Simulating the Doctor's Behaviour: A Preliminary Study on the Identification of Atrial Fibrillation through Combined Analysis of Heart Rate and Beat Morphology

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Keywords: Recommender System, Deep Learning, ECG Analysis, Atrial Fibrillation, Arrhythmia.

Abstract: Atrial fibrillation (AF) is a medical disorder that affects the atria of the heart. AF has emerged as a worldwide cardiovascular epidemic affecting more than 33 million people around the world. Several automated approaches based on the analysis of the ECG have been proposed to facilitate the manual identification of AF episodes. Especially, such approaches analyze the heartbeat morphology (absence of P-wave) or the heart rate (presence of arrhythmia). In this article, we present AMELIA (AutoMatic dEtection of atriaL fIbrillation for heAlthcare), an approach that simulates the doctor's behavior by considering both the sources of information in a combined way. AMELIA is basically composed of two components; one integrating a LSTM (Long Short-Term Memory) Recurrent Neural Network (RNN) and the second integrating a rhythm analyzer. When the RNN reveals a heartbeat with abnormal morphology, the rhythm analyzer is activated to verify whether or not there is a simultaneous arrhythmia. AMELIA has been experimented by using well-known datasets, namely Physionet-AF and NSR-DB. The achieved results provide evidence of the potential benefits of the approach, especially regarding sensitivity. AMELIA has an incredibly high potential to be used in applications of continuous monitoring, where the detection of AF episodes is a fundamental and crucial activity.

1 INTRODUCTION

In modern healthcare systems the vital signals of patients are acquired, collected, and analyzed within the system itself.

This is the case of *ATTICUS* (Laudato et al., 2021), an innovative tele-service and remote monitoring system for ambient-assisted living based on the analysis of vital and behavioral parameters. The data are acquired through a smart t-shirt (Balestrieri et al., 2019; De Vito et al., 2021) and then transmitted to an Ambient Intelligence device located nearby, which, in turn, predicts potentially anomalous situations and it communicates them to a Decision Support System (DSS). Such a system can perform deeper and more accurate analysis and, if it confirms the anomaly, it can alert a monitoring station in which human experts (e.g., doctors) manually analyze the data and plan an intervention.

In this paper, we present an approach that we aim at integrating into the DSS of *ATTICUS*. The approach is in charge of analyzing the ECG to identify atrial fibrillation (AF) events, an abnormal heart rhythm characterized by rapid and irregular beating of the atria. The process of AF episodes diagnosis involves two ECG sources of information: (i) *morphology-based*, because during an AF episode,

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Laudato, G., Rosa, G., Capobianco, G., Colavita, A., Forno, A., Divino, F., Lupi, C., Pareschi, R., Ricciardi, S., Romagnoli, L., Scalabrino, S., Tomassini, C. and Oliveto, R.
Simulating the Doctor's Behaviour: A Preliminary Study on the Identification of Atrial Fibrillation through Combined Analysis of Heart Rate and Beat Morphology.
DOI: 10.5220/0010823900003123
In *Proceedings of the 15th International Joint Conference on Biomedical Engineering Systems and Technologies (BIOSTEC 2022) - Volume 5: HEALTHINF*, pages 446-453
ISBN: 978-989-758-552-4; ISSN: 2184-4305

fluctuating waveforms instead of P waves can be observed and (ii) *rhythm-based*, because of the heart rate irregularity, which may appear.

A lot of effort was devoted by the research community to the definition of approaches for the automatic detection of AF by using Machine Learning (ML) techniques based on one of the above sources of information. Indeed, a widespread approach is the Support Vector Machines (SVM) (Sepulveda-Suescun et al., 2017; Islam et al., 2017; Padmavathi and Ramakrishna, 2015), while other authors chose Neural Network (NN) to classify ECG segments (Yuan et al., 2016; Xiong et al., 2017) or novel recursive algorithms (Zhou et al., 2015). The most common features for the ML tools used in these methods are based on RR Intervals (RRI) analysis. There are also approaches, such as the one by Padmavathia and Ramakrishnab (Padmavathi and Ramakrishna, 2015), where it is proposed the use of autoregressive coefficients as derived morphological ECG features.

