

Article

Identification of Electrocardiographic Patterns Related to Mortality with COVID-19

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Abstract: COVID-19 is an infectious disease that has greatly affected worldwide healthcare systems, due to the high number of cases and deaths. As COVID-19 patients may develop cardiac comorbidities that can be potentially fatal, electrocardiographic monitoring can be crucial. This work aims to identify electrocardiographic and vectorcardiographic patterns that may be related to mortality in COVID-19, with the application of the Advanced Repeated Structuring and Learning Procedure (AdvRS&LP). The procedure was applied to data from the “automatic computation of cardiovascular arrhythmic risk from electrocardiographic data of COVID-19 patients” (COVIDSQUARED) project to obtain neural networks (NNs) that, through 254 electrocardiographic and vectorcardiographic features, could discriminate between COVID-19 survivors and deaths. The NNs were validated by a five-fold cross-validation procedure and assessed in terms of the area under the curve (AUC) of the receiver operating characteristic. The features’ contribution to the classification was evaluated through the Local-Interpretable Model-Agnostic Explanations (LIME) algorithm. The obtained NNs properly discriminated between COVID-19 survivors and deaths (AUC = 84.31 ± 2.58% on hold-out testing datasets); the classification was mainly affected by the electrocardiographic-interval-related features, thus suggesting that changes in the duration of cardiac electrical activity might be related to mortality in COVID-19 cases.

Keywords: Advanced Repeated Structuring and Learning Procedure; COVID-19; deep learning; electrocardiography; local-interpretable model-agnostic explanations; neural network



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1. Introduction

COVID-19 is an infectious disease caused by the SARS-CoV-2 virus, which has greatly affected healthcare systems on a worldwide level due to its high transmission rate and health consequences [1]. As of 25 October 2023, there had been more than 700 million cases since the beginning of the pandemic [1]. Among these cases, the virus has manifested in different manners, as infected people have experienced mild to severe symptoms related to the respiratory system [2,3]. Severe manifestations of COVID-19 can require hospitalization in intensive care units [2,3] and may also be lethal, as proven by the great number of deaths (773,819,856 from the beginning of the pandemic until the time of writing) [1], especially in elderly groups and/or in subjects with preexisting conditions like, for example, overweight. Even when not requiring hospitalization, COVID-19 infection often contributes to the worsening of an already unstable health status [1].

It has also been observed that COVID-19 may lead to manifestations in biological systems other than the respiratory system. Some of the most common manifestations of COVID-19 outside the respiratory system arise at the cardiac level, for example, arrhythmias, bundle branch blocks, acute coronary syndrome, myocarditis, and heart failure [4–13]. As cardiac complications are prevalent among COVID-19 patients and have been observed in more than 50% of COVID-19 deaths [5,6], timely identification by cardiac monitoring is essential. A common form of cardiac screening is the standard 10-second 12-lead electrocardiogram (ECG, Figure 1a), which, together with the vectorcardiogram (VCG, Figure 1b), can be used to identify the presence of cardiac abnormalities. Usually, ECG and VCG analyses are automatically performed, and cardiologists combine their interpretation with patients' anamnesis. However, interpretation is highly dependent on cardiologists' experience and can be affected by limitations in the data or intra-subject and intra-rater variability [14–16].

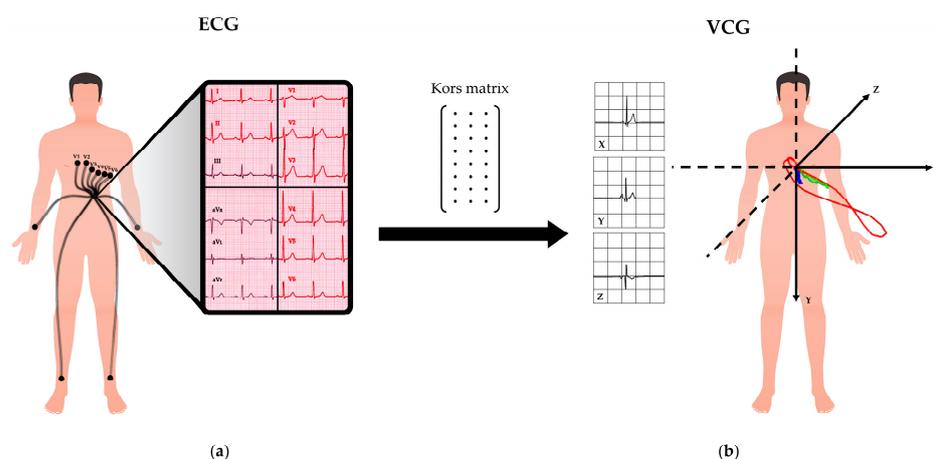


Figure 1. Representation of ECG and VCG: (a) the 12-lead ECG is acquired through electrodes; (b) the VCG is obtained from the ECG through the Kors matrix transformation.

