MULTIPLE INSTANCE LEARNING FRAMEWORK USED FOR ECG PREMATURE CONTRACTION LOCALIZATION

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Abstract: We propose the model combining convolutional neural network with multiple instance learning in order to localize the premature atrial contraction and premature ventricular contraction. The model is based on ResNet architecture modified for 1D signal processing. Model was trained on China Physiological Signal Challenge 2018 database extended by manually labeled ground truth positions of premature complexes. The presented method did not reach satisfying results in PAC localization (with dice = 0.127 for avg-pooling implementation). On the other hand, results of localization of PVCs were comparable with other published studies (with dice = 0.952 for avg-pooling implementation).

Keywords: EEICT, ECG, PAC, PVC, CNN, MIL, arrhytmia, localization

1 INTRODUCTION

Premature atrial contractions (PAC) are one of the common diagnosed arrhythmias characterized by premature heartbeat originated in atria. When occurred isolated, they are not life-threatening. When combined with more underlying medical conditions, PAC could result in early death. Detection of PAC is often combined with early diagnostics of atrial fibrillation (AF) [1]. PACs, from the point of view AF detection, are recorded and quantified by 24 h Holter recordings, and may thus serve as a surrogate marker for paroxysmal AF [2].

Primary, PAC were detected by decision rules mostly based on rhythm features [3]. Since PAC is morphologically very similar to normal QRS complex, morphological features are not usually used for detection (contrary to detection of premature ventricular contractions, PVC). On the other hand, in most of the previously published approaches of PAC detection, temporal features based on RR intervals were used [4]. Such approach requires one-to-one QRS complex detection, which could end up being very time consuming.

Deep-learning approaches are current state-of-the-art methods for PAC classification and detection. Here, we propose method based on deep neural network. Our model uses only global labeling from train dataset and does not require QRS complex detection for identification of local abnormalities in ECG. We trained the model on data demonstrated mentioned arrhythmias (PAC and PVC). We, thus, tested the model capability to localize pathologies with characteristic temporal and morphological manifestation, respectively. Presented results are the attempt to extend the previous work [5]. Briefly, the algorithm for PAC localization contains several steps. First, ECG signal is classified into selected arrhythmia types. Second, the feature signal is derived using so called multiple instance learning (MIL) tool. Finally, PAC are localized via peak detection in the feature signal. Following chapters describe the proposed method in more detail.

2 DATASET

Recordings analysed in this paper come from publically available database from China Physiological Signal Challenge 2018 (CPSC2018) [6]. The database consists of recordings assigned to 9 different arrhythmias. To create the model, we used only three labels (global annotations): Normal, PVC and PAC. Altogether, 2145 signals were used (653, 574 and 918 for PVC, PAC and Normal, respectively). The database was split into the training and testing datasets in the 8:2 ratio. All the provided signals included 12 lead recordings. Proposed model is also suited for the use of reduced number of recorded leads. In the database, only global annotations (e.g. label "PVC" means that there are some PVCs in the whole ECG) are available. To evaluate the results of PAC/PVC localization, the local true PAC/PVC positions are needed. We, therefore, analysed the whole dataset manually and added the positions of pathological complexes in the database.

3 MODEL ARCHITECTURE

3.1 CLASSIFICATION NETWORK

Convolutional neural network (CNN) was chosen for presented algorithm. The model is based on residual neural network (ResNet) [7]. ResNet CNN is mostly used for image processing, so we modified it for signal processing. All parts, which are originally designed to be applied on 2D data (images) were replaced by operators suitable for 1D data (signals). Classification network follow up is presented on Figure 1. The input ECG enters the model to CNN network, which consists of repeating block of convolutional layer, batch normalization and ReLu activation function. Max pooling or average pooling are applied after. All convolutional blocks are followed by sigmoid activation function and global max pooling layer, out of which final label for the signal is gained.

