the triple data encryption standard to encrypt and expand the size of the key by using different keys three consecutive times. Triple data encryption standard can prevent attacks by expanding the key size of the data encryption standard so that no new encryption algorithm is designed.
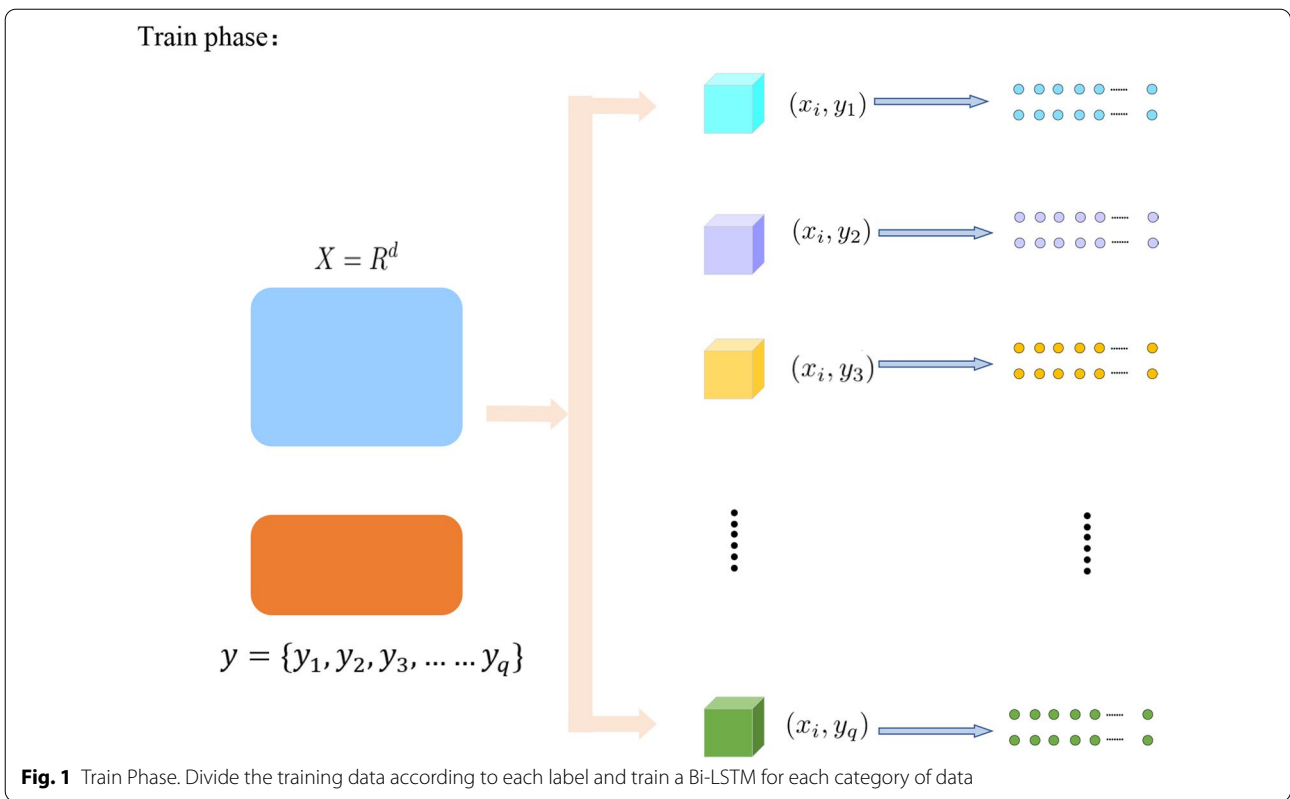
Our methods