Despite the high accuracy of the above methods, we conjecture that there is still room for improvement. We believe that an approach – based on the combination of morphological and rhythmic analysis – can reproduce the exact procedure used by cardiologists when manually checking an ECG for AF diagnosis. Our conjecture is supported by the results of previous works proposed in Laudato et al. (2020b,a), where a machine learning approach, named *MORPHYTHM* was defined to combine morphological and rhythmic information to support the identification of AF events. Despite the promising results achieved, the main limitation of such an approach was represented by the difficulties to explain a specific prediction. Indeed, all the features extracted from the ECG were put together in one single learning algorithm. This made it difficult to identify the event that triggered the prediction.

Based on the willingness to have an accurate and explainable method for detecting AF events, we present AMELIA (AutoMatic dEtection of atriaL fIbrillation for heAlthcare). AMELIA is an automated AF detector based on (i) an LSTM Recurrent Neural Network (Hochreiter and Schmidhuber, 1997) for the ECG Morphology classification and on (ii) statistical heuristics to identify arrhythmia. The proposed approach aims at simulating as much as possible the doctor's behaviour during the detection of AF episodes. Especially, AMELIA first analyzes the morphology of the heartbeat (as it is and not in terms of derived features as shown in the literature) in order to identify the absence of p-wave and then confirm the anomaly by checking the presence of arrhythmia.

The proposed approach was experimented on two publicly accessible sets of clinical data (MIT-BIH Atrial Fibrillation Database[1] and MIT-BIH Normal Sinus Rhythm Database[2]). The accuracy of AMELIA was compared with the work by Zhou et al. (2015), one of the most accurate methods of AF detection based on RRI analysis (therefore based on only rhythmic features) and with the work recently proposed by Laudato et al. (2020b) which, as AMELIA, also takes in consideration morphological and rhythmic features. The results reported in Section 4 show that it is possible to achieve benefits with respect to the chosen baselines.

We believe that AMELIA can be better employed in telemedicine applications, where e-AI (explainable-Artificial Intelligence) is often a strong requirement. Indeed, AMELIA– thanks to the conceptual and *de facto* separation of the data sources between rhythmic and morphological – can provide highly accurate information in the process of diagnosis. For example, AMELIA– beyond the generation of a warning indicating a potential AF episode – can provide the additional information of which is the heartbeats not showing a P wave with a high accuracy.

The premise that AMELIA can reproduce the exact procedure used by cardiologists is based on the consideration that the approach takes as input a sequence of heartbeats that are submitted only to noise-removal and downsampling processing stages, therefore preserving the ECG shape. AMELIA aims at simulate the manual diagnosis by observing the rhythm and the shape of a pattern of heartbeats.

The rest of the paper is structured as follows: Section 2 presents the proposed approach for AF detection, Section 3 describes the experimental choices for the design of the study, while Section 4 presents the results of the evaluation of the proposed approach on the Physionet data set. Finally, Section 6 concludes the paper by discussing the results and by reporting all the potential future works which can be undertaken with AMELIA in the context of *ATTICUS* (Balestrieri et al., 2019; Laudato et al., 2021).

2 AMELIA

An AF episode is diagnosed by a doctor when the morphology of the heartbeat is abnormal (no P-wave), RR intervals are irregularly irregular, and f-waves appear. AMELIA aims at simulating as much as possible such a behavior. The workflow of AMELIA is

[1] https://physionet.org/physiobank/database/afdb/

[2] https://physionet.org/physiobank/database/nsrdb/

depicted in Fig. 1. In the preprocessing stage, AMELIA extracts all the heartbeat signals and all the R peak positions from a raw single lead digital ECG acquired with a given sampling frequency. These signals are submitted to a *Morphology analyzer*.