In the context of the detection and investigation of cardiac risk associated with COVID-19, the use of machine learning and deep learning methods has already been largely investigated [17–22]. The methods proposed in [17–22] showed good accuracy, ranging from 85% to 100%, in detecting cardiovascular changes that may be related to COVID-19. However, complex deep learning models, such as convolutional neural networks (CNN), are not easily interpretable due to their nature (being black boxes). The non-explainability of the reasoning behind these complex models causes a lack of trust among clinicians and, thus, hampers their usage in clinical practice as diagnostic methods.

Sbrollini et al. [23,24] proposed a new machine learning method, called the Repeated Structuring & Learning Procedure (RS&LP), and tested it to detect heart failure, ischemia, and atrial fibrillation, with promising results. This method allows the construction of supervised neural networks (NNs) that were created by considering features as inputs and proved to be more interpretable than other deep learning models, which consider entire signals as inputs. The recent application of an advanced version of the RS&LP, namely Advanced Repeated Structuring & Learning Procedure (AdvRS&LP), for myocardial ischemia detection has seen further improvements in terms of NN performance [25].

Considering the good results obtained, the current work aims to investigate the use of the novel AdvRS&LP for the identification of electrocardiographic and vectorcardiographic patterns related to mortality with COVID-19. With this aim, the presented paper contributed to revealing the hidden electrocardiographic and vectorcardiographic patterns related to mortality with COVID-19, assessing the reliability of NNs created by AdvRS&LP in electrocardiographic feature interpretation and investigating interpretable solutions to support clinical practice using AI-based methods.

2. Materials and Methods

2.1. Database

Data pertain to the database collected during the “automatic COmputation of cardioVascular arrhythmIc risk from ECG data of COVID-19 patients” (COVIDSQUARED) project [21]. This database is composed of 1123 ECGs (12 leads), acquired from 646 subjects (age range: 19–100 years) hospitalized due to COVID-19 symptoms at the Ospedale San Matteo in Pavia, Italy (from 7 June 2020 to 21 September 2021). For research purposes, COVIDSQUARED can be obtained for free by contacting the authors.

The review board of the Fondazione Policlinico San Matteo approved the publication of anonymized case series of COVID-19 patients using data collected for routine clinical practice and waived the requirement for specific informed consent. The ECGs were recorded with a sampling frequency of 500 Hz, had a duration of 10 s, and were acquired by the standard 12-lead ECG configuration (I, II, III, aV_R, aV_L, aV_F, V1, V2, V3, V4, V5, V6). Survival of COVID-19 was assessed by follow-up, one year after hospitalization, using the Lombardy region death register (SISS). The database comprises multiple acquisitions for the same subject, obtained in different days; for each subject, only the ECG closest to hospitalization was included in this study. Moreover, ECGs that presented null leads were excluded. Subjects were divided into cases and controls: subjects that survived the infection were considered as controls, while subjects that died within one year after the infection were considered as cases. According to these criteria, 492 ECG recordings were classified as controls, and 148 ECG recordings were classified as cases.

2.2. Signal Pre-Processing and Feature Extraction

All computations were performed on MATLAB (Mathworks, version 2022a).

The ECG recordings included in the database were filtered with a digital bidirectional third-order Butterworth high-pass filter (cut-off frequency equal to 0.5 Hz) to reduce baseline wander. On lead I, R-peak positions were identified by the Pan–Tompkin’s algorithm [26] and considered as synchronization points for all heartbeats in all 12 ECG leads. For each ECG lead, synchronization points were used to select beat-related ECG segments spanning the time interval between 0.25 s before and $0.40 \cdot RR^{1/2}$ s after the synchronization point (where RR corresponds to the median RR interval in s) [24]. These ECG segments were used to compute 12 lead-dependent median ECG beats. Next, median VCG beats of the X, Y, and Z leads were computed by multiplying the median ECG beats of the 8 independent leads I, II, V1–V6, by using the Kors matrix [27–29]. From the median VCG components, the median vector magnitude signal was obtained.

