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PAPER

Predicting Heart Failure: A Comparative Approach between Artificial Neural Networks and Support Vector Machines

José Luis Herrera Salazar(✉), Magdalena Talla Linderman, Orlando Iparraguirre-Villanueva

Facultad de Ingeniería, Ciencias y Administración, Universidad Autónoma de Ica, Ica, Perú

jose210281@hotmail.com

ABSTRACT

In recent years, cardiovascular diseases have become increasingly important as a leading cause of death globally. heart failure (HF), a chronic disease affecting some 26 million people worldwide, has become a growing pandemic. Its prevention is a national and global emergency. In India, between 1.3 and 4.6 million adults suffer from HF, and despite advances in therapy and prevention, mortality and morbidity remain high, with significant costs to the healthcare system. The purpose of this study is to conduct a comparative evaluation of ML models for predicting HF. The support vector machine (SVM) and artificial neural network (ANN) models were analyzed to determine which model offers superior accuracy. A dataset from the Kaggle platform with x records and x features was used to train the models. The results indicated that the SVM model is the best predictor of HF with an accuracy of 79%, which far exceeds the ANNs with 77%. It is concluded that the machine learning (ML) method known as SVM shows outstanding and effective performance in the task of predicting heart failure.

KEYWORDS

machine learning (ML), models; heart failure (HF), prediction

1 INTRODUCTION

In recent years, cardiovascular conditions have emerged as a major cause of death in populations around the world [1]. Heart failure (HF) is a growing global public health problem, affecting approximately 26 million people worldwide [2]. This chronic disease has become an ever-increasing pandemic [3], and its prevention is an urgent need both nationally and globally [4]. In India, the prevalence of HF is between 1.3 and 4.6 million adults, and it is a complex clinical syndrome caused by several cardiovascular diseases [6]. Despite advances in therapy and

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prevention, [5] mortality and morbidity remain high, with considerable healthcare costs [7]. The death rate due to HF remains high, with approximately 50% over five years in recent years [8]. In addition, HF has become the leading cause of hospitalization and mortality in Germany [9] and worldwide. The risk of developing HF affects a significant part of the population in Taiwan [11], and the burden of the disease on healthcare systems requires alternative strategies to long and costly hospitalizations [12]. In addition, the incidence and prevalence of HF continue to increase annually, putting increasing pressure on healthcare systems worldwide [13]. It is estimated that approximately 1–3% of the adult population globally suffers from HF [14], and in the United States, the prevalence exceeds 6 million adults, with a steadily increasing incidence [15]. The World Health Organization (WHO) reports that there are about 17 million cases of HF [16] and defines HF as the inability of the heart to pump sufficient blood and oxygen to vital organs [17]. In this context, accurate and reliable prognostic prediction tools for patients and healthcare providers are crucial [18].

Over the last ten years, an astonishing advancement in the field of technology has taken place [19]. Artificial intelligence (AI) has proven to be beneficial in clinical research [20]. This technology has intrigued the healthcare industry, allowing its integration into various areas of medicine [21]. In the past five years, AI has challenged and transformed medicine in multiple aspects, from diagnostics and medical image analysis to drug development and patient management [22]. In addition, AI can harness a wide range of medical data, such as electronic records, biosensors, and molecular data, to improve medical care and address pressing challenges in the sector [23]. The application of AI and machine learning (ML) in medicine focuses on extracting valuable information from large datasets, which can improve accuracy and efficiency in the diagnosis and treatment of patients [24]. AI is poised to revolutionize medicine, playing a crucial role in data analysis, pattern recognition, anomaly identification, and decision-making [25]. The most widely used AI architectures in medical image recognition are ML and deep learning (DL) [26]. AI has the potential to revolutionize healthcare by driving innovation, automation, and optimization in various areas of medicine [27]. As access to healthcare has improved and patient volume has increased, the amount of medical data has grown significantly [28]. The successful implementation of technologies such as ML, AI, and data science has proven to be of great use in the healthcare field, enabling more effective decision-making and the ability to make accurate predictions using the vast amount of data generated by this industry [29]. Furthermore, the application of AI in medical data analytics can provide doctors with the ability to diagnose diseases and anticipate patient outcomes, which could lead to earlier detection of medical conditions and the development of personalized treatment plans [30].

