Fetal Arrhythmia: Deep Learning and Clustering Techniques, Analysis Through Permutation Entropy and Genetic Algorithms in Its Early Diagnosis

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Abstract

Fetal arrhythmias occur in 1-2% of pregnancies and involve irregular fetal heart rhythms, typically outside the 100-200 bpm reference range. This condition can be diagnosed as benign in most cases due to its subsequent natural regularization, but 10% of the registered cases indicate that the presence of irregularities in the fetal heart rhythm can trigger morbidity, fetal hydrops or even imminent death of the fetus. In this context, early and precise diagnosis is crucial for addressing this condition and reducing fetal deaths. That is why, a deep learning model is proposed based on a classifying neural network trained with an ECG database of 6 channels (fetal and maternal) accompanied by an intelligent arrangement of clustering techniques, analysis by permutation entropy and data augmentation based on genetic algorithms. This set of techniques aims to form an effective system for the rapid diagnosis of heart rhythm irregularities present in fetuses, ensuring an overall accuracy greater than 92% in fetal arrhythmia risk stratification.

1. Introduction

Fetal heart defect is one of the most common birth defects that may be undetectable in seemingly healthy babies for many years after birth or be so severe that they pose an immediate threat to the infant's life [1, 2]. Fetal cardiac arrhythmias (ARRs) are characterized by any fetal cardiac rhythm that falls outside the reference range of 100 to 200 beats per minute (bpm), whether it's irregular or regular [4]. Approximately 1% of fetuses are found to have RRs, with around 10% of these RRs having the potential to cause morbidity [5]. While the majority of fetal ARRs are harmless, a subset of them can result in fetal hydrops and ultimately lead to fetal mortality [6]. This implies that as many as 1 in every 100 fetuses may require close monitoring of their ARRs and, if necessary, in utero treatment with antiarrhythmic therapy.

In this way, early diagnosis is important for the treatment of the reported condition. While existing studies utilize ECG signal analysis and neural networks for detecting and categorizing cases [7–9], the paramount goal remains to enhance accuracy, speed, and efficiency to diminish the annual incidence of fetal deaths attributed to this condition. Consequently, this research introduces a deep learning model that employs a classifier neural network trained on ECG data preprocessed with permutation entropy. Since the latter has demonstrated great efficiency for the treatment of physiological data and specifically ECG. It also incorporates the strategic application of clustering and data augmentation techniques guided by genetic algorithms. This holistic approach is designed to ensure accurate classification of fetal arrhythmia presence.

2. Database

The considered database was extracted from Physionet [10] and is titled Non-Invasive Fetal ECG Arrhythmia Database (NIFEAD). It comprises a set of 25 records, including 11 arrhythmia records and 14 normal records, with a total of 6 recording channels: one from the maternal thorax and 5 from abdominal channels. These records have a range limitation of 5 mV and a recording frequency of 1000 Hz. The duration of each record varies from 7 to 32 minutes, from which 1 minute was selected for each channel. This minute was further divided into segments of 2 seconds in duration and subsequently organized into 11 arrays (for arrhythmia records) and 14 arrays (for normal rhythm records), each with dimensions of 6x30x(2000).

3. Method

It is well-known that during the recording of ECG signals, data with noise can be acquired, which could significantly impact the performance of optimization algorithms included in classification models. Therefore, a two-stage

filtering approach was considered. In the first stage, the Approximate Entropy (ApEn) [12] parameter was calculated for each 30x2000 matrix corresponding to the maternal channel of each record.

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

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

The result was then comparatively filtered with a reference ApEn value corresponding to white noise (not exceeding 2), replacing values above the threshold through polynomial interpolation. The second stage involved the application of the Normalized Least-Mean-Square (NLMS) adaptive filter, using the maternal record as the reference signal and extracting data from the 5 abdominal channels.

It is evident that the obtained arrays can be analyzed using a wide range of methods for time series, and it is possible to describe their characteristics through statistics aimed at measuring their regularity and complexity in terms of existing patterns within them. Hence, the use of Permutation Entropy (PE) was considered, which was defined by Band and Pompe [11].

$$H(n) = -\sum p(\pi)\log p(\pi) \tag{3}$$

The corresponding PE value was calculated for each 2-second segment in each of the 5x30x2000 arrays, resulting in 5x30 matrices for each of the records. The obtained matrices were transformed into vectors of dimension 1x150 and labeled according to their condition (”Control” and ”Arrhythmia”). Both established groups were analyzed using the Mann-Whitney-Wilcoxon test to verify and determine the existence of significant differences between them, successfully identifying the 2-second segments whose heterogeneity would contribute to the correct performance of the classification algorithm. The aforementioned process allowed for the reduction of the arrays to vectors of dimension 1x111.

It was decided that the database could be expanded through a data augmentation procedure, driven by an unsupervised learning model for classification, coupled with the application of genetic algorithms for data generation. The 25 records were divided into 2 groups, with 13 of them (7 labeled as ”Control” and 6 as ”Arrhythmia”) used for data augmentation processing, while the remaining 12 were reserved for the subsequent evaluation of the neural network for classification. Techniques such as K-means clustering were leveraged to partition the vector space corresponding to the 1x111 arrays into the well-known Voronoi cells, establishing the number of clusters at k=2. Additionally, the ’elkan’ optimization algorithm, which utilizes the triangular inequality and has demonstrated good performance with a small number of clusters, was employed.

