Singular Value Decomposition Entropy Analysis and Deep Learning Models Based on Genetic Algorithms for Early Diagnosis of Fetal Arrhythmia

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Abstract

The term fetal arrhythmia refers to irregular fetal heart rhythms, with the established heart rate range being 120 to 160 beats per minute (bpm). Fetal arrhythmias occur in 1 to 2% of pregnancies; and although the majority of these are benign and transient, both tachyarrhythmia and bradyarrhythmia in some cases can indicate a serious condition for the fetus or the mother. Thus, a persistent fetal arrhythmia can lead to decreased cardiac output, heart failure, hydrops, and even fetal demise. As a result of this situation, an early diagnosis is crucial to adequately address this condition and reduce related mortality. Therefore, this study proposes the use of SVD entropy for characterizing ECG data from 6 channels (fetal and maternal), aiming to differentiate between healthy and diseased individuals. Consequently, a neural network could classify them, thus enabling a non-invasive early diagnosis of fetal arrhythmia. Additionally, it aims to enhance the performance of this technique by employing genetic algorithms for data augmentation and selecting the optimal architecture for the neural network, thereby ensuring a global accuracy of over 88% in fetal arrhythmia risk stratification.

1. Introduction

The fetal cardiac defect is among the most prevalent congenital anomalies, and it may go unnoticed in seemingly healthy infants for many years post-birth or be so severe as to pose an immediate threat to the baby's life [1, 2]. Typically, a healthy fetal heart rate ranges between 120 and 160 beats per minute, displaying a regular rhythm. Fetal arrhythmias, on the other hand, denote irregular cardiac rhythm and/or heart rates outside the normal range [3]. These arrhythmias can be categorized into three types: irregular, tachycardic, and bradycardic [4]. A comprehensive echocardiographic investigation into fetal heart arrhythmias within a significant fetal cohort uncovered an incidence rate of irregular fetal heart rhythms at 12.7% (614 out of 4838) [5]. While the majority of fetal arrhythmias are benign, a subset of them can lead to fetal hydrops and ultimately fetal demise [7]. This suggests that up to 1 in every 100 fetuses may necessitate close monitoring of their arrhythmias and, if required, in utero treatment with antiarrhythmic therapy.

For this reason, early diagnosis is of paramount importance for the proper and timely treatment of this condition. While there are already diagnostic techniques utilizing ECG signals and neural networks [8–10], as well as innovative data augmentation techniques for improving classification performance [11], the main objective of this study is to enhance these techniques and thus, the outcomes yielded by them. Hence, considering their successful application in previous studies on physiological data [12], this study aims to adapt and enhance these techniques for early fetal arrhythmia detection. While these methods have been applied to physiological datasets in prior research, their adaptation to clinical settings, specifically for fetal arrhythmia diagnosis, remains limited. Therefore, this paper builds on prior work and demonstrates the potential for broader clinical application.

2. Database

The dataset used in this study was obtained from Physionet [13], specifically the Non-Invasive Fetal ECG Arrhythmia Database (NIFEAD). This dataset contains 25 records, 11 of which are from patients with arrhythmia, and 14 from those with normal heart rhythms. Each record was collected from 6 channels—1 from the maternal thorax and 5 from the maternal abdomen. The recordings were made with a 5 mV voltage range and sampled at a rate of 1000 Hz. For analysis, a 1-minute segment was ex-

tracted from each record, further subdivided into 2-second segments to ensure consistent input size across the model. Each record's duration varies from 7 to 32 minutes, from which 1 minute was selected for each channel. This minute was further segmented into 2-second segments and subsequently organized into 11 arrays (for arrhythmia records) and 14 arrays (for normal rhythm records), each with dimensions of 6x30x (2000).

3. Method

The influence of noise in the training set on the performance of optimization algorithms in Machine Learning is significant and relevant. From this point of view, the two-stage filter proposal mentioned in [11] is favorable for the processing of ECG signals and their subsequent analysis.

The double-stage filter considers the calculation of the Approximate Entropy (ApEn) [14] parameter for each 30x2000 matrix corresponding to the maternal channel of each record to then be compared with the white noise reference value (said value should not be higher to 2). The proposed threshold allows replacement of ECG values by polynomial interpolation. The Normalized Least-Mean-Square (NLMS) adaptive filter represented the second filtering stage in which the maternal recording channel was considered as a reference signal for the remaining 5 abdominal channels.

$$\phi^m(r) = \frac{1}{n}\sum_{i=1}^{n} log(C_i^m(r)) \tag{1}$$

$$ApEn(m, r, N)(u) = \phi^m(r) - \phi^{m+1}(r) \tag{2}$$

The resulting records are capable of being analyzed using a wide spectrum of statistical parameters capable of describing their periodicity, dimensionality and complexity. Related works report the predictive capacity of SVD Entropy, [12] mentions a 94% accuracy in binary classification for ECG data records analyzed with SVD Entropy, a value comparable to the 94.12% recorded in the same work and at 92% accuracy reported in [11] for Permutation Entropy (EP). In this way, the use of the Entropy of Singular Value Decomposition (SVD Entropy) was considered.