Data preprocessing

We selected CPSC Database [44], the PTB Diagnostic ECG Database [44], Georgia database [44], St Petersburg INCART 12-lead Arrhythmia Database [44], and the PTB-XL Database [44] as our experiment data. The CPSC Database contains 6877 twelve lead ECG records, lasting from 6 to 60 s. The St Petersburg INCART Database contains 74 annotated records extracted from 32 Holter records, 30 min per record. The PTB-XL Database contains 21,837 clinical twelve lead ECGs with a length of 10 s and a sampling frequency of 500 Hz. The Georgia Database also contains 10,344 twelve lead ECGs with a length of 10 s and a sampling frequency of 500 Hz. Since there are unequal lengths between records, we uniformly take a 10-s segment for each record as a representative. Considering the different record lengths, we only take 10 s segments for each record and selectively discard the segments less than 10 s. Besides, the sampling frequency of the CPSC Database, Georgia Database, and PTB-XL Database is 500 Hz. The sampling frequency of PTB is 1000 Hz, and St Petersburg's is 257 Hz. We resample the PTB and St Petersburg by 500 Hz. We use the wavelet transform to denoise. Finally, we normalize the data.
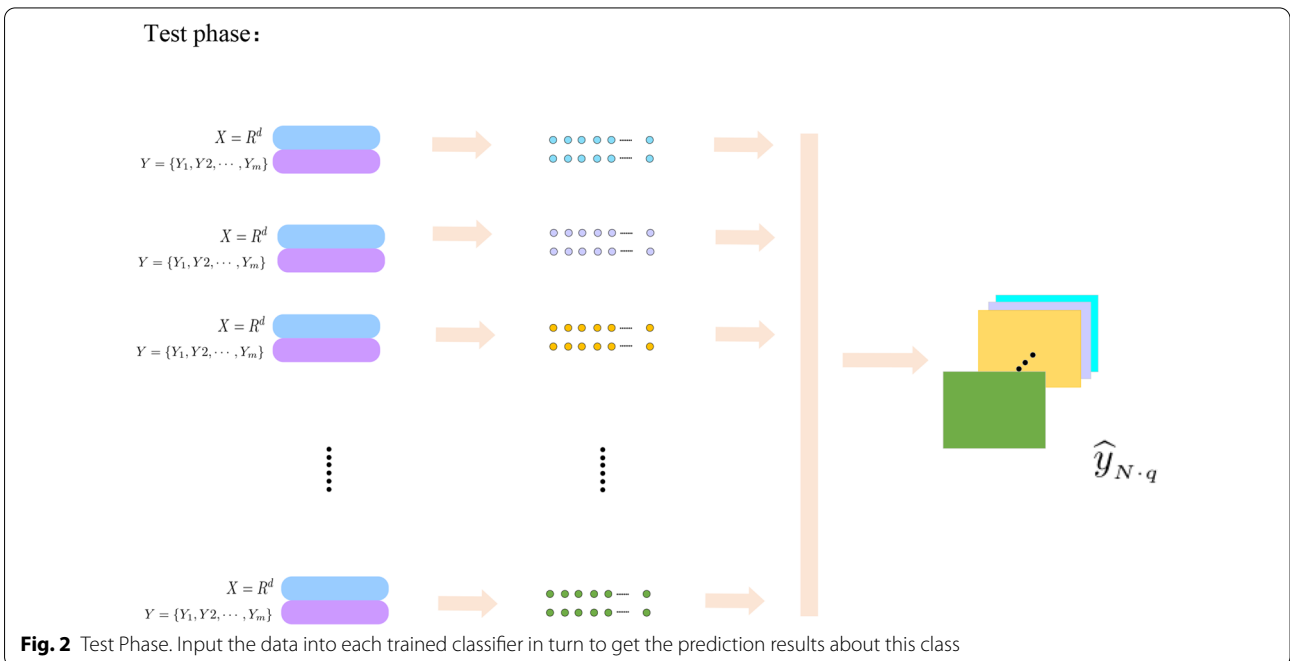
Binary relevance methods

In this paper, we perform a multi-label classification of physiological signals. We adopt a binary relevance method. For each class, we train a double-layer Bi-LSTM model as a classifier. For each class of classifiers, those that contain the label of that class belong to positive samples, and those that do not contain the label of this class belong to negative samples. The task of each model is to perform anomaly detection on positive and negative samples. Figures 1 and 2 is the model learning process. For each sample, x belongs to R^d, where d is the sample space. Labels $y = \{y_1, y_2, , y_3 \cdots y_q\}$. We split the dataset based on labels. Get the dataset (x_i, y_1), $(x_i, y_2), (x_i, y_3), \cdots (x_i, y_q)(1 < i < N)$ about each label. We train a binary classifier $f(*)$ per class as a counter example. The role of each binary classifier is to distinguish positive samples from negative samples. Finally, we get an $N \times q$ matrix by combining the inputs of each binary classifier. N is the number of samples, and q is the number of labels. This is the predicted output of the model.