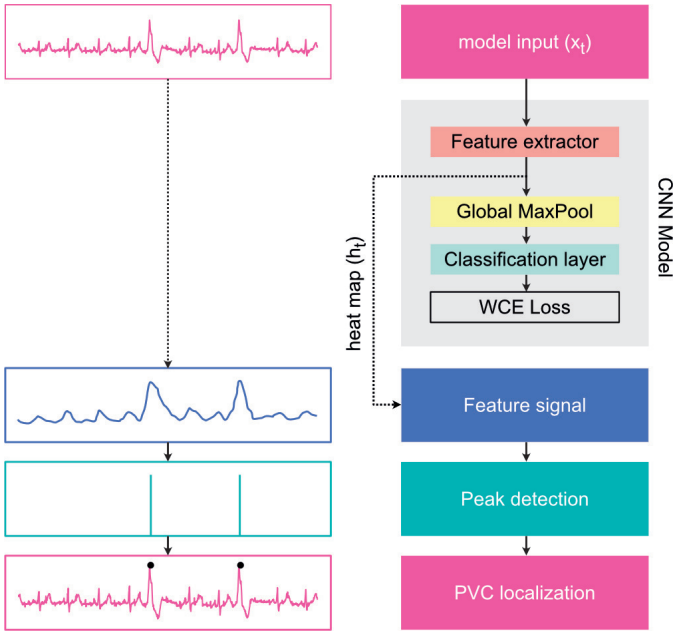

Figure 1: Architecture of proposed model. CNN Model: $Conv(3, i \times 12)$ - convolution layer with filter size 3 and $i \times 12$ filters; $MaxPool(2,2)$ - max pooling with filter size 2 and stride 2.

3.2 MIL FRAMEWORK

MIL framework [8] process the output of previous applied convolutional layers. The effect of convolution is in the multiple sub-sampling of the input ECG. The output signal can be referred as MIL feature signal. The feature signal contains the information of pathology (PAC/PVC) position likelihood: the peaks in the feature signal correspond with the part(s) of the input ECG contributing the most significantly to the final classification. MIL feature signal is of variable length (bag of instances) and is projected to a single output label by global max pooling. Global pooling layer was followed by standard weighted cross-entropy loss (WCE), which is defined as:

$$WCE_{MIL} = w_{pos} t \log\left(\max_i s_i\right) + w_{neg}(1-t)\log\left(1-\max_i s_i\right), \tag{1}$$

where s_i is MIL feature signal (which is the output of the sigmoid activation function), t is a binary signal label, w_{pos} and w_{neg} are weights for positive and negative classes, respectively. The weight itself is in inverse proportion to the frequency of class label. The feature signal, representing the arrhythmia position likelihood, is an input for further processing.

3.3 MODEL IMPLEMENTATION DETAILS

Since the dataset used for training the model is not initially balanced, data augmentation was needed. Various augmentation techniques were applied on ECGs. Particularly, each lead was randomly multiplied by 0.3 and signal was stretched by 20 %. Circular shifting of selected signal parts was performed, too. Batch size, which is constant, does not reach the size of every analysed signal, so zero-padding was applied. More implementation specifications of the model are: optimisation with Adam optimiser ($\beta_1 = 0.9$; $\beta_2 = 0.999$) [9]); decoupled weight decay regularization ($\lambda = 10^{-5}$) [10]; initial learning rate 0.001 (with every 50 epochs multiplied by 0.1). Weighted cross-entropy loss was applied in the training phase. Batch size was initially set to 32 and weights were set via Xavier initialisation [11].

3.4 ARRHYTHMIA LOCALIZATION

Premature complexes localization is performed by the peak detector applied on MIL feature signal. The detector was set up with three specific parameters: threshold, minimal distance and peak prominence [12]. The parameters' optimal values were set to: minimum-maximum of all feature signals (likelihood maps) for each arrhythmia, respectively; 0 - min-max range as for peak prominence; 0 - 2 s for minimal distance between peaks. These values were obtained by Python implementation of Bayesian optimization [13].