The purpose of this study is to carry out a comparative evaluation of ML models to predict HF. Support vector machine (SVM) and artificial neural network (ANN) models are examined and evaluated to determine which model offers superior accuracy. The article is structured in six main sections. Section 1 introduces the context of the problem addressed in the study. Section 2 is devoted to a review and discussion of related work. Section 3 contains a detailed description of the methodology used in the study, divided into two parts: the first part describes the models, and the second part presents the development of the case study. The results of the model training are presented in Section 4. Finally, in sections 5 and 6, an analysis is carried out, and the results obtained are concluded.

2 RELATED WORK

Over time, scientists have developed ML models to anticipate the occurrence of HF and to provide medical professionals with more effective tools in the diagnostic process [31]. For example, the authors of [32] proposed to predict the survival of HF patients. To achieve this, five ML methods were employed: decision tree (DT), decision tree regression (DTR), random forest (RF), XGBoost, and gradient boosting (GB) algorithms. The results of the study highlight that the RF model achieves the highest accuracy, reaching 97.78%. Similarly, the study [33] explored various ML models for heart disease prediction, including logistic regression (LR), k-nearest neighbors (KNN), RF, and ANN. RF demonstrated a remarkable accuracy level of 83.15%, outperforming other evaluated algorithms.

Also, in [34], seven ML algorithms were used to predict the presence of HF in patients. The methods applied included KNN, Naïve Bayes (NB), LR, SVM, RF, DT, and neural network (NN). The results revealed that LR, SVM, and NN provided the best results, reaching an impressive accuracy of up to 94.57%. In [35] they improved the accuracy in predicting HF in patients. The researchers applied four ML classifiers: SVM, RF, DT, and XGBoost, to assess patients' chances of survival. SVM stood out with the highest accuracy, reaching a remarkable 96.67%, outperforming the other classification techniques. They also proposed an improved prediction model for HF [36]. To achieve this, they used an ensemble learning model that combines a variety of algorithms, such as RF, DT, GB, LR, ANN, NB, SVM with a radial basis kernel, SVM with a linear kernel, kNN, recurrent neural network (RNN) based on short-term memory (LSTM), and LR with selected features. The result is an accuracy of 99.5%, significantly outperforming contemporary techniques. On the other hand, [37] developed an HF prediction model using SVM. The methodology included building this SVM-based prediction model. The results revealed that the model achieved an impressive classification accuracy of 87.50% on the final test set. The study [38] developed an innovative solution to predict HF by using an ensemble learning approach combining 10 different classification algorithms, such as AdaBoost, CatBoost, DT, KNN, LR, Light GBM, NB, RF, SVM, and XGBoost. This joint model achieved an outstanding test accuracy of 85.2% and a recall rate of 87.50%.

Similarly, in [39] they sought to anticipate HF through the application of seven ML classification algorithms. They performed a comparative performance analysis of these algorithms. The research results indicate that naive bias, RF, and SVM algorithms outperform the others in HF prediction, reaching an accuracy close to 85.86%. In [40] they presented a hybrid model that combines an optimized ANN with an artificial bee colony to improve the accuracy of HF diagnosis through ML. The model achieves 99.3% accuracy. The study [41] evaluated the effectiveness of various ML algorithms, such as SVM, DT, RF, and ANN, in predicting heart disease. The results of the analysis revealed that the RF model achieved the highest prediction accuracy, with a performance of 83%. Finally, in [42], they analyzed and contrasted different ML models (GB, RF, KNN, LR, and SVM) to evaluate the effectiveness of these algorithms in cardiovascular disease prediction. After comparing all the aforementioned ML approaches, SVM was found to be the most suitable, with an efficiency of 94.56% for predicting the presence of cardiovascular diseases.