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Fig. 1 Train Phase. Divide the training data according to each label and train a Bi-LSTM for each category of data
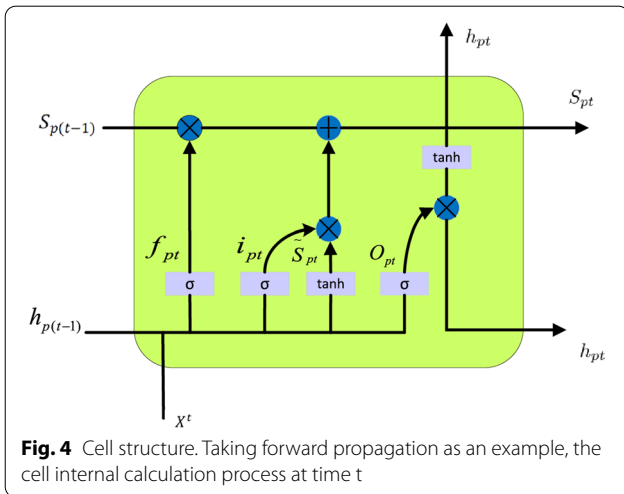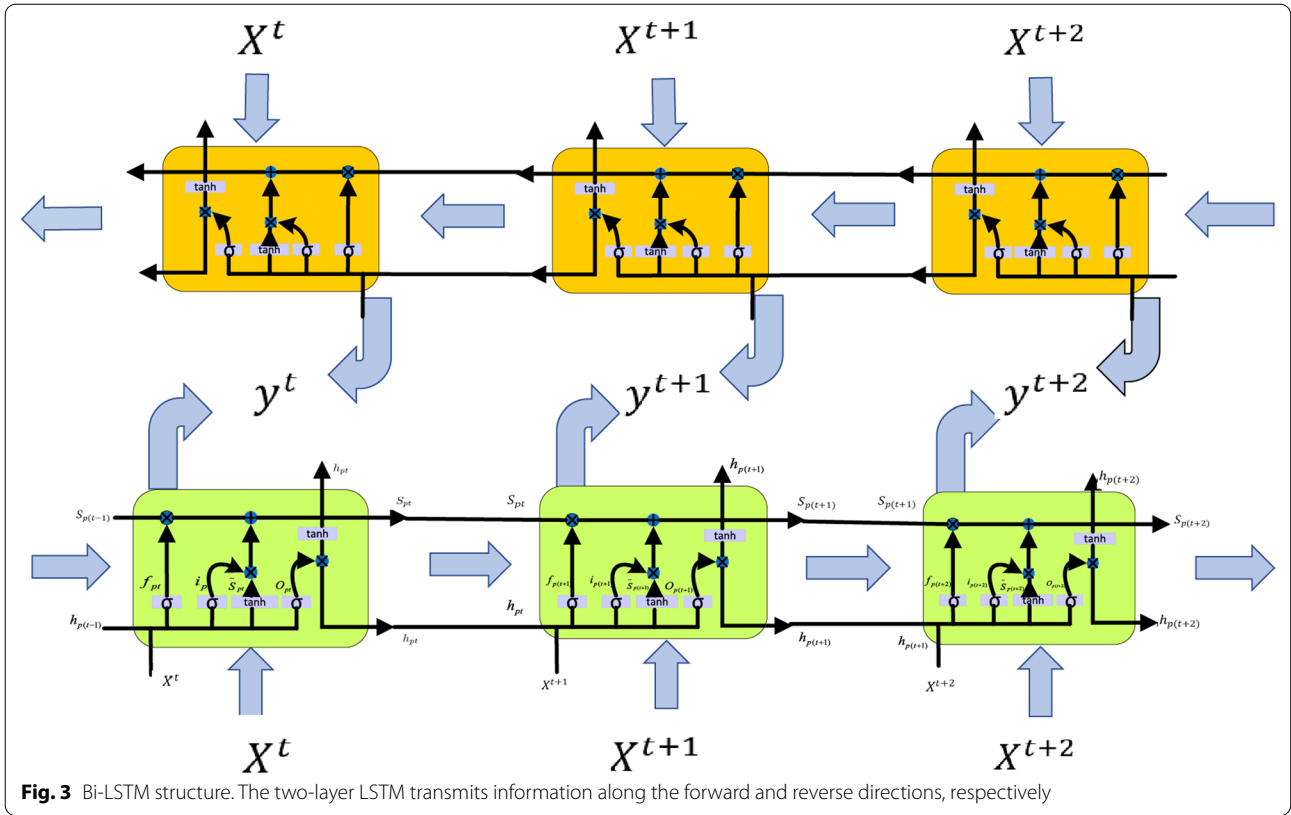
After passing through the sigmoid activation function, it is determined whether each sample belongs to class $y_j (1 < j < q)$ according to the threshold (Figs. 3, 4).