4 RESULTS AND DISCUSSION

Results reached by presented model are summarized in Table 1. Main goal of this study was to extend our previous model in order to reach the results comparable with another recent reports. From Table 1 (see gray rows), this was achieved for PVC localization performed by the model with max pooling layer (e.g. compare with [14]). The results for PAC localization (black rows in the Table 1), were not satisfying. The reason for such difference in localization of PVC and PAC may lay in their characteristics, mostly the morphological point of view. On Figure 2, we can see that QRS complexes labeled as PAC (both red and grey) are not as different in it's shape, duration and power, compared to the normal QRS complexes. Features distinguishing PAC from normal QRS are mainly temporal. From Table 1, it is obvious that presented MIL framework is not as sensitive to temporal pathology manifestations as to morphological ones. As a result, PACs cannot be accurately localized via obtained MIL feature signal.

In future work, we well focus on the improvement of PAC localization. We suppose that the main

temporal feature contributing to the PAC recognition is the ECG part corresponding to the compensation pause. We therefore believe that appropriate post-processing of MIL feature signal could result in improved detection efficacy. Further enhancement of the method may consist in extension of the model for most common arrhythmias (such as atrioventricular blocks, atrial fibrillation, atrial flutter, etc.).

Method	Arrhytmia	Prec.	Recall	Dice	ACC
MIL - max-pool	PAC	0.032	0.187	0.055	0.506
MIL - avg-pool	PAC	0.097	0.181	0.127	0.789
MIL - max-pool	PVC	0.922	0.805	0.810	0.975
MIL - avg-pool	PVC	0.877	0.752	0.952	0.967

Table 1: Results of PAC localization compared to PVC localization, coming from the same model.

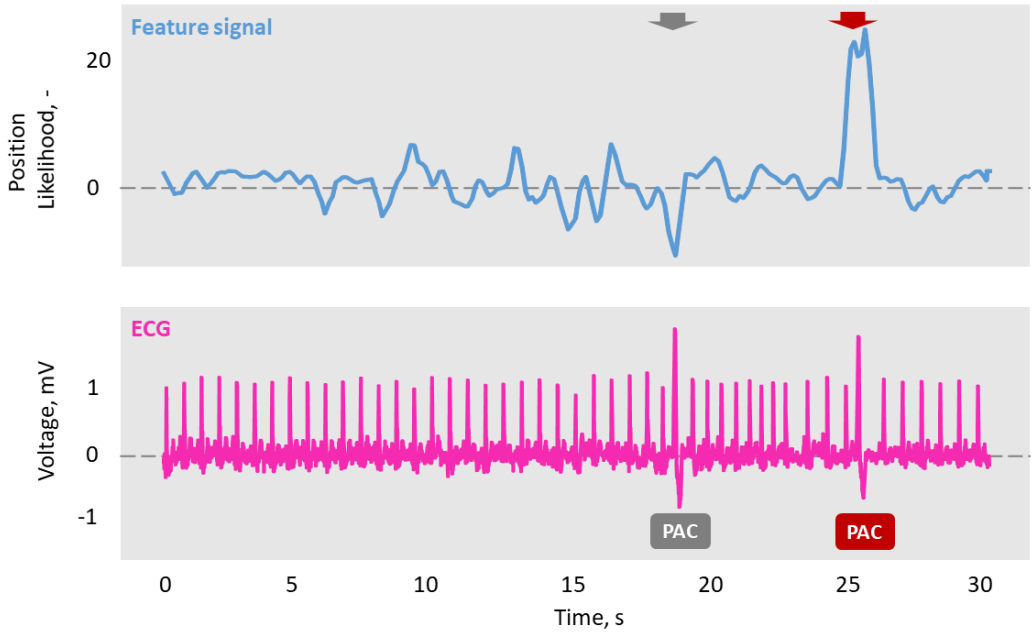

Figure 2: MIL feature signal and PAC beats detection. PAC position likelihood is represented by upper blue signal, where the amplitude of the signal represents the contribution to the final classification. One PAC was detected, one was not.

5 CONCLUSION

In conclusion, proposed method was previously proven to work well on localization of PVC, which has significantly different morphology as compared to normal QRS complex. In case of PAC, the results were not satisfactory. One of the most benefits of presented model is almost whole absence of pre- and post-processing of the output. Adding the post-processing part could result in better outcome of the model for PAC localization, which will be the subject of further research.

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