The ECG landmarks were then identified in the 12 median ECG beats and in the vector-magnitude signal. These landmarks are the positions of the P-wave peak, QRS onset, R peak position, QRS offset (or J point), T-wave peak, and T-wave offset [24,30]. These landmarks in time plus the synchronization points were finally used to characterize each ECG recording by using the 254 features in Tables 1–3: 216 features (18×12 [features \times leads], ID from f1 to f216 in Table 1) describe the morphological and temporal characteristics regarding 12-lead median ECG beats’ lead-dependent features; 16 features (ID from f217 to f232 in Table 2) are related to the global QT interval, global QRS duration, heart rate (HR), HR variability, and dispersion of the ECG temporal characteristics, that are variability among ECG leads’ lead-independent features; 22 features (ID from f233 to f254 in Table 3) are related to the median vector-magnitude signal. These 254 features are designed to represent the most clinically relevant morphological, spatial, and temporal information of 10-second 12-lead ECG signals.

Table 1. Lead-dependent ECG features. The 18 features reported here, considered in all 12 leads for a total of 216 features, are related to morphological and temporal information of the ECG.

Feature ID	Feature Name	Feature Description
f1–f12	PA (μV)	P-wave peak amplitude
f13–f24	QA (μV)	Q-wave amplitude at QRS-complex onset position
f25–f36	QRSA (μV)	QRS-complex amplitude at R-wave peak position
f37–f48	SA (μV)	J-point amplitude
f49–f60	TA (μV)	T-wave peak amplitude
f61–f72	QRS/P (adi)	Ratio between the QRSA and PA
f73–f84	QRS/T (adi)	Ratio between the QRSA and TA
f85–f96	ToTpS ($^\circ$)	Angle between the baseline and the left front of the T wave
f97–f108	TpTeS ($^\circ$)	Angle between the baseline and the right front of the T wave
f109–f120	PR (ms)	Time interval between P-wave peak and R-wave peak
f121–f132	PS (ms)	Time interval between P-wave peak and J point
f133–f144	PT (ms)	Time interval between P-wave peak and T-wave end
f145–f156	QT (ms)	Time interval between QRS-complex onset and T-wave end
f157–f168	QRS (ms)	Time interval between QRS-complex onset and QRS-complex end
f169–f180	RS (ms)	Time interval between QRS-complex peak and QRS-complex end
f181–f192	ToTp (ms)	Time interval between T-wave onset and T-wave peak
f193–f204	TpTe (ms)	Time interval between T-wave peak and T-wave end
f205–f216	ρ (adi)	Median correlation coefficient between ECG beats and median ECG beat

For each lead-dependent feature, the feature ID considers the leads listed in the following order: I, II, III, aV_R, aV_L, aV_F, V1, V2, V3, V4, V5, V6.

Table 2. Lead-independent ECG features. The 14 features reported here are related to HR, HR variability, and ECG morphological dispersion.

Feature ID	Feature Name	Feature Description
f217	GQT (ms)	Global QT interval
f218	GQRS (ms)	Global QRS duration
f219	mnRR (ms)	Mean RR interval
f220	mnHR (bpm)	Mean HR
f221	MHR (bpm)	Maximum value of HR
f222	mHR (bpm)	Minimum value of HR
f223	mHR/MHR (-)	Minimum over maximum values of HR
f224	stdRR (ms)	Standard deviation of RR intervals
f225	PRD (ms)	Dispersion of the time intervals between P-wave peak and R-wave peak over the 12 leads
f226	PSD (ms)	Dispersion of the time intervals between P-wave peak and J point over the 12 leads
f227	PTD (ms)	Dispersion of the time intervals between P-wave peak and T-wave end over the 12 leads
f228	QTD (ms)	Dispersion of the time intervals between QRS-complex onset and T-wave end over the 12 leads
f229	QRSD (ms)	Dispersion of the time intervals between QRS-complex onset and QRS-complex end over the 12 leads
f230	RSD (ms)	Dispersion of the time intervals between QRS-complex peak and QRS-complex end over the 12 leads
f231	ToTpD (ms)	Dispersion of the time intervals between T-wave onset and T-wave peak over the 12 leads
f232	TpTeD (ms)	Dispersion of the time interval between T-wave peak and T-wave end over the 12 leads

Table 3. VCG features. The 22 features here reported are related to the median vector magnitude.

Feature ID	Feature Name	Feature Description
f233	MPV (μV)	Magnitude of the maximal P vector
f234	EPV ($^\circ$)	Elevation of the maximal P vector
f235	APV ($^\circ$)	Azimuth of the maximal P vector
f236	MQRSV (μV)	Magnitude of the maximal QRS vector
f237	EQRSV ($^\circ$)	Elevation of the maximal QRS vector
f238	AQRSV ($^\circ$)	Azimuth of the maximal QRS vector
f239	MJV (μV)	Magnitude of the maximal J vector

Table 3. Cont.