3 METHODOLOGY

At this stage, we will provide a thorough exposition of the SVM and ANN models that will be used in the context of predictions associated with HF disease.

3.1 Support vector machine

Support vector machine is a tool used to address classification and prediction issues in both regression and classification problems [43]. The SVM classifier operates by classifying training instances into two classes, adjusting a separating hyperplane between them to maximize the margin between the hyperplane and each of the classes. The determination of the class of a new instance is based on which side of the hyperplane it lies on [44]. The key to the SVM classifier lies in identifying the support vectors that define the boundary hyperplanes, seeking to maximize the margin between these planes [45]. The quality of SVM classification is related to the maximization of the margin between the class data points surrounding the hyperplane [46]. Compared to other methods, SVM has been shown to produce accurate results that are easily interpretable [47]. In the two-dimensional context, the hyperplane is characterized by equation (1).

$$\beta 0 + \beta 1x1 + \beta 2x2 = 0 \tag{1}$$

With parameters $\beta 0$, $\beta 1$, and $\beta 2$ given, any pair of values $x = (x1, x2)$ satisfying the equality represents points on the hyperplane.

3.2 Artificial neural network

A neural network is composed of a set of neurons interconnected by weighted links [48]. These neurons, also known as nodes, transform a set of inputs into outputs, whose transformation is defined by the characteristics of the nodes and the weights of the connections between them [49]. The learning process involves adjusting the weights and biases to strengthen the connections between neurons in different layers, reducing the classification error rate measured by the loss function. This process, known as neural network training, is based on supervised learning from labeled data [50]. Furthermore, the structure of an ANN includes input layers, possibly hidden layers, and an output layer, and resembles the organization of synapses in a brain [51]. Ultimately, an artificial neural network is a system with parallel distributed processes [52]. Figure 1 presents the ANN architecture.

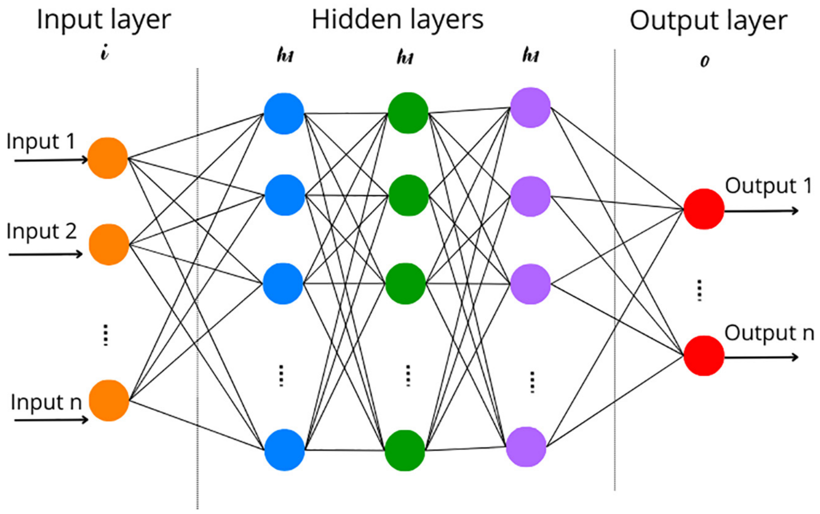

Fig. 1. Artificial neural network architecture

3.3 Understanding the dataset

This study used a dataset hosted on the Kaggle platform. The dataset is composed of a total of 299 entries and consists of 13 main variables, which are: Age (patient's age in years), anemia (hemoglobin level), creatinine_phosphokinase (level of this enzyme in the blood), diabetes (whether the patient suffers from diabetes), ajection_fraction (percentage of blood ejected from the heart per beat), high_blood_pressure (in case the patient presents hypertension), platelets (blood platelet count), serum_creatinine (blood serum creatinine level), serum_sodium (blood serum sodium level), sex (gender of the patient), smoking (whether the patient is a smoker or not), time (the duration of follow-up in days), DEATH_EVENT (whether the patient has died during the observation period). Variables with binary values represent characteristics that can have only two possible states: zero for "Negative" or "No" and one for "Positive" or "Yes." Figure 1 shows the development process of the case study.