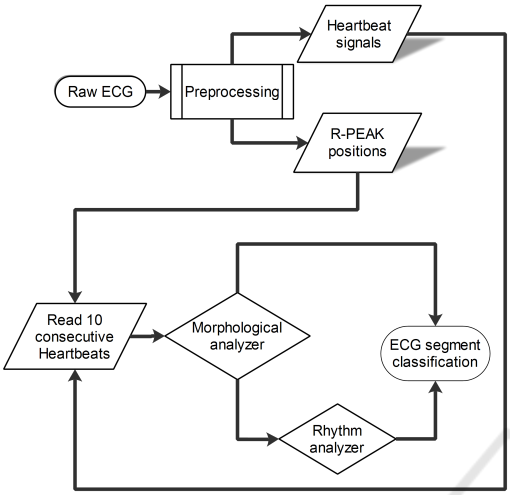

Figure 1: AMELIA workflow.

If the morphology of the heartbeat is abnormal, the *Morphology analyzer* triggers the *Rhythm analyzer*. The *Rhythm analyzer* takes as an input the extracted R peak positions and tries to consolidate the initial warning identified by the *Morphology analyzer*. If the *Rhythm analyzer* identifies through the analysis of ten consecutive R-R intervals an arrhythmia, then an *AF episode* is identified. Otherwise, the initial warning of the *Morphology analyzer* is rejected. In this case, the abnormal morphology of the heartbeat could be due to the wrong classification of the NN or just to some noise in the ECG.

2.1 Definition of a Heartbeat

It is necessary to clarify the concept of *heart beat signal*. In AMELIA, a heartbeat signal is a raw ECG segment included between two successive R peaks (see Fig. 2). The choice to define a heartbeat signal in this way is due to the consideration that the morphological features – observable during AF episodes – are (i) the absence of *P wave* and (ii) the potential fibrillation waves in its place. The concept of the *heartbeat signal* is also faced in the work by Xu *et al.* (Xu et al., 2018) with the difference that the authors define it as the signal between the two middle points of three consecutive R peaks. We decided to work with heart dynamics included between two successive R peaks because the fibrillating phenomena are inscribed between those waves. We used the Pan-

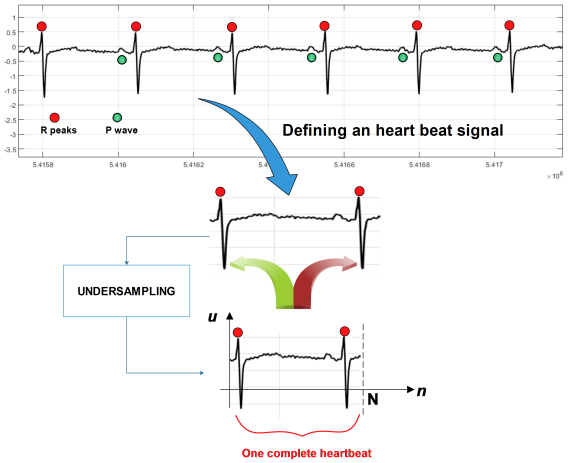

Figure 2: Definition of heartbeat signal in AMELIA.

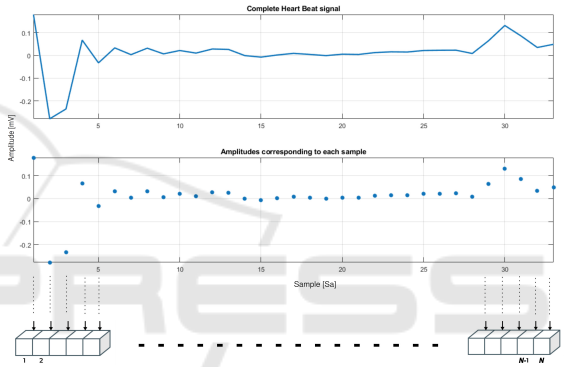

Figure 3: Representation of a complete heartbeat in AMELIA.