Feature ID	Feature Name	Feature Description
f240	EJV (°)	Elevation of the maximal J vector
f241	AJV (°)	Azimuth of the maximal J vector
f242	MTV (μV)	Magnitude of the maximal T vector
f243	ETV (°)	Elevation of the maximal T vector
f244	ATV (°)	Azimuth of the maximal T vector
f245	MVG (μV)	Magnitude of the ventricular gradient
f246	EVG (°)	Elevation of the ventricular gradient
f247	AVG (°)	Azimuth of the ventricular gradient
f248	PI (μV·ms)	Integral of the P wave in the vector magnitude
f249	QRSI (μV·ms)	Integral of the QRS complex in the vector magnitude
f250	TIon (μV·ms)	Integral of the left front of the T wave on the vector magnitude
f251	TIoff (μV·ms)	Integral of the right front of the T wave on the vector magnitude
f252	PQRS-SA (°)	Spatial angle between the P vector and the QRS vector
f253	QRST-SA (°)	Spatial angle between the QRS vector and the T vector
f254	PT-SA (°)	Spatial angle between the P vector and the T vector

2.3. Advanced Repeated Structuring and Learning Procedure

Extracted features are considered as inputs to an NN created with the Advanced Repeated Structuring and Learning Procedure (AdvRS&LP) [25], an enhanced version of the RS&LP algorithm by Sbröllini et al. [23,24], a procedure to create architecture specifically designed for the problem of interest. The AdvRS&LP (Figure 2) builds a supervised NN, starting by fixing a defined number of inputs (IN) and classification outputs (OUT). Next, the procedure iteratively allows a gradual structuring, which starts with 1 neuron in a single hidden layer. During each structuring phase (Figure 2, block 1), the current NN is extended in multiple new NNs thanks to the insertion of additional neurons (AD) in one of the existing hidden layers or in a new hidden layer. New AD neurons are initialized (Figure 2, block 2) with random weights and biases, which range between -1 and $+1$, and sigmoid activation function. The weights and biases of neurons that are already part of the current NN do not vary. Insertion of new AD neurons is considered successful if the performance of the extended NNs is greater than the performance of the current NN after a single learning step. If performance improvement does not occur, the addition of AD neurons is discarded. Successful new structures are then trained (Figure 2, block 3) by optimizing the loss function (mean squared error) using the scaled-conjugate-gradient algorithm [31], considering the early stopping criterion to prevent overfitting [32] and the inverse of class prevalence as input to counterbalance possible class disparities [33].

The performance of the new NN is evaluated and compared with the current NN, and the NN with the lowest error is considered the best NN (Figure 2, block 4). If the best NN is different from the current NN, the best NN becomes the new current NN, and the procedure restarts (Figure 2, block 5). By contrast, if the best NN corresponds to the current NN, the number of AD neurons is decreased by 1 (Figure 2, block 6), and the procedure restarts. Finally, the procedure concludes when the number of AD neurons becomes zero (Figure 2, block 7). More details about AdvRS&LP can be found in [25].

For this study, IN was equal to 254 (ECG/VCG features), OUT was equal to 2 (case and control classes), and AD was equal to 30. A 5-fold cross-validation procedure was employed [34]. The dataset was divided into 5 folds, of which 4 folds were used for creating the NN by AdvRS&LP, while the remaining fold was used as a hold-out testing dataset. The data division was performed by maintaining the case–control prevalence in all folds and without mixing patients in the training and hold-out testing datasets.

