

Personalized Zero-Shot ECG Arrhythmia Monitoring System

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Abstract. This project proposes a low-cost and highly accurate ECG monitoring system to detect ECG arrhythmias for wearable mobile sensors. Earlier supervised learning approaches required normal as well as abnormal heartbeats to train classifiers. However, in the real world, such training data for a person is not available if the person is healthy with no history of cardiac disorder. In this project (i) I propose null space analysis on the healthy signal space obtained via sparse dictionary learning. (ii) I introduce a sparse representation-based domain adaptation technique to project other existing users' normal and abnormal signals onto the new user's signal space, allowing training the classifier without having any abnormal heartbeat of the new user. Therefore, zero-shot learning can be achieved without the need for the synthetic abnormal heartbeat of the new user. Experiments performed on the benchmark MIT-BIH ECG dataset show that when this domain adaptation-based training data generator is combined with a 1-D CNN classifier, it outperforms prior works by a very good margin. Afterwards, by combining (i) and (ii), an ensemble classifier is proposed that further improves the performance. Implementation of the proposed technique is available at this link.

Keywords: Personalised ECG monitoring · Zero-Shot Anomaly Detection · Domain based adaptation · Sparse Representation · Dictionary Learning.

1 Introduction

Cardiac arrhythmia is a predictor of a major health threat such as heart failure, hypertension, or stroke. Past statistics show that cardiovascular diseases continue to be the number one cause of death. Approximately 32.84% of all deaths in 2019 were caused by cardiovascular diseases [1]. Detecting cardiac arrhythmias in real time can significantly reduce the number of casualties. Numerous methods have been proposed for the identification of electrocardiogram (ECG) waveforms using machine learning and signal processing, such as support vector machines (SVMs) [2], frequency analysis [3], and statistical analysis [4]. The problem with these methods is that they are based on a set of hand-crafted features, which makes them unfit for changes in ECG patterns. The morphology of the ECG varies

from person to person and even from heartbeat to heartbeat. In addition, it is unique to each individual according to their cardiovascular system. Thus, it has become essential to design a person-based arrhythmia detection system, which is not possible by the traditional methods mentioned above.

Such personalized classification and arrhythmia detection systems are proposed in [5], [6], [7]. Such methods require both normal and abnormal heartbeats from a patient to train a dedicated classifier, and thus they cannot serve as an early detection system for a healthy person with no history of such diseases. The landmark study in [8] has proposed a system to model the degradation between normal and abnormal beats by learning linear filters from several patients with arrhythmias. After that, for a new user, the potential abnormal beats can be synthesized directly from the normal beats, and finally, a dedicated 1-D CNN is trained over the synthesized abnormal heartbeats and real normal heartbeats to monitor the signs of arrhythmia in the user.

Sparse approximation (SA) is a method that involves selecting a set of wave-forms, often referred to as a dictionary or basis set. A signal is then represented as a linear combination of only a few elements from this dictionary—this is known as a sparse representation of the signal. SA has been successfully used in ECG classification tasks. However, these methods attempt to learn SA dictionaries from the extracted features, and so their performance is still limited by the discrimination power of the handcrafted features. Another way to bypass the need to collect abnormal ECG data for a person is to use outlier detection schemes.

In this project, I introduce a novel approach to improve normal heartbeat detection performance using advanced machine learning techniques. The key innovation is that the method requires no abnormal beats and only a small number of normal beats from the target user. First, I introduce the concept of the left null space matrix of the normal dictionary, which enables a faster computation of the approximate representation error. Additionally, a domain transformation technique is employed to project a patient’s heartbeats into the space of a new user’s heartbeats—without requiring any knowledge of the new user’s abnormal data.