Tompkins method (Pan and Tompkins, 1985) to obtain all the expected heartbeat signals of a given full ECG signal. We opted for the validation of AMELIA in the online scenario (worst case), therefore without using the beat annotations available from Physionet.

A complete heartbeat is represented by a vector defined as:

$$\mathbf{hbs} = [u_1, u_2, ..., u_N] \quad (1)$$

where u_1 and u_N are the raw amplitudes of the samples corresponding to the position of the left and right R peak, respectively (see Fig. 3).

In order to provide fixed-length instances to the *Morphology analyzer* component – all the heartbeat signals were submitted to a process of down-sampling (in section 4.3, more details are provided). N is the fixed length of each complete heartbeat signal.

2.2 Morphology Analyser

The *Morphology Analyser* is in charge of analyzing the morphology of a heartbeat. The input of this component is represented by a heartbeat. Ideally, the out-

put is **no-AF** if the morphology of the heartbeat is normal and **AF** if the morphology of the heartbeat does not have the P wave and shows fluctuating waveforms (f-waves), *i.e.,* the morphological characteristics of a heart beat in the presence of an AF event. The morphology classification of the heartbeat is based on a Recurrent Neural Network (RNN) (Hochreiter and Schmidhuber, 1997) with multiple LSTM cells. The choice is justified by the consideration that LSTM cells better adapt to time-series classification (Karim et al., 2017) (as in the case of ECG).

2.3 Rhythm Analyser

The *Rhythm Analyser* aims at identifying normal rhythm or arrhythmia by evaluating a buffer of ten successive heartbeats. It is worth noting that– based on a consolidated opinion from cardiologists – ten consecutive heartbeats can be can be deemed enough to diagnose atrial fibrillation. This number is also confirmed by the works in (Kurzweil et al., 2009; Zurro et al., 1995) where a minimum of 3 and 6 successive heartbeats was evaluated.

In details, the *Rhythm Analyser* classifies each beat as *short*, *long*, or *normal*. Considering that the normal heart rate during rest for teenagers is around 70-120 beat per minute (bpm) and adults is around 60-90 bpm (D. Limmer, 2005), each beat is classified as follows: ***short*** if bpm $>$ 120, ***long*** if bpm $<$ 50 and ***normal*** otherwise. Once the *Rhythm Analyser* has buffered and labeled ten consecutive heartbeats, computes the entropy of the buffer B.

2.4 Putting All Together

Algorithm 1 shows how the *Morphology Analyser* and the *Rhythm Analyser* are combined in order to detect AF events.

For each heartbeat signal, a fixed-length buffer hbs_i is instantiated, containing the amplitudes of the signal. The buffer hbs_i then is submitted to the *Morphology Analyser*, which provides its classification. When the morphology is classified as *AF*, a new buffer of heartbeats is created. Once the buffer of heartbeats has reached the max size (set as 10, in our case), it is submitted to the *Rhythm Analyser*. Based on the entropy information evaluated on the buffer, a classification in terms of rhythm is provided. If also the rhythm is identified as *IRREGULAR*, a warning is generated.

Algorithm 1: Detection of Arrhythmia.

```
Require: ECG                                   ▷ Raw ECG
  HBS = ExtractHeartBeatSignals(ECG)
  RRI = ExtractRRInterval(ECG)
  for each hbs_i ∈ HBS do
      Morphology = MorphologyAnalyser(hbs_i)
      if Morphology == AF then
          buffer_i ← ∅    ▷ new buffer for the i^th heart
  beat
          BUFFERS ← BUFFERS ∪ buffer_i
      end if
      for each buffer_j ∈ BUFFERS do
          buffer_j ← buffer_j ∪ RRI_i
          if size(buffer_j) == MAX_SIZE then
              Rhythm = RhythmAnalyser(buffer_j)
              if Rhythm == ABNORMAL then
                  GenerateWarning()
              end if
              BUFFERS ← BUFFERS \ buffer_j
          end if
      end for
  end for
```