$$H = -\sum_{i=1}^{M} \bar{\sigma}_i log_2(\bar{\sigma}_i) \tag{3}$$

The SVD Entropy value was obtained for each 2-second segment in each of the stacked matrices of dimension 5x30x2000. The matrices obtained corresponding to each of the recordings were stacked in a 1x150 vector for each patient and were labeled according to her recording condition ("Control" and "Arrhythmia"). The established and labeled groups were compared using the Mann-Whitney-Wilcoxon test to establish significant differences between them, identifying heterogeneous 2-second segments capable of contributing to the performance of the rating model.

The test reduced the dimensionality of the vectors to dimension 1x9. The Data Augmentation method based on genetic algorithms driven by an unsupervised learning model is mentioned in [11]. In this case, 11 records were randomly selected (6 labeled as "Control" and 5 as "Arrhythmia"), while the remaining 14 records were reserved for the evaluation of the classification model. K-Means was chosen as the clustering technique to divide the vectorial space into the corresponding Voronoi cells by setting the number of clusters to k=2. The unsupervised learning model reached 85.5% accuracy, achieving the calculation of the centroids that best characterize the data grouping. The genetic algorithm presented in Figure 1 maintains a

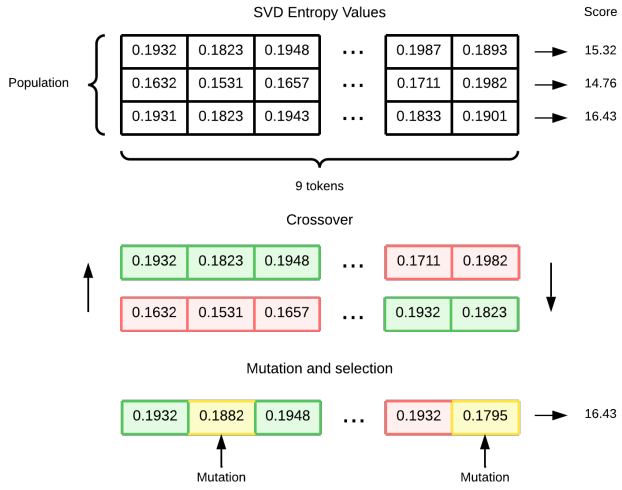

Figure 1. Genetic algorithm: Initial population = 150, mutation rate = 0.02, maximum generations = 150.

specific threshold for the fitness function in order to generate vectors close to the centroids without compromising their generality. In this way, it was possible to expand the training set with 65 vectors labeled as "Arrhythmia", and 70 labeled as "Control". The proposed artificial neural network was implemented as a sequential model with 5 stacked layers (with a total of 955 trainable parameters) whose output function "Softmax" expressed the result as a probability distribution. EarlyStopping was considered as a threshold criterion to avoid overfitting and the initial generation of the Neural Network weights was established through a second genetic algorithm implemented to accelerate convergence towards the optimal model considering the inverse value of the Categorical Crossentropy parame-

ter. as a fitness function to be maximized.

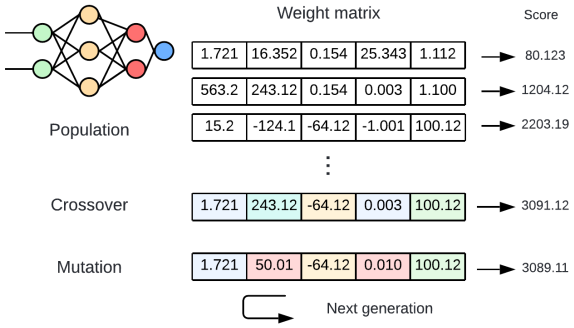

Figure 2. Genetic algorithm - Trainable values of the classifier model: Initial Population = 100, mutation rate = 0.2, maximum solutions = 10

4. Results

The progression of the loss function, which indicates the error incurred by the densely connected neural network at the end of each epoch, is depicted in Figure 3. The figure demonstrates a favorable trend where both the training and validation curves exhibit a steady and gradual convergence towards zero error. Interestingly, the neural network's classification error for patients approaches levels close to zero shortly before the initial 40 epochs and continues to decrease gradually in subsequent epochs. Notably, the graph does not show any signs of overfitting or underfitting behavior in the model.