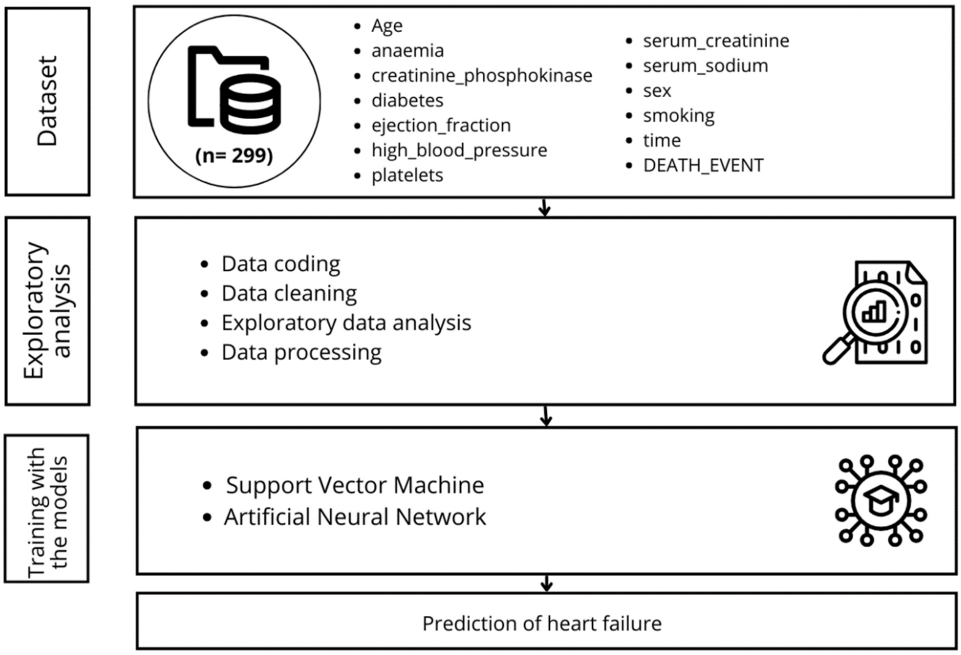

Fig. 2. Development process

3.4 Data preparation

In this section, a comprehensive analysis of the data was performed before the modeling and training phase. We started by importing the essential libraries for data manipulation. Subsequently, the dataset is evaluated as shown in Table 1. Furthermore, it can be seen that most of the attributes have 'float64' or 'int64' data types, which facilitates their compatibility with ML algorithms. The other features seem to follow a normal distribution since their means coincide with the medians. Also, it is observed that the average age of the patients is 60.83 years; the minimum age is 40 years, and the maximum age is 95 years. The column "anemia" shows that 43.14% of the patients have anemia (value 1), and 56.86% do not have anemia (value 0). The creatinine_phosphokines variable has a mean value of approximately 581.84, with a high variability, as the standard deviation is high. Also, 41.81% of people have diabetes (value 1), and 58.19% do not have diabetes (value 0). As for the variable "ejection_fraction," it has a mean value of approximately 38.08. At the same time, 35.12% of people have high blood pressure (value 1), and 64.88% do not have high blood pressure (value 0). Blood platelet counts ranged from 25,100 to 850,000. Similarly, 32.11% of people experienced a death event, while 67.89% did not, as shown in Table 2. These findings provide valuable information for future data preparation and processing decisions.