3 STUDY DESIGN

We compared AMELIA to the method proposed in (Zhou et al., 2015), where AF episodes are identified by using only an RRI analysis. Thus, in the context of the study, we formulated the following research question:

Does AMELIA *outperform state-of-the-art AF detection approaches?*

We chose as baseline the approach by Zhou (2015) *et al.* (Zhou et al., 2015) because in the state of the art, it is one of the most accurate approaches based on RRI analysis. We also keep a recent tool *MORPHYTHM* (Laudato et al., 2020b) as a reference, because it is based on a combination of rhythmic and morphological analysis, too.

3.1 Context of the Study

The proposed approach was experimented on the MIT-BIH AFDB (Goldberger et al., 2000). For this DB, Physionet offers 25 2-lead ECG recordings. These were acquired with a sampling frequency of 250 Hz, 12-bit resolution over a range of $\pm$ 10 millivolts. In this preliminary study, we performed a detection based on a single-lead ECG, thus we took into account only the first lead. Furthermore, for this data set, Physionet does not provide distinction among beat types (but only in terms of rhythm); indeed, all

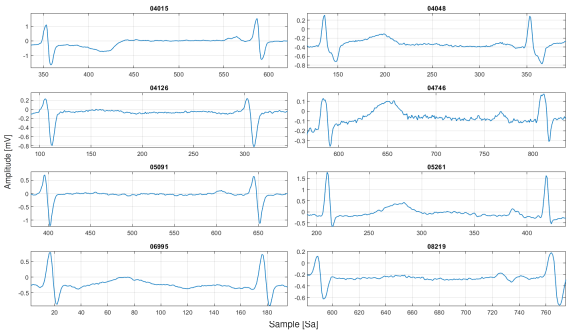

Figure 4: The records chosen for this study.

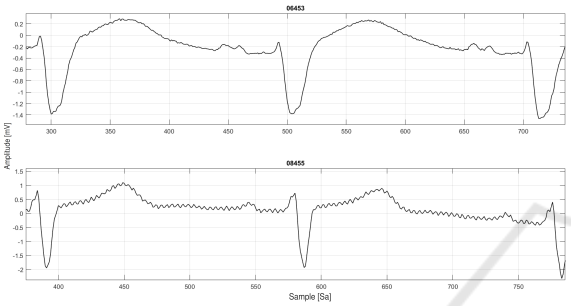

Figure 5: The records ignored for the study.

beats are labeled as normal. Considering the diversity of the ECG shapes – in order to guarantee consistency of information – we manually selected only those recordings with a common shape. This choice is due to specificity of AMELIA's morphology component. Thus, in this preliminary study, we considered records #04015, #04048, #04126, #05091, #05261, #06995, #08219, #08455. Indeed, this group of patients presents a high similarity between the ECG waveform shapes (see Fig. 4). For the moment, the other records were ignored. Examples of ignored records are #06453 and #08455, where in the available signal 1 from the database, the shapes differ from the ones of the above group of recordings (Fig. 5).

Each heartbeat signal was manually observed and analyzed, with the help of a medical equipe. Only signals presenting a clear AF effect were selected. The operation was carried out for all the chosen records. A total of 1637 heartbeat signals from the 8 different recordings were manually extracted. The minimum length for each of these signals varies from 33 to 111 samples. By doing that, we obtained two types of signal: *AF* and *Normal (no-AF)* heart-beat signals.

To conclude the experiment, we tested the final version of AMELIA also on the MIT-BIH Normal Sinus Rhythm Databases because it contains patients with a healthy ECG except for some no significant arrhythmia episodes. Therefore, at the end of the study, we will experiment AMELIA under several circumstances: the detection of AF and NO-AF episodes. These latter include normal sinus rhythm and pathological rhythm. Indeed, both the chosen database include pathological rhythm different from AF episodes. Specifically, the AFDB contains atrial flutter episodes and the NSRDB arrhythmia episodes (Goldberger et al., 2000).