2 Related Work

2.1 Sparse Representation Based Classification

Let $\mathbf{s}_i^p \in \mathbb{R}^N$ be the i^{th} ECG heartbeat of the p^{th} user which can be represented by a linear combination of n wave-forms, i.e.,

$$\mathbf{s}_i^p = \mathbf{D}^p \mathbf{x}_i^p, \quad (1)$$

where $\mathbf{D}^p \in \mathbb{R}^{N \times n}$ is the dictionary of these wave-forms (atoms) and $\mathbf{x}_i^p \in \mathbb{R}^n$ is the corresponding coefficient vector. In the case of being overcomplete ($n > N$) the representation will be enriched; however, the representation formed by (1) will not be unique. It is possible to make it unique by making it represent the

signal in \mathbf{D}^p with the smallest number of significant coefficients (i.e. sparseness), i.e.,

$$\min_{\mathbf{x}_i^p} \|\mathbf{x}_i^p\|_{\ell_0^n} \text{ subject to } \mathbf{D}^p \mathbf{x}_i^p = \mathbf{s}_i^p, \quad (2)$$

which is known as the sparse representation of the signal \mathbf{s}_i^p .

Sparse Approximation Error (SAE) is used to detect anomalies, which can be calculated as

$$r_i = \|\mathbf{D}^p \hat{\mathbf{x}}_i^p - \mathbf{s}_i^p\|_2^2, \quad (3)$$

where \mathbf{D}^p is the user-specific dictionary for the normal heartbeats. Normal beats are assumed to be collected for a limited duration from a new user without obtaining or labeling the abnormal beats. Having the pre-trained dictionary, when a new ECG beat \mathbf{s}_i^p comes into the picture, its sparse coefficients are obtained with the OMP algorithm. Then, the estimation $\hat{\mathbf{x}}_i^p$ is back-projected to the dictionary and the residual or SAE is calculated as in Eq. (3). Then, they use a simple thresholding method on r_i to detect anomaly i.e., detect anomaly if $r_i > \gamma$, where γ is the defined threshold.

2.2 Abnormal Beat Synthesis for Early Arrhythmia Detection

Using both normal and abnormal ECG beats collected from a patient, an anomaly detection system for ECG signals can be trained effectively. However, in real-world scenarios—particularly when aiming to develop an early warning system—this approach faces a significant challenge: for a newly registered healthy user, no abnormal beats are typically available. To address this issue, the authors of [8] proposed a personalized abnormal beat synthesis (ABS) method.

In this system, when a new user joins, their normal ECG beats are recorded over a short duration. Since it is assumed that these signals do not contain any anomalies, synthetic abnormal heartbeats are generated based on the collected normal data.

To achieve this, the authors first modeled how common heart conditions affect the morphology of ECG beats. Specifically, they assumed that certain heart diseases induce predictable distortions in normal heartbeats, transforming them into characteristic abnormal patterns. This transformation was modeled as a linear time-invariant (LTI) system. Mathematically, it is assumed that any observed abnormal signal \mathbf{s}_A^l for user l can be approximated as a linearly degraded version of an underlying (latent) normal signal \mathbf{s}_N^l :

$$\mathbf{s}_N^l \circledast \mathbf{h}^l = \mathbf{s}_A^l, \quad (4)$$

where $\mathbf{h}^l \in \mathbb{R}^M$ is the M -length filter coefficient vector of the LTI system and \circledast is the convolution operation. As part of the process of obtaining a filter bank, the authors first select an average normal beat for a user l , by taking the average of all normal beats of the user and finding the normal beat closest to the average. Then, using this average normal beat $\bar{\mathbf{s}}_N^l$, for each abnormal observation \mathbf{s}_A^l , a filter \mathbf{h}^l is estimated from Equation $\bar{\mathbf{s}}_N^l \circledast \mathbf{h}^l = \mathbf{s}_A^l$ via regularized least-squares

filtering. The final **ABS** filter library is the remaining set of filters after similar ones have been pruned.