The model did not aim to be particularly accurate since its primary function was related to computing centroids that best characterized the data clustering. The accuracy when altering the initialization seed of the centroids was approximately 85%, with the maximum Euclidean distance corresponding to each group not exceeding the value of 2.9. The values of 111 EP (which we referred to as tokens) for the 13 records laid the foundation for the genetic algorithm based on the classical stages:

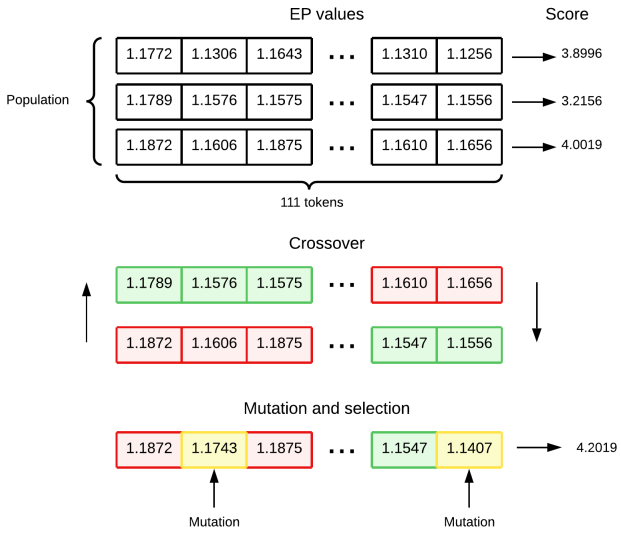

Figure 1. Genetic algorithm: Initial population = 150, mutation rate = 0.02, maximum generations = 150.

The algorithm in question had a maximum number of generations set to 150 and considered a fitness target value greater than or equal to 4 to ensure the production of vectors close to the vicinity of each centroid without compromising their generality.

The proposed procedure succeeded in expanding the training database, resulting in up to 56 instances labeled as ’Arrhythmia’ and 102 as ’Control.’ The artificial neural network was implemented with a sequential model consisting of 4 stacked layers (with a total of 2582 trainable parameters), with a ’Softmax’ output function that allows expressing the result as a probability distribution. Consequently, the artificial neural network considered a matrix of dimension 158x111 as the training set and a 1x158 vector corresponding to the input values, which were encoded using One-Hot-Encoding. Adaptive Moment Estimation was the optimization algorithm considered, and EarlyStopping was used as the criterion to prevent overfitting. The supervised learning model was evaluated with a set of 12 records, which were excluded from the Data Augmenta-

tion process, resulting in a 50:50 training-evaluation ratio.

4. Results

In Figure 2, the progression of the loss function is depicted, representing the error incurred by the densely connected neural network at the conclusion of each epoch. The figure illustrates a favorable trend where both the training and validation curves exhibit a consistent and gradual convergence towards zero error. Remarkably, the neural network's classification error for patients approaches near-zero levels shortly before the initial 100 epochs and continues to decrease gradually in subsequent epochs. Notably, the graph does not display any indications of overfitting or underfitting behavior in the model.

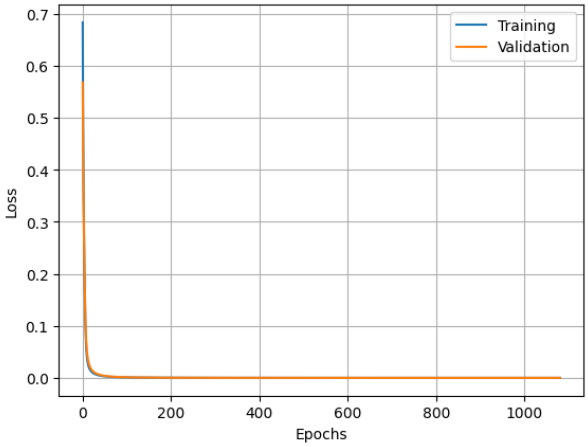

Figure 2. Evolution of the Loss function through the epochs

Figure 3 illustrates the progression of categorical precision across epochs. This metric reflects the proportion of subjects accurately classified relative to the total count, with values approaching one indicating a more proficient network classification. The figure demonstrates that both curves closely mirror each other, maintaining a consistent alignment throughout. Moreover, both curves rapidly converge toward values approaching one within the initial 100 epochs, and this high level of precision persists in subsequent epochs.

Figure 4 presents the confusion matrix of the model, offering crucial insights into the classification performance of the densely connected neural network. Within this matrix, we find counts for true positives, true negatives, false positives, and false negatives, accompanied by their respective rates. These metrics serve as the basis for calculating key performance indicators for the model, including accuracy, precision, recall, and the F-score.