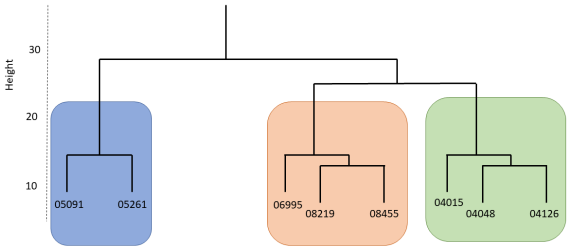

Figure 6: The dendrogram for the manually selected records from AF Database, based on an AF heartbeat.

3.2 Patient-centered Data Clustering

The 8 records were manually observed and selected. Therefore, before reporting the classification results, we aimed at validating the manual selections performed in the previous steps. To do so, the data was submitted to a clustering algorithm to assess effectively if the 8 patients group together in an individual cluster. To this aim, we selected one AF-labelled heartbeat from each of the chosen records, and we described each of these heartbeats using several descriptors, such as: entropy measures (e.g. the one proposed in (Zhou et al., 2015)), Statistical Features (e.g. the mean, variance, and norm of the amplitude samples), Fast Fourier Transform and AR model coefficients. After creating this data set, we applied a technique of Hierarchical clustering with *Euclidean distance* as the similarity function and the *average* as the agglomeration method. We obtained the dendrogram depicted in Fig. 6. Thus, even if they seemed to have a common ECG waveform shape – when they are observed from an AF heartbeat perspective – the clustering process assigns them to distinct groups. This separation could be due to physiological aspects that are embedded in an ECG.

From this step of clustering, we obtained a refined view of the groups to which our records belong. This will be used to represent the results for each patient, according to the reference cluster.

3.3 Training of the LSTM RNN

The training of the LSTM RNN was performed on a balanced data set composed of 1637 instances for the **AF Class** and 1653 for the **no-AF Class**. To the

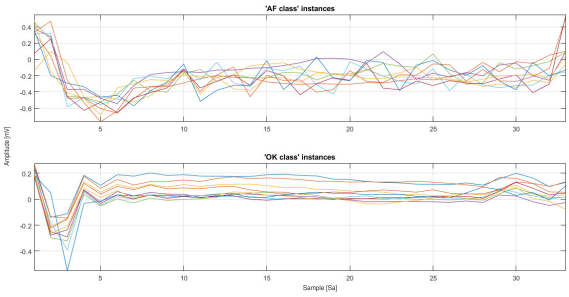

Figure 7: Examples of the manually selected instances from the Physionet AFDB.

aim of guaranteeing an alignment, all the instances were downsampled to 33 data points. An example of selected and downsampled instances is depicted in Fig. 7. The LSTM parameters were experimentally defined through a *trial & error* approach. In order to validate the network, a classical Leave-one-person-out (LOPO-CV) cross-validation was applied to the data set. LOPO-CV means that one person at a time is left out from the training set, so that the training set contains no data specific to the individual who is being tested (the classifier was not tuned with the test data of that person).

4 ANALYSIS OF THE RESULTS

We experimented with the proposed approach on two freely accessible data set, the Physionet MIT-BIH AFBD and the Normal Sinus Rhythm Database (NSRDB) (Goldberger et al., 2000). We considered the following classification metrics: **TP** (beat labeled as AF and classified as AF), **FP** (beat labeled as no-AF and classified as AF), **TN** (beat labeled as no-AF and classified as no-AF), and **FN** (beat labeled as AF and classified as no-AF).