When a new user p registers to the system, their average normal beat \bar{s}_N^p is computed based on the collected normal beats. A filter \mathbf{h}^l is then selected from the previously constructed ABS filter library of an existing user l . Using this filter, a synthetic abnormal beat for user p is generated by applying the filter to their average normal beat, i.e., \bar{s}_N^p as $\mathbf{s}_A^p = \bar{s}_N^p \otimes \mathbf{h}^l$.

Through this process, personalized training data for user p is constructed using their own normal beats along with the synthetically generated abnormal beats derived via the ABS filter library.

This artificial generation of personalized data allows for training a conventional classifier, such as a 1-D (CNN). Figure 1 illustrates how linear degradation filters derived from an existing user can be applied to the normal ECG signals of a new user to simulate abnormal beats.

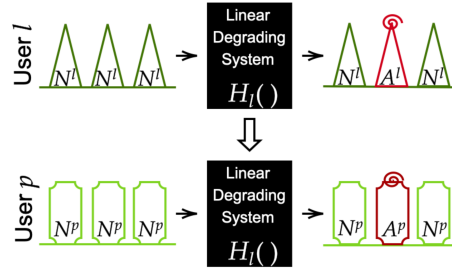


Fig. 1: The schema of ABS, the estimated linear degrading system of the existing user j can be applied to the healthy ECG beats of a new user p to synthesize possible abnormal beats for user p .

3 Proposed Solution

3.1 Null Space Projection Based Classifier (NPE)

The proposed method is based on the assumption that a normal ECG beat from a user can be accurately represented using a dictionary learned from that user's own healthy beats. Each normal beat \mathbf{s}_i^p is approximated as $\mathbf{s}_i^p = \mathbf{D}^p \mathbf{x}_i^p + \mathbf{e}$, where \mathbf{D}^p is the user-specific dictionary, \mathbf{x}_i^p is a sparse coefficient vector, and \mathbf{e} is the residual error. Since solving the original ℓ_0 -minimization problem is NP-hard, it is relaxed into a convex ℓ_1 -minimization form using the Lasso formulation: $\min_{\mathbf{x}_i^p} \|\mathbf{s}_i^p - \mathbf{D}^p \mathbf{x}_i^p\|_2^2 + \lambda \|\mathbf{x}_i^p\|_1$, which yields stable solutions even in noisy conditions. To learn the dictionary \mathbf{D}^p and sparse coefficients \mathbf{X}^p from a collection of normal beats \mathbf{S}^p , a Lasso-based dictionary learning method is used: $\min_{\mathbf{X}^p, \mathbf{D}^p} \|\mathbf{S}^p - \mathbf{D}^p \mathbf{X}^p\|_2^2 + \lambda \|\mathbf{X}^p\|_1$. Unlike previous approaches that

use K-SVD with a fixed sparsity level, this method allows more flexible sparsity. The core insight is that normal ECG beats tend to be well reconstructed by the dictionary, resulting in low sparse approximation error (SAE), while abnormal beats produce higher errors, making classification possible based on reconstruction performance.

3.2 Sparse Representation Based Domain Adaptation

As previously noted in several studies, ECG morphology varies between individuals due to differences in their cardiovascular systems [9]. This inter-individual variability has recently gained attention in the context of ECG-based biometric identification [10], [11]. Building upon the work of [8], where the transformation of a normal heartbeat into an abnormal one was modeled using a linear transformation, this project presents an investigation into the relationship between the ECG morphologies of users l and p . In what follows, we show that this relationship can also be effectively modeled by a linear transformation.

Specifically, for any ECG heartbeat signal \mathbf{s}_i^l from user l , whether normal or abnormal, we aim to linearly transform it using a matrix $\mathbf{Q}_{l \rightarrow p}$ such that the transformed signal $\hat{\mathbf{s}}_i^l = \mathbf{Q}_{l \rightarrow p} \mathbf{s}_i^l$ resembles the morphology of heartbeats from user p . We emphasize that this transformation matrix — referred to as the **Morphology Transformation Matrix (MTM)**, $\mathbf{Q}_{l \rightarrow p} \in \mathbb{R}^{N \times N}$ — is designed specifically to map the ECG morphology space of user l into that of user p . An illustration of this transformation is provided in Figure 2.