$$f_{pt} = \sigma(W_{pf} * [h_{pt-1}, X_t] + b_{pf}) \tag{1}$$

$$f_{rt} = \sigma(W_{rf} * [h_{rt-1}, X_t] + b_{rf}) \tag{2}$$

Fig. 2 Test Phase. Input the data into each trained classifier in turn to get the prediction results about this class

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Fig. 3 Bi-LSTM structure. The two-layer LSTM transmits information along the forward and reverse directions, respectively

Fig. 4 Cell structure. Taking forward propagation as an example, the cell internal calculation process at time t

$$i_{pt} = \tanh(W_{pi} * [h_{pt-1}, X_t] + b_{pi}) \quad (3)$$

$$i_{rt} = \tanh(W_{ri} * [h_{rt-1}, X_t] + b_{ri}) \quad (4)$$

$$\tilde{S}_{pt} = \tanh(W_{pc} * [h_{pt}, X_t] + b_{ps}) \quad (5)$$

$$\tilde{S}_{rt} = \tanh(W_{rc} * [h_{rt}, X_t] + b_{rs}) \quad (6)$$

$$S_{pt} = f_{pt} * S_{pt-1} + i_{pt} * \tilde{S}_{pt} \quad (7)$$

$$S_{rt} = f_{rt} * S_{rt-1} + i_{rt} * \tilde{S}_{rt} \quad (8)$$

$$o_{pt} = \sigma(W_{po} * [h_{pt-1}, X_t] + b_{po}) \quad (9)$$

$$o_{rt} = \sigma(W_{ro} * [h_{rt-1}, X_t] + b_{ro}) \quad (10)$$

$$h_{pt} = o_{pt} * \tanh(S_{pt}) \quad (11)$$

$$h_{rt} = o_{rt} * \tanh(S_{rt}) \quad (12)$$

Formulas 1 to 12 are calculation formulas of Bi-LSTM. The subscripts *pt* and *rt* stand for forward propagation and backward propagation, respectively. Equations 1 and 2 describe what information will be forgotten. Equations 3 and 4 represent the input gate, which controls the learning and updating of new information. Formulas 5 and 6 indicate that the hidden state at the last moment and the current time step data are activated by *tanh*. Formulas 7 and 8 represent the update process of the current

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cell state, which is determined by the information left at the previous moment and the information currently obtained together to determine the information update. Equations 9 and 10 represent output information. Formulas 11 and 12 represent the information calculation process of the current hidden state of the cell.

Experiment

Experiment setup

The experiment settings are as follows: In this experiment, we use Hold-out Method. After all datasets are merged, the whole dataset is divided as 90% and 10% for training and testing, respectively. The parameter settings of the model are as follows: the learning rate is 0.0001, the number of sample training batches is 200, the number of iterations is 10, the optimizer used is Adam, and the loss function is binary crossentropy.

Experiment evaluation

We introduced several multi-label evaluation indicators, namely F1 score, Hamming loss, coverage rate, and ranking label loss. Formulas 13 to 17 are their calculation formulas.

In formulas 13 and 14, $\widehat{y}_i$ is the predictions and y_i is the true labels. m is the number of samples. N in formula 15 is the number of samples. L is the number of labels, $Y_{i,j}$ is the true value of the jth component in the ith prediction result, $P_{i,j}$ is the predicted value of the jth component in the ith prediction result. For coverage error, the N is the number of samples, $M_{l_i}(i \in 1, 2, 3, \ldots, n)$ is the label l_n is ranked from large to small according to all prediction probabilities. In formula 17, L_i is the positive label set and the $\overline{L}_i$ is the

negative label set which is possibly higher than the positive label set.

$$
\begin{aligned}
PRE &= \frac{1}{m} \Sigma_{i=1}^{m} \frac{|\widehat{y}_i \bigcap y_i|}{|\widehat{y}_i|}, \\
REC &= \frac{1}{m} \Sigma_{i=1}^{m} \frac{|y_i \bigcap \widehat{y}_i|}{|y_i|}
\end{aligned}
\tag{13}
$$

$$
F_1 = \frac{2 * PRE * REC}{PRE + REC}
\tag{14}
$$

$$
H - Loss = \frac{1}{N} \Sigma_{i=1}^{N} \frac{XOR(Y_{i,j}, P_{i,j})}{L}
\tag{15}
$$

$$
Coverage = \Sigma_{i=1}^{N} \frac{\max(M_{l_1}, M_{l_2}, \ldots, M_{l_n})}{N}
\tag{16}
$$

$$
Ranking\ loss = \frac{\Sigma_{j \in L_i} \Sigma_{k \in \overline{L}_i} I(P_{ij} \leqslant P_{ik})}{|L_i| \cdot |\overline{L}_i|}
\tag{17}
$$