Unfortunately – for the chosen baseline (Zhou et al., 2015) – the authors did not report classifications at patient-level. Therefore, we replicated the method and obtained the desired level of classification. The classification results are shown in Tables 1, 2, 3 according to the clusters previously obtained. The difference in the number of heartbeats is due to the nature of AMELIA. Our online tool embeds the Pan-Tompkins algorithm as a peak detector (while the methods of the state of the art use the peak annotations provided from Physionet). Therefore, even if highly accurate, the performances of AMELIA integrate an additive error due to potential wrong classifications of this algorithm. Therefore, the only way to compare AMELIA—with respect to the chosen baselines—is to evaluate the overall statistics as: *Sensitivity* $= \frac{TP}{TP+FN}$, *Specificity* $= \frac{TN}{TN+FP}$ and *Accuracy* $= \frac{TP+TN}{TP+TN+FP+FN}$.

Table 1: AMELIA classification performance compared to the chosen baseline on MIT-BIH AF-db cluster 1.

Cluster 1	Method	TP	TN	FP	FN
#04015	AMELIA	500	42088	2886	25
	MORPHYTHM	491	40650	2836	27
	(Zhou et al., 2015)	478	40707	2779	40
#04048	AMELIA	792	38967	165	90
	MORPHYTHM	443	38982	145	363
	(Zhou et al., 2015)	419	38990	137	387
#04126	AMELIA	3345	39581	960	51
	MORPHYTHM	3154	38149	1424	132
	(Zhou et al., 2015)	3082	38743	830	204

Method	Sens	Spec	Acc
AMELIA	**0,965**	0,968	**0,968**
MORPHYTHM	0,887	0,964	0,961
(Zhou et al., 2015)	0,863	**0,969**	0,965

Table 2: AMELIA classification performance compared to the chosen baseline on MIT-BIH AF-db cluster 2.

Cluster 2	Method	TP	TN	FP	FN
#05091	AMELIA	44	35470	986	98
	MORPHYTHM	0	36640	4	133
	(Zhou et al., 2015)	0	36644	0	133
#05261	AMELIA	881	43739	1953	51
	MORPHYTHM	766	43015	1595	157
	(Zhou et al., 2015)	655	44215	395	268

Method	Sens	Spec	Acc
AMELIA	**0,861**	0,964	0,963
MORPHYTHM	0,725	0,980	0,977
(Zhou et al., 2015)	0,620	**0,995**	**0,990**

From the achieved results, it is possible to observe that for records belonging to: **Cluster 1:** AMELIA outperforms both the baseline and *MORPHYTHM* in terms of all the metrics of validation; **Cluster 2:** AMELIA provides significantly higher sensitivity with slightly lower specificity and accuracy; **Cluster 3:** AMELIA presents a significant loss, mostly in terms of sensitivity and accuracy.

From the LOPO-CV cross-validation, we chose the best network in terms of accuracy on the test data set. With this, we experimented with the proposed approach also on the MIT-BIH Normal Sinus Rhythm

Table 3: AMELIA classification performance compared to the chosen baseline on MIT-BIH AF-db cluster 3.

Cluster 3	Method	TP	TN	FP	FN
#06995	AMELIA	11215	27160	490	17784
	MORPHYTHM	27240	25901	1767	280
	(Zhou et al., 2015)	27072	25648	2020	448
#08219	AMELIA	7946	42595	4286	6207
	MORPHYTHM	13420	40934	4203	735
	(Zhou et al., 2015)	12627	42637	2500	1528
#08455	AMELIA	32705	15265	22	12470
	MORPHYTHM	44111	15244	45	151
	(Zhou et al., 2015)	44103	15250	39	159

Method	Sens	Spec	Acc
AMELIA	0,587	0,947	0,768
MORPHYTHM	**0,986**	0,932	0,959
(Zhou et al., 2015)	0,975	**0,948**	**0,962**

Table 4: AMELIA's accuracy on MIT-BIH NSR-db.