However, learning such transformation matrices is inherently challenging due to the limited availability of healthy beats and the lack of abnormal data for user p , which can lead to overfitting in many learning algorithms.

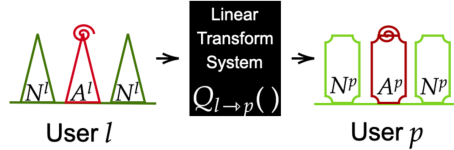


Fig. 2: Linear Morphology Transformation System

Based on the discussion above, we formulate our MTM learning problem as finding a transformation matrix, $\mathbf{Q}_{l \rightarrow p} \in \mathbb{R}^{N \times N}$, which results in the \mathbf{S}^l being sparsely represented in \mathbf{D}^p after transformation:

$$\begin{aligned} \hat{\mathbf{Q}}_{l \rightarrow p}, \hat{\mathbf{X}}^l = \arg \min_{\mathbf{Q}_{l \rightarrow p}, \mathbf{X}^l} & \|\mathbf{Q}_{l \rightarrow p} \mathbf{S}^l - \mathbf{D}^p \mathbf{X}^l\|_2^2 \\ & + \lambda \|\mathbf{X}^l\|_1 + \gamma \|\mathbf{S}^l - \mathbf{Q}_{l \rightarrow p} \mathbf{S}^l\|_2^2 \quad (5) \end{aligned}$$

where λ and γ are positive hyper-parameters and the last term, $\gamma\|\mathbf{S}^l - \mathbf{Q}_{l \rightarrow p}\mathbf{S}^l\|_2^2$, is a trade-off term. For large values of γ , it ensures that $\hat{\mathbf{S}}^l$ does not deviate much from \mathbf{S}^l . For small values of γ , $\hat{\mathbf{S}}^l$ fits better onto dictionary \mathbf{D}^p . Without the last term, or for $\gamma = 0$, Eq. (5) has a trivial minimum at $\mathbf{X}^l = 0$ and $\mathbf{Q}_{l \rightarrow p} = \mathbf{0}$. In other words, Eq (5) solves for a mapping that compromises between projecting the signal onto subspace \mathbf{D}^p and remaining close to the original signal. In order to solve the problem defined in Eq. (5), we follow an iterative optimization strategy —

Algorithm 1 SR-based MTM Finding Algorithm

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1: procedure DOMAIN_ADAPTATION( $\mathbf{D}^p, \mathbf{S}^l, \gamma, \eta$ , epochs)
2:    $\mathbf{Q}_{l \rightarrow p} \leftarrow \mathbf{I}_{N \times N}$ 
3:   for  $i \leftarrow 1$  to epochs do
4:      $\hat{\mathbf{S}}^l \leftarrow \mathbf{Q}_{l \rightarrow p}\mathbf{S}^l$  ▷ Domain Adaptation
5:      $\hat{\mathbf{s}}_i^l \leftarrow \frac{\hat{\mathbf{s}}_i^l}{\|\hat{\mathbf{s}}_i^l\|_2}$  ▷ Normalization
6:      $\mathbf{X}^l \leftarrow \arg \min_{\mathbf{X}^l} \|\hat{\mathbf{S}}^l - \mathbf{D}^p \mathbf{X}^l\|_2^2 + \lambda \|\mathbf{X}^l\|_1$ 
7:      $\nabla \mathbf{Q}_{l \rightarrow p} \leftarrow ((1 + \gamma) \mathbf{Q}_{l \rightarrow p} - \gamma \mathbf{I}_{N \times N}) \mathbf{S}^l \mathbf{S}^{lT}$ 
        $\quad - \mathbf{D}^p \mathbf{X}^l \mathbf{S}^{lT}$ 
8:      $\mathbf{Q}_{l \rightarrow p} \leftarrow \mathbf{Q}_{l \rightarrow p} - \eta \nabla \mathbf{Q}_{l \rightarrow p}$ 
9:   end for
10:  return  $\mathbf{Q}_{l \rightarrow p}$ 
11: end procedure