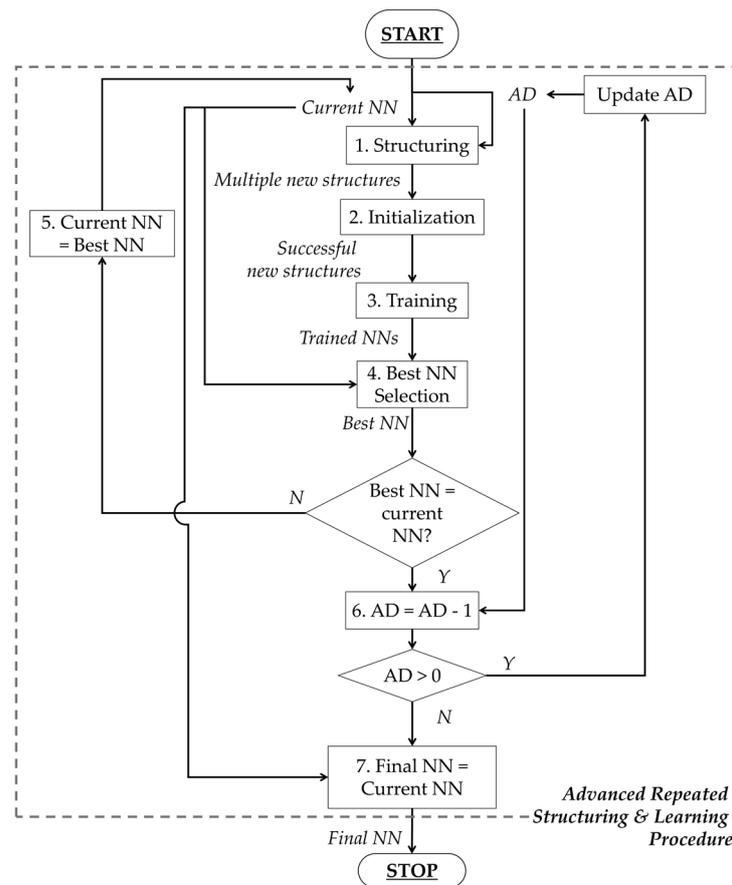


Figure 2. Flow chart of the Advanced Repeated Structuring and Learning Procedure.

2.4. Deep Learning Interpretability Module

To investigate the contribution of each ECG/VCG feature to the classification by the NNs, the Local-Interpretable Model-Agnostic Explanations (LIME) algorithm [35–37] was applied. The LIME is an explainer algorithm that allows the interpretation of deep learning models' decisions, taken for each observation in a dataset, by approximating the model with a local, interpretable, and much less complex model. Explanations come in the form of features ranked according to the amount of influence they had on classification. In practice, LIME was applied to locally approximate the NN with a linear model and to obtain feature rankings for each recording included in the database. Next, to obtain a general view of the ECG/VCG features' contribution to classification, feature relevance (FR) was computed as the weighted average of the percentage of recordings presenting each feature in each ranking position. Consequently, 254 FR values, each associated with the corresponding ECG/VCG feature, were obtained. Features were then sorted according to FR values.

2.5. Statistics

The performance of the NNs created by AdvRS&LP was quantified by considering the architecture, by computing the area under the curve (AUC) of the receiver operating characteristic (ROC) and the accuracy (ACC) in training and validation datasets and the FR. Moreover, to compare deep learning analysis with standard statistical analysis, univariate AUC of the ROC was computed for each of the 254 ECG/VCG features. Features, as previously undertaken with FR, were sorted according to AUC values. Agreement between AUC and FR for each NN and between the FRs of the different NNs was assessed by computing Pearson's correlation coefficient. Statistical significance was set at 0.05.

3. Results

The AdvRS&LP produced 5 NNs (one for each cross-validation fold), whose architectures and performance are listed in Table 4. Despite the different architectures, all the NNs presented high-level performances, comparable across folds, in the hold-out testing sets (AUC > 80% and ACC > 79%). The best NN, composed of 714 neurons distributed in three layers, was related to the second fold: the highest AUC on the validation dataset (AUC = 86.42% and ACC = 83.17%). The worst performance was obtained in the 4th fold (AUC = 80.89% and ACC = 79.21%).

Table 4. Architecture and performance of the neural networks created by the Advanced Repeated Structuring and Learning Procedure.

	Architecture		AUC (%)		ACC (%)	
	Number of Layer	Distribution of Neurons	Training	Hold-Out Testing Fold	Training	Hold-Out Testing Fold
fold 1	3	[101 100 555]	99.11	86.05	99.01	79.21
fold 2	3	[101 100 513]	95.75	86.42	97.28	83.17
fold 3	1	[736]	94.61	86.00	97.24	81.19
fold 4	3	[196 188 245]	100.00	80.89	100.00	79.21
fold 5	4	[101 100 100 228]	97.41	82.18	98.51	79.21
Overall	-	-	97.38 ± 2.25	84.31 ± 2.58	98.42 ± 1.17	80.40 ± 1.77

ACC: accuracy; AUC: area under the curve of the receiver operating characteristic curve. Overall performance is reported in terms of average ± standard deviation.

Table 5 shows the first 10 features of the ranking obtained for the univariate AUC and FR computed for each NN created by AdvRS&LP, while Figure 3 depicts the scatter plots of the comparisons between the AUC and FR for each NN and between the FRs of the different NNs. The FRs obtained by all the folds presented a poor correlation with the univariate AUC ($\rho < 0.30$, $p < 0.05$), but the agreement between the FRs obtained in the different folds was statistically strong ($\rho > 0.97$, $p < 0.05$).

Table 5. List of the first 10 features on the ranking obtained for univariate AUC and FR computed for each NN created by AdvRS&LP.