Result and comparison

In Tables 1 and 2, we make a comparison with the related work of multi-label classification. Our experiment is more complete and the evaluation metrics are more sufficient. Our F1-score was 0.092 higher than TCN and 0.14 higher than ResBlocks+GRU+GCN [45]. Besides, we also compare it with the TCN model in other metrics. According to the experiment results, our new methods get lower H-Loss, lower coverage error, and lower ranking loss. It proves that our method performs better.

Table 1 Compare advantages and disadvantages of machine learning methods

Model	Advantages	Disadvantages
Multi-classifier [17]	Each classifier has its own advantages	Manually extracting features
SVM [18]	Simple model	Manually extracting features
SVM & MLP [20]	Simple model combination	No experimental data support
Autoencoder [21]	Simple model construction	No experimental data support
PAC & SVM [22]	Classification performance well	Heavily rely on Feature Engineering

Table 2 Compare with TCN and other works

Model	F1 score	H-Loss	Coverage	Ranking loss
Bi-LSTM + Binary Relevance	0.767	0.073	3.40	0.262
TCN(2021)	0.675	0.10	3.63	0.317
Res-Blocks+Bi-GRU(2020)	0.564	–	–	–
Res-Blocks+Bi-GRU+GCN (2020)	0.627	–	–	–
1DCNN	0.481	–	–	–

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Discussion

In the field of disease diagnosis, for patients with multiple arrhythmias, research on multi-label problems is very necessary. Since most of the current work is a single-label classification study, it is not enough to identify all diseases. If it is used for medical examination, it can only be used to identify abnormal heartbeats. Multi-label classification is a difficult problem in classification problems. We simplify complex problems by building shallow sequence models to classify each type of labeled data separately. In order to get a better solution, we tried cropping different parts of each record, as well as cropping input signals of different lengths for training. In feature engineering, we use the wavelet transform to remove signal noise to improve classification accuracy. In summary, we provide a feasible scheme for the multi-label classification of ECG signals.

The datasets used for the experiments have no heartbeat labels. But each header file contains a diagnostic result, which has an impact on the model's observation of ECG signatures to make predictions. For example, the length of each record in the data set is not equal and can only be processed by uniformly intercepting a fixed length. However, since there is no heartbeat label, it is unknown whether the intercepted part contains abnormal heartbeats. In this case, a patient with heart disease records that the intercepted 10-s heartbeats are all normal heartbeats. Unfortunately, we may mark this normal heartbeat segment with an exception diagnostic result. In addition, multi-label classification adopts a binary correlation method, which ignores the correlation between labels by default. For example, when we classify the y_1 class, all samples containing y_1 are positive samples, and the samples of $\{y_2, y_3 \cdots, y_q\}$ is a negative sample. Nevertheless, when a class is paired with many classes like y_1 and y_2, y_1 and y_3, y_1 and y_5. We need a deeper model to observe the data when training a binary classification model for class y_1, because the diversity of the data increases. The samples of $[y_1, y_2]$ and $[y_1, y_3]$ are not exactly the same, and the model needs more parameters to memorize. Data imbalance is also a major difficulty affecting the classification effect. At present, the commonly used methods to balance data include the following categories: the first category achieves almost the same number of category samples through hierarchical sampling. Secondly, by changing the weight to balance the data, we can balance the data by adjusting the importance of the sample weight in the training process. The third type is data enhancement. Some data models can be used to generate false data or add noise and expand data on the basis of existing data.

Next, we consider incorporating the correlation between tags into our learning objectives. Graph neural networks would be used to construct graph structure data to learn the potential relationship between data, so as to better carry out multi-label classification. In addition, we will also consider new data balancing methods.

Conclusion

In this article, we analyze the importance of the multi-label classification of ECG signals and propose a classification scheme combining binary correlation methods as required. We build a set of shallow neural networks based on Bi-LSTM to learn different classes of samples. Different from other methods, we use a more lightweight network structure, and we decompose the complex multi-label classification into multiple simple binary classification tasks. The experimental results demonstrate the effectiveness of our method.

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