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3.3 Ensemble Learning

This project gives a probabilistic approach to automatically determine the classification threshold based on each user’s generated training data (the training data generation details are provided in Section 4). To begin with, we compute the null space projection errors (NPEs) for both normal and abnormal beats as described in Section 3.1. Using these values, we fit two probability distributions—one for normal and one for abnormal errors—by estimating their parameters via maximum likelihood estimation (MLE). During the testing phase, we calculate the likelihood that a given test beat’s NPE belongs to each distribution and classify it based on the higher likelihood. Rather than relying solely on this probabilistic method for classification, we also train a user-specific 1-D CNN. When the CNN exhibits low confidence in its prediction, we fall back on the probabilistic model to make the final decision. This collaborative use of models forms an ensemble classifier that combines the strengths of both approaches.

4 Results

4.1 Experimental Setup

This project uses ECG data from the benchmark MIT-BIH arrhythmia database [12], [13]. The database consists of 2-channel ECG records from 48 different patients. Each record is approximately 30 minutes long with beat labels for different types of heartbeats.

Each beat is represented by 128 samples by resampling it. A single beat and a beat-trio are the two most often used forms of showing a beat. Regarding both of them, the reference point for the given beat is regarded to be the central R-peak. We locate the nearby R-peaks, move 10% inward towards the central peak, extract that segment, and resample to 128 samples to get the single-beat representation. We build a beat-trio to grasp the temporal morphological features of the beats. Once more finding the adjacent R-peaks will help us to obtain the beat-trio representation; now, we move 10% outward, hence the segment comprises the adjacent R-peaks. We find any R-peaks using the annotations from the MIT-BIH database.

In this study the Association for the Advancement of Medical Instrumentation (AAMI) recommendations [14] are followed: AAMI categorizes heartbeat types as N (beats occurring in the sinus mode), V (ventricular ectopic beats), S (supraventricular ectopic beats), F (fusion beats) and Q (uncategorizable beats). In this study, we considered N beats as normal beats and the other 4 types as abnormal beats. Among 48 patients 34 records are used. Patients 102, 104, 107, 217 are excluded because their records come from a pacemaker. Patients 105, 114, 201, 202, 207, 209, 213, 222, 223, and 234 are excluded as they show high variations among their beats. According to the AAMI recommendation, only normal heartbeats captured during the first five minutes are used as training data for a user's classifier; any abnormal beats are not included. The datasets of the remaining 33 users are then combined with this small set of typical heartbeats using the algorithms outlined in Section 4.2 (e.g., with/without domain adaptation, ABS, etc.). The test data for that user consists of the abnormal beats during the first five minutes and the beats during the next twenty-five minutes.

The performances of the proposed and competing methods are compared using the following metrics:

$$\text{F1-Score} = 2 \cdot \frac{\text{Precision} \cdot \text{Recall}}{\text{Precision} + \text{Recall}}, \quad (6)$$

$$\text{Specificity} = \frac{\text{TN}}{\text{TN} + \text{FP}}, \quad (7)$$

$$\text{Precision} = \frac{\text{TP}}{\text{TP} + \text{FP}}, \quad (8)$$

$$\text{Recall} = \frac{\text{TP}}{\text{TP} + \text{FN}}, \quad (9)$$

where a positive response corresponds to an abnormal beat, and true positives (TP), true negatives (TN), false positives (FP), and false negatives (FN) are computed from the predicted and ground-truth binary labels. We used the macro-average method for overall tables unless otherwise noted. In some specific cases, we analyzed user-specific performance metrics.