Ranking	AUC (%)	FR				
		Fold 1	Fold 2	Fold 3	Fold 4	Fold 5
1	TpTeS on lead V6 (0.65)	mnNN (0.78)	mnNN (0.78)	mnNN (0.78)	mnNN (0.78)	mnNN (0.78)
2	PR on lead aVL (0.65)	PT on lead V2 (0.78)	QT on lead V6 (0.77)	PT on lead II (0.71)	PT on lead V6 (0.74)	QT on lead aVR (0.75)
3	SDNN (0.64)	PT on lead aVR (0.78)	QT on lead aVR (0.77)	PT on lead aVR (0.72)	PT on lead V4 (0.77)	PT on lead aVR (0.76)
4	PTD (0.64)	PT on lead II (0.77)	QT on lead aVF (0.77)	QT on lead aVR (0.77)	PT on lead V5 (0.74)	PT on lead I (0.75)
5	PS on lead aVL (0.64)	PT on lead I (0.77)	QT on lead II (0.76)	PT on lead V4 (0.75)	PT on lead II (0.78)	QT on lead II (0.75)
6	QA on lead II (0.63)	PT on lead V3 (0.76)	QT on lead V4 (0.76)	PT on lead V1 (0.71)	PT on lead aVR (0.78)	QT on lead V6 (0.75)
7	TpTeS on lead V5 (0.63)	PT on lead V1 (0.76)	QT on lead V5 (0.76)	QT on lead II (0.76)	QT on lead aVR (0.77)	PT on lead V6 (0.78)

Table 5. Cont.

Ranking	AUC (%)	FR				
		Fold 1	Fold 2	Fold 3	Fold 4	Fold 5
8	QA on lead V6 (0.63)	QT on lead II (0.75)	PT on lead V6 (0.76)	QT on lead aVF (0.77)	QT on lead II (0.76)	PT on lead II (0.77)
9	QRST-SA (0.63)	QT on lead aVR (0.75)	QT on lead V3 (0.76)	PT on lead I (0.72)	PT on lead I (0.76)	QT on lead I (0.74)
10	ToTpD (0.63)	PT on lead V4 (0.75)	QT on lead V2 (0.75)	QT on lead V1 (0.75)	PT on lead aVL (0.73)	QT on lead aVL (0.74)

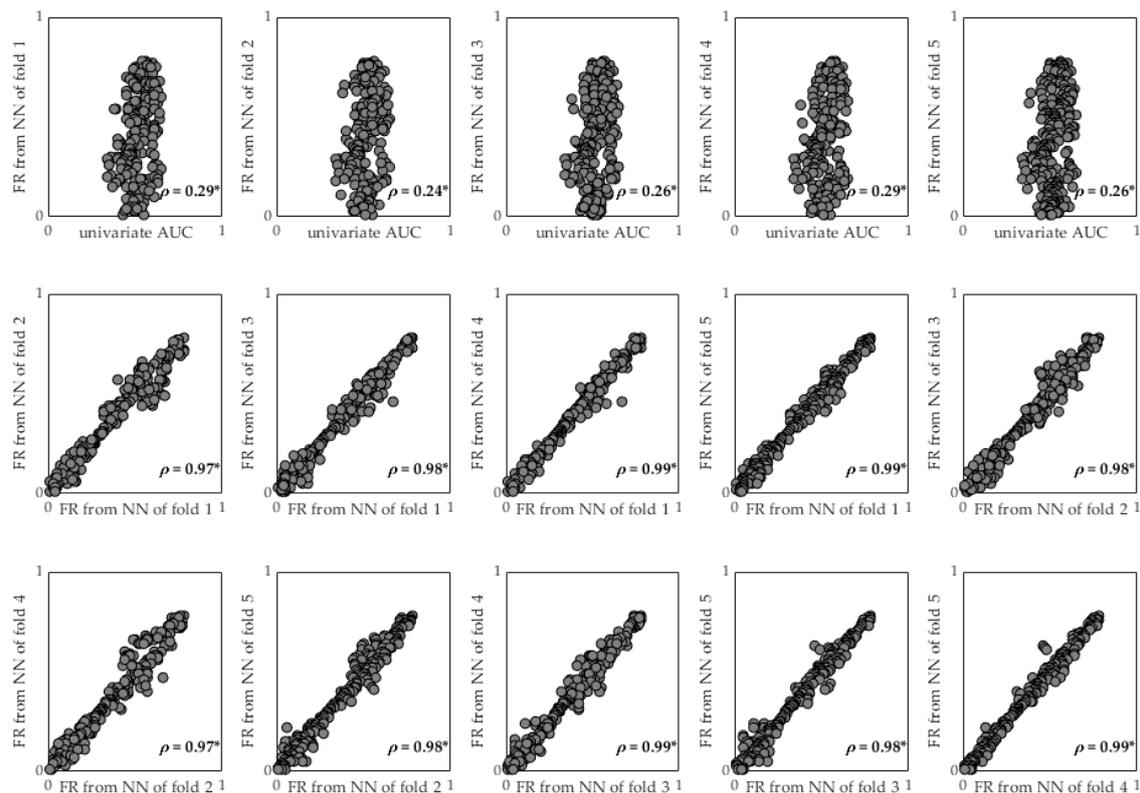


Figure 3. Comparisons between AUC and FR for each NN and between the FRs of the different NNs. * refers to p -value lower than 0.05.