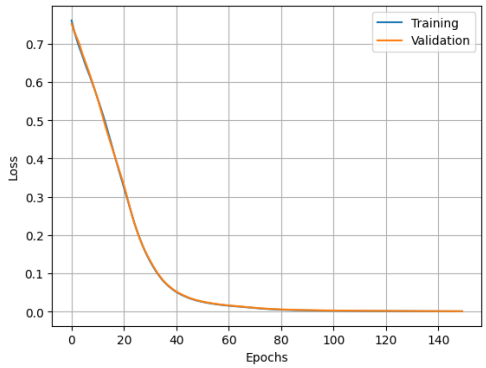

Figure 3. Evolution of the Loss function through the epochs

Figure 4 depicts the advancement of categorical accuracy over epochs. This measure represents the ratio of accurately classified subjects to the total count, with values nearing one indicating a more proficient network classification. The figure demonstrates that both curves follow the same trend, differing slightly only at the beginning (between epochs 5 to 9) and around epochs 17-18.

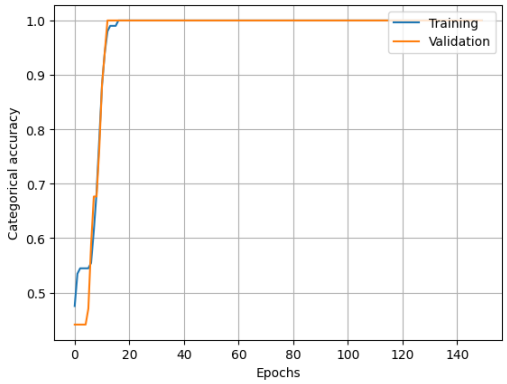

Figure 4. Evolution of the Categorical Accuracy through the epochs

The confusion matrix of the model is depicted in Figure 5, revealing that the model achieves an overall accuracy of 93%. Furthermore, in the classification of control and arrhythmia patients, precision of 100% and 86% respectively was obtained. Regarding the recall rates, 89% for control and 100% for arrhythmia were achieved. It is important to note that the values of the confusion matrix are significantly lower than those used for training. This is because the original data have not been subjected to the data augmentation method, and therefore represent over 50% of the original set.

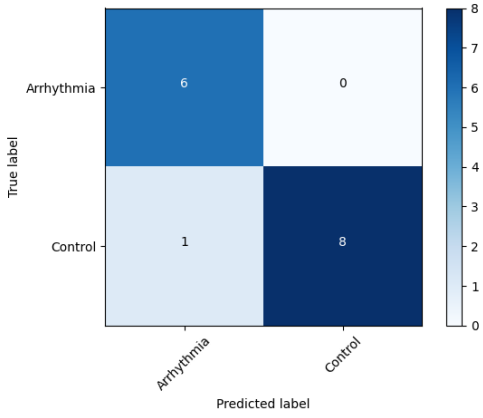

Figure 5. Confusion matrix

Figure 6 illustrates the ROC curve for the performed classification. The y-axis represents the true positive rate (sensitivity), while the x-axis corresponds to the false positive rate (specificity - 1); thus, the closer the points are to the upper left corner (ideal point), the better the classification performance, meaning that as the area under the curve (AUC) approaches one, the classification becomes more

accurate. From Figure 6, it is observed that its AUC value is very close to 1, precisely at 0.944, indicating a very good classification performance of the network.

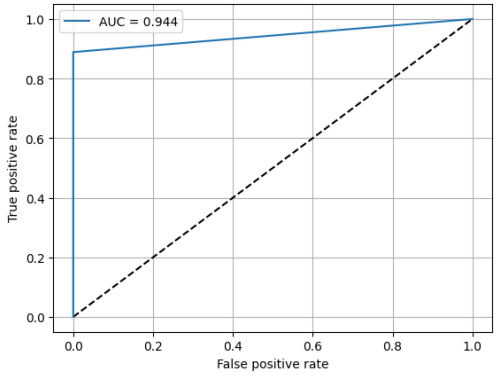

Figure 6. ROC curve

5. Discussion and conclusions

This study explores the use of SVD entropy and neural networks, optimized via genetic algorithms, for early detection of fetal arrhythmia. While the methodology shows promise, it presents certain challenges. The two-stage filtering method effectively reduces noise, but it may introduce biases that affect the generalizability of results. Similarly, while genetic algorithms improved classification accuracy (93%), their use in data augmentation raises concerns about real-world applicability, as the dataset remains small. The model's high precision (100% for control and 86% for arrhythmia) indicates its potential clinical utility. However, the risk of misclassifying arrhythmias as normal (false negatives) could delay critical interventions. The ROC curve (AUC of 0.944) supports the model's effectiveness, but caution is advised given the life-threatening consequences of misclassification.

A key limitation is the small dataset, which, despite augmentation, cannot fully capture the variability seen in clinical cases. Future work should focus on validating the model with larger datasets and improving robustness by integrating more diverse physiological data. Enhancing real-time applicability through further clinical testing will be crucial.

Acknowledgements

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