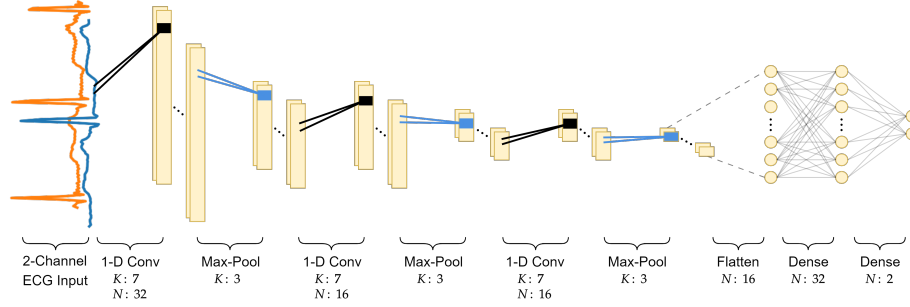


Fig. 3: CNN architecture used in all experiments. K is the filter size, and N is the number of neurons in the layer.

4.2 1-D CNN Classifier with ABS vs SR-based Domain Adaptation

To build a personalized ECG anomaly detection system for each user, we adopt the state-of-the-art method from [8] and train it using user-specific data. Following AAMI guidelines, only the normal heartbeats from the first five minutes of the user’s recording are used for training. This limited data is then augmented using the datasets of the remaining 33 users through three different strategies:

(i) **Baseline Method:** Normal beats of the target user are combined with both normal and abnormal beats from other users, ensuring balance between the two classes.

(ii) **Abnormal Beat Synthesis (ABS):** Synthetic abnormal beats are generated and added to the target user’s normal beats, as described in Section 2.2.

(iii) **Domain Adaptation:** A sparse representation-based domain adaptation approach transforms signals from other users to match the target user’s style using 33 learned MTMs. Both normal and abnormal beats are transformed and included in the training set.

All methods use the same 1-D CNN architecture for a fair comparison. The network includes three convolutional layers (kernel size 7, stride 1) each followed by max-pooling (stride 3) and **tanh** activation, followed by two fully connected layers (ReLU, log-softmax). Training uses an 80-20 train-validation split with early stopping (15 epochs) based on validation loss. We use cross-entropy loss

Method	Accuracy	Specificity	Precision	Recall	F1-Score
CNN					
Kiranyaz <i>et al.</i> [5] \diamond	0.959	0.971	0.842	0.888	0.864
Zhai <i>et al.</i> [16] \diamond	0.968	0.976	0.879	0.920	0.899
Li <i>et al.</i> [17]	0.920	0.918	0.628	0.933	0.751
SR-based \diamond*					
SAE-based	0.947	0.968	0.779	0.794	0.786
NPE-based (ours)	0.947	0.968	0.779	0.80	0.79
CNN \diamond*					
ABS [9]	0.977	0.995	0.956	0.825	0.886
Baseline (ours) \diamond *	0.965	0.987	0.899	0.809	0.852
Domain Adaptation (ours)	0.990	0.991	0.940	0.987	0.963
Ensemble (ours)	0.990	0.991	0.939	0.983	0.961
Ensemble (avg.) (ours)	0.988	0.990	0.933	0.979	0.955

Table 1: Comparison of other CNN methods, NPE-Based (ours) Baseline (ours), Domain Adaptation (ours), and Ensemble Classification (ours) methods. The classification performances of former studies, including global and one-shot classifiers, are presented. The results show that our personalized zero-shot ensemble classifier surpasses in F1-Score all the other methods.

\diamond Personalized classifiers.

* Zero-shot classifiers.

with AdamW [15] optimizer, and report the average results over 10 runs to reduce randomness. Let me know if you'd like the diagram code for Figure 3 as well!

As mentioned in Tables 1 and 2, the proposed domain adaptation technique significantly outperforms both the baseline and the abnormal beat generation (ABS) methods, particularly in terms of recall and F1-score. This improvement translates into fewer missed arrhythmia detections, highlighting the practical value of domain adaptation for more accurate ECG classification.