4. Discussion

This work aims to identify, with the application of the novel AdvRS&LP, electrocardiographic and vectorcardiographic patterns that may be related to mortality in subjects affected by COVID-19.

The definition of “death due to COVID-19” is still under discussion. Indeed, most of the subjects whose mortality is associated with COVID-19 are also affected by other, pre-existing diseases; thus, the infection aggravates an already compromised condition. For this reason, we considered the ECG acquisition closest to the hospitalization date, considering the infection active during the recording, and we defined cases as subjects that died within one year from the infection, assuming the deaths were correlated with COVID-19. Due to the limited size of the database, the selected ECG signals were all employed for the 5-fold cross-validation procedure. Although this procedure is widely accepted in the literature [17,18,20,21], the validation of the method in a testing holdout dataset would demonstrate the applicability of the method in a real-world application. Consequently, the classification results are purely indicative. Future studies will aim to demonstrate the reliability of the method in a real-world clinical scenario.

Despite these limitations, the NNs created through AdvRS&LP showed very promising classification capabilities, with a training AUC and ACC higher than 94% and 97%, respectively, and a validation AUC and ACC higher than 80% and 79%, respectively (Table 4). The AUC performed a little better than the ACC because the dataset was unbalanced (the number of controls was much larger than the number of cases). Considering the good performances, the application of AdvRS&LP for the identification of ECG/VCG patterns associated with mortality in COVID-19 patients seemed fitting.

The architectural structuring of the artificial NNs was accomplished using the novel AdvRS&LP algorithm [25], an enhanced version of RS&LP recently proposed by Sbröllini et al. [23,24]. Thanks to the removal of structural rules (previously included in RS&LP) and to a variable number of neurons to be added in each structuring step of the procedure, AdvRS&LP fosters the creation of NNs that adapt to the task for which they are needed, without compromising classification performance. Indeed, the architectures of the NNs obtained for the different folds are structurally different, since they are created with different data divisions, although they provide similar classification performances in both training (AUC = $97.38 \pm 2.25\%$ and ACC = $98.42 \pm 1.17\%$) and hold-out testing (AUC = $84.31 \pm 2.58\%$ and ACC = $80.40 \pm 1.77\%$).

Classifiers created by AdvRS&LP can take into account a number of inputs that correspond to the number of features included in the training dataset. In this work, 254 features that covered the clinically relevant morphological, spatial, and temporal information for the ECG/VCG signals were extracted from 10-second 12-lead ECG signals. The use of features, as in this work, rather than raw or processed signal sequences guarantees a certain level of interpretability in NN classification. We decided not to normalize the input features: this design choice will guarantee the interpretability of the features by clinical personnel, which allows comparisons with normality ranges. Moreover, we decided not to apply the preprocessing feature-selection method. During the training of the NN, the adjustment of weights and biases automatically selects the feature of interest, embedding the feature-selection procedure inside the NN construction. The complexity of deep learning models can hinder the uncovering of the decision process behind classification, which is, however, fundamental in a diagnostic context. Notably, no anamnestic or clinical features were considered as inputs for the NNs, with the aim of underlining hidden cardiac patterns associated with mortality with COVID-19.

To permit the interpretability of the NN created by AdvRS&LP, LIME was applied [35–37]. The use of LIME allowed the construction of a feature ranking, which highlighted the ECG/VCG features that most significantly affected the classification performed by the NNs and, therefore, the ECG/VCG features whose changes could be mainly associated with mortality in cases involving COVID-19. According to this analysis, HR and electrocardiographic intervals seem to be of relevance for classification, as features involving the mnNN, PT interval, and QT interval appeared in the top 10 on the FR ranking of all the NNs (Table 5), suggesting that changes in the duration of cardiac electrical activity might be related to mortality in COVID-19 cases. This finding is in agreement with the body of clinical research, which already revealed the modification of the QT interval [38], ST-T pattern [39–41], and PR interval [42] induced by COVID-19 infection. Notably, modifications to the QT interval are, indeed, often associated with a higher risk of developing arrhythmias or heart failure [2,43], both of which have been observed in COVID-19 patients [4–13]. The agreement between the FRs extracted from the different NNs ($\rho > 0.97$, Figure 2) suggests robust feature interpretation by LIME.