Record	**Rhythm Analyser**	**AMELIA**
ID	# FP	# FP
16265	2	0
16272	0	0
16273	1	0
16420	1	0
16483	0	0
16539	13	0
16773	0	0
16786	0	0
16795	4	0
17052	29	0
17453	0	0
18177	5	0
18184	0	0
19088	10	1
19090	0	0
19093	0	0
19140	0	0
19830	16	14

Databases. In this DB, all the recordings present a shape with high similarity with respect to the ones used in this study. The individuals included in the NSRDB were found to have no significant arrhythmia. Tables 4 show the results achieved on this DB. This experimentation represents a boundary validation for our proposed methods because the goal is to avoid all the phenomena with arrhythmia (different from AF) by using the useful information provided by the morphological module of AMELIA.

In this validation of AMELIA, we expected that the proposed tool do not get confused with (not significant) arrhythmia episodes affecting the patient from this data set. As we can see from the tables - by using our rhythm analyzer - an arrhythmia can be detected as an Atrial Fibrillation episode. With the introduction of the morphological Analyzer in AMELIA we reduced the chance of misclassifying several heartbeats.

5 THREATS TO VALIDITY

One of the limitations of the present study is that the evaluation is performed on a reduced number of selected recordings. This choice was due to the consideration that the Neural Network—used in this context as a morphology analyzer —is strictly dependent on several features related to an ECG recording, such as the lead, physiological aspects (smoker, BMI, etc.), and the instrumentation used to acquire the ECG.

Therefore, we opted for manually selecting the available recordings from the AF database to be involved in this preliminary study. Of course, in the real-world application of arrhythmia detection, the detectors are subject to a broad range of beat morphologies, including patients with ectopic beats, different types of arrhythmia, recordings corrupted by noise, and so on. The evaluation results of this study are to be intended only for a limited number of ECGs, such as the ones with common features as the ones selected for the validation of AMELIA. We also decided to validate the manual selection of ECG recordings in order to assess the similarity between them. From a refined perspective offered by the dendrogram, we observed that the 8 recordings could be further grouped into three sub-clusters. Thanks to this result, we could report the evaluation in terms of 'clusters' in order to highlight the specificity of AMELIA in the detection of AF episodes

The comparison with state of the art should be considered only illustrative because the validation was performed with different procedures: (i) Zhou et al. (2015) used the Physionet Long-Term AF Database[3] to tune their entropy threshold and the MIT-BIH Atrial Fibrillation Database to validate it, (ii) in the validation of *MORPHYTHM* (Laudato et al., 2020b) a LOPO-CV among all the patients from the MIT-BIH Atrial Fibrillation Database was performed while (iii) in AMELIA a LOPO-CV between only the selected patients from the MIT-BIH Atrial Fibrillation Database was executed.

6 CONCLUSION

We have presented AMELIA, an approach for automated detection of atrial fibrillation in the context of real-time monitoring of vital parameters. The approach is based on the combined use of two different sources of information that have paramount importance in the detection of AF events: (i) morphological analysis of the heartbeats; and (ii) RRI analysis. An empirical study conducted on two different well-known public data sets has shown the potential of the proposed approach compared with the state-of-the-art methods based on (i) just RRI analysis and (ii) on both sources of information.

Future works will be devoted to extending the experimentation of AMELIA on other datasets.

Also, we plan to further improve the accuracy of AMELIA, by replacing the manual selection of ECG recordings with a fully automated process.

[3]https://archive.physionet.org/physiobank/database/ltafdb/

Finally, we plan to improve the classification performances by refining some clue parameters in our proposed method. We specifically refer to the downsampling resolution, the Neural Network structure, and the length of the rhythm pattern.

ACKNOWLEDGMENT

The authors have been supported by the project PON 2014-2020—ARS01_00860 "*ATTICUS: Ambient-intelligent Tele-monitoring and Telemetry for Incepting and Catering over hUman Sustainability*" funded by the Ministry of Education, University and Research—RNA/COR 576347.

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