In particular, domain adaptation proves to be highly beneficial for users whose normal heartbeats differ noticeably from those of other individuals. According to AAMI standards, beats such as normal (N), left bundle branch block (L), right bundle branch block (R), atrial escape (e), and nodal (junctional) escape (j) are all categorized as normal. However, in practice, these beats can vary considerably.

Ground Truth						
Predicted						
		A	N		A	N
	A	63832	18081	A	78618	5016
	N	15798	546199	N	1012	559264

Table 2: Confusion matrices of the NPE (left) and Domain Adaptation (right) methods, accumulated over 10 independent training runs. A = Abnormal, N = Normal.

4.3 Ensemble Classification

We estimate the probabilistic model as described in Section [3.3] following CNN training. We model both normal NPEs with an exponential distribution and abnormal NPEs with a Gaussian distribution for all of our experiments. The exponential distribution has a probability density function (PDF) of

$$f(x; \beta) = \begin{cases} \frac{1}{\beta} e^{-x/\beta} & x \geq 0 \\ 0 & x < 0 \end{cases}. \quad (10)$$

The maximum likelihood estimate for the parameter β is

$$\hat{\beta} = \arg \max_{\beta} \prod_{i=1}^n \frac{1}{\beta} e^{-x_i/\beta} = \frac{\sum_{i=1}^n x_i}{n}, \quad (11)$$

which is the sample mean. Similarly, the PDF of the Gaussian distribution is

$$f(x; \mu, \sigma) = \frac{1}{\sigma\sqrt{2\pi}} e^{-\frac{1}{2}\left(\frac{x-\mu}{\sigma}\right)^2}, \quad (12)$$

and the maximum likelihood estimate for the parameters μ and σ are

$$\hat{\mu} = \frac{1}{n} \sum_{i=1}^n x_i, \quad \hat{\sigma} = \sqrt{\frac{1}{n} \sum_{i=1}^n (x_i - \mu)^2}, \quad (13)$$

which are the sample mean and sample standard deviation respectively.

CNN output is passed through the softmax function rather than log-softmax at test time. We then select the CNN's confidence—that of greater neuron output. The network output is employed for classification if the confidence exceeds some threshold \mathcal{C} . Otherwise the test sample's NPE is computed using a probabilistic model for classification. Just the CNN output is used if $\mathcal{C} \leq 0.5$; if $\mathcal{C} \geq 1$, only the probabilistic model is used. We choose \mathcal{C} as the confidence maximizing F1-Score in the validation set. Regarding equally performing confidences, we choose the more confident one can be.

5 Conclusion

Through the use of sparse representation-based domain adaptation, and ensemble classifier that achieves state-of-the-art performance on the MIT-BIH Arrhythmia Database, this paper tackles the problem of personalized and zeroshot abnormal heartbeat detection. Based on the thorough experiments described in Section 4, we make the following final observations about the suggested methodology —

Method 3.1: Rather than solving a sparse recovery problem iteratively, we can directly project the error component of a given test signal \mathbf{s}_i^p onto the null space of \mathbf{D}^p by building the left annihilator matrix \mathbf{F}^p of the dictionary \mathbf{D}^p for user p .

We demonstrate that classification based on the representation error component, $\tilde{\epsilon}$, offers substantial computational gains (up to 20 times) without compromising performance.

Method 3.2: Inter-patient beat transfer with modified ECG morphology is feasible with our new sparse representation-based domain adaptation technique and the morphology transformation matrices outlined in Algorithm 1. In this way, original healthy and abnormal beats from all the other users can be transferred to create large training sets for each user. When trained on these datasets, our CNN classifier achieves an intermediate state-of-the-art performance, with an accuracy of 99.0% and an F1-Score of 96.3%.

Method 3.3: In this case, an ensemble classifier was created by combining methods 3.1 and 3.2. Based on a confidence threshold, the CNN classifier consults the straightforward NPE error-based classifier. Table 1 shows the performance levels attained by our approach and the prior art for comparison.

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