The rankings obtained from LIME and the conventional statistical analysis, with the latter usually evaluated by clinicians, showed disagreement ($\rho < 0.30$). This disagreement was surely due to the different approaches: while conventional ROC analysis is based on a linear separation boundary between samples by considering the role of each single variable regardless of possible interactions, NNs build highly nonlinear separation boundaries by considering all variables simultaneously during model training. The conventional statistical analysis gave relevance to the features related to repolarization and RR-interval variability,

as evidenced by the top 10 on the univariate AUC ranking (Table 5). From a physiological perspective, a relationship between the RR interval and the QT interval cannot be denied, as changes in one lead to variations in the other [44]. Thus, future studies will be needed to investigate the correlation between QT and RR features exclusively.

In the context of the detection and investigation of cardiac risk associated with COVID-19, the use of machine learning and deep learning methods has already been investigated [17–22] (Table 6). All these studies are based on electrocardiography, but they differ in terms of the type of input: three papers [17–19] considered the ECG paper scan of the open access “ECG image dataset of Cardiac and COVID-19 patients” database [45], two studies [20,22] considered ECG signals collected on a private database, and one paper [21] considered ECG signals on the COVIDSQUARE database. Most of the papers [17–19,21] investigated the detection of COVID-19 among those with healthy status or other diseases, one study [23] assessed the severity of the COVID-19 infection, and Sridhar et al. [20] aimed to predict COVID-19-related mortality. All the studies applied CNN [17–22], which was validated by the k-fold cross-validation method [17,18,20,21], or static train/test data division. Regarding performance, methods that were designed to identify patients affected by COVID-19 presented very high levels of performance (accuracy higher than 85%) [17–19,21], and the method that was designed to predict COVID-19-related mortality presented a good performance (AUC equal to 60%) [20]. Finally, only two out of six papers applied post-processing algorithms for ECG interpretation, both of which were based on color maps [19,22]. Thus, in comparison with the literature, the method presented here is a unique approach that considers ECG features as NN inputs and includes an interpretability-post-processing algorithm (LIME) that is able to sort ECG features according to their importance to the classification performance. This design choice ensures the high level of acceptability of the AI-based method in a real clinical scenario. Indeed, the non-explainability typical of CNN causes a lack of trust among clinicians and, thus, hampers their usage in clinical practice as diagnostic methods. Finally, in comparison with the work of Sridhar et al. [20], our NN, created by using AdvRS&LP, provided a higher level of performance in detecting mortality correlated with COVID-19 after it was assessed with the same type of validation procedure, albeit on a different database.

Table 6. Qualitative comparison with the literature.

Ref.	Input	Output	Method	Validation	Performance	Interpretation
[17]	Hexaxial feature mapping computed by extracting signal from ECG-image dataset of cardiac and COVID-19 patients	COVID vs. No COVID	CNN	5-fold cross-validation	AUC = 95%	-
[18]	ECG-image dataset of cardiac and COVID-19 patients	TEST1: COVID vs. Other vs. Normal TEST 2: COVID vs. Myocardial Infarction vs. Abnormal heartbeat vs. History of Myocardial Infarction vs. Normal	CNN	10-fold cross-validation	AUC = 99%	-
[19]	ECG-image dataset of cardiac and COVID-19 patients	COVID vs. No COVID	Efficient ECGNet	Static train/test data division	ACC = 99%	Grad-CAM
[20]	1386 ECGs recorded from hospitalized COVID-19 patients	Survived vs. Dead	CNN-LSTM	10-fold stratified cross-validation	AUC = 60%	-

Table 6. Cont.

Ref.	Input	Output	Method	Validation	Performance	Interpretation
[21]	ECG of COVIDSQUARED and ECG of Physionet database	COVID vs. Non COVID	CNN	7-fold cross-validation	ACC = 85%	-
[22]	1453 adult patients affected by COVID-19	Severity Stratification	CNN	Static train/test data division	AUC = 73%	Heatmap
This work	ECG features extracted from COVIDSQUARED	Survived vs. Dead	NN	5-fold cross-validation	AUC = 84%	LIME

5. Conclusions

The application of an NN-based algorithm combined with an interpretability approach highlighted features related to electrocardiographic intervals as those mainly affecting the classification performed by NNs trained on ECG signals from COVID-19 patients. This application highlighted the promising applicability of the neural networks created by Advanced Repeated Structuring and Learning Procedure in the clinical environment, supporting clinical personnel in the interpretation of the electrocardiographic patterns associated with a specific pathology.

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