Based on the observed values, the model achieves an overall accuracy of 92%. For the classification of control

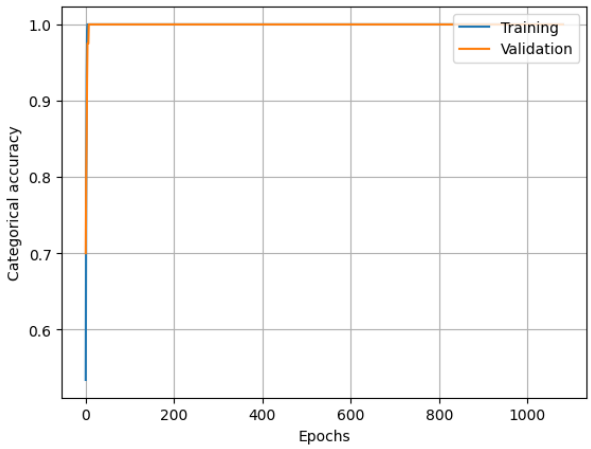

Figure 3. Evolution of the Categorical Accuracy through the epochs

patients and those with arrhythmia, the precision rates are 83% and 100%, respectively. Additionally, the recall rates are 100% for control patients and 86% for arrhythmia patients, while the F1-scores stand at 91% and 92% for control and arrhythmia classifications, respectively.

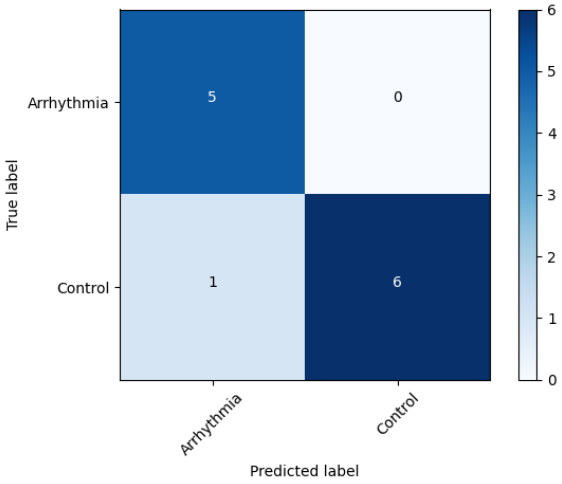

Figure 4. Confusion matrix

An ROC curve provides a visual representation of the classification performance achieved by the densely connected neural network. In this curve, the y-axis represents the true positive rate, known as "sensitivity," while the x-axis corresponds to the false positive rate, referred to as "1-specificity." The "ideal" point on this graph is one where both specificity and sensitivity values approach 1. Therefore, the closer the points are to the upper-left corner, the better the classification performance. In other words, a larger area under the curve (AUC) signifies superior classification accuracy.

Figure 5 depicts the ROC curve for this specific classification task. Here, it is evident that the AUC value is very close to 1, precisely at 0.929. This serves as compelling evidence of the network's effective classification performance.

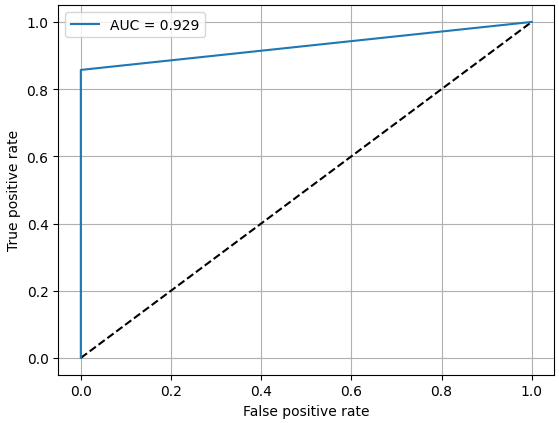

Figure 5. ROC curve

5. Discussion and Conclusions

The two-stage filter proposed in this study was conceived with the objective of enhancing ECG records to facilitate and optimize the acquisition of Permutation Entropy (EP) values corresponding to each record, here referred to as 'tokens.' This enhancement manifested in the heterogeneity observed within the 'Control' and 'Arrhythmia' labeled groups, as the Mann-Whitney-Wilcoxon test enabled the preservation of a substantial number of tokens. In contrast to other works addressing the treatment of ECG signals for early diagnosis of fetal arrhythmia, this study advocated the employment of Permutation Entropy as the sole value or feature that the neural network should discern for the classification task. However, it is not asserted that the proposed two-stage filter is exclusively suitable for EP; rather, it could also demonstrate strong performance when applied to other feature sets tailored to the problem.

The utilization of clustering techniques in conjunction with genetic algorithms demonstrated remarkable efficiency in data augmentation tasks, facilitating the generation of vectors that ensured similar characteristics, primarily determined by their distribution in the vector space. This was achieved without compromising the generality of these samples. The aforementioned findings were substantiated by the performance exhibited by the artificial neural network, achieving an overall accuracy of 92% and precision values of 83% and 100% for the classification of the 'Control' and 'Arrhythmia' groups, respectively. These results suggest that the implemented data augmentation system maintains heterogeneity even after the application of the Mann-Whitney-Wilcoxon test.

Acknowledgements

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