Table 1. Dataset characteristics

Age	Anemia	Creatinine_ Phosphokinase	Diabetes	Ejection_ Fraction	Platelets	Serum_ Creatinine	Serum_ Sodium	Sex	Smoking	Time	DEATH_ EVENT
75	0	582	0	20	265000	1.9	130	1	0	4	1
55	0	7861	0	38	263358	1.1	136	1	0	6	1
65	0	146	0	20	162000	1.3	129	1	1	7	1
50	1	111	0	20	210000	1.9	137	1	0	7	1
65	1	160	1	20	327000	2.7	116	0	0	8	1
...	...	...	...	...	...	...	...	...	...	...	...
62	0	61	1	38	155000	1.1	143	1	1	270	0
55	0	1820	0	38	270000	1.2	139	0	0	271	0
45	0	2060	1	60	742000	0.8	138	0	0	278	0
45	0	2413	0	38	140000	1.4	140	1	1	280	0
50	0	196	0	45	395000	1.6	136	1	1	285	0

Table 2. Numerical analysis of the dataset

	Count	Mean	Std	Min	25%	50%	75%	Max
age	299	60.833893	11.894809	40	51	60	70	95
anemia	299	0.431438	0.496107	0	0	0	1	1
creatinine_ phosphokinase	299	581.839465	970.287881	23	116.5	250	582	7861
diabetes	299	0.41806	0.494067	0	0	0	1	1
ejection_fraction	299	38.083612	11.834841	14	30	38	45	80
high_ blood_pressure	299	0.351171	0.478136	0	0	0	1	1
platelets	299	263358.029	97804.2369	25100	212500	262000	303500	850000
serum_creatinine	299	1.39388	1.03451	0.5	0.9	1.1	1.4	9.4
serum_sodium	299	136.625418	4.412477	113	134	137	140	148
sex	299	0.648829	0.478136	0	0	1	1	1
smoking	299	0.32107	0.46767	0	0	0	1	1
time	299	130.26087	77.614208	4	73	115	203	285
DEATH_EVENT	299	0.32107	0.46767	0	0	0	1	1

3.5 Exploratory data analysis

Figure 2 shows that the duration of patient follow-up has a significant impact on the probability of mortality. With fewer days of follow-up, mortality tends to occur at older ages, while the more days of follow-up applied, the greater the likelihood of mortality events occurring, even at younger ages. This suggests that longer follow-up tends to identify mortality events at younger ages, whereas, with shorter follow-up, deaths are observed at older ages. This relationship between length of follow-up and probability of mortality highlights the importance of considering observation time when analyzing data related to patient health.

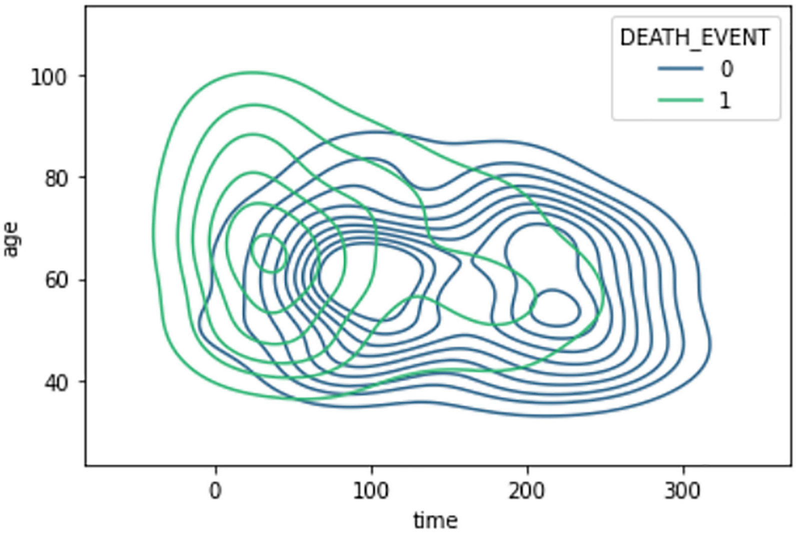

Fig. 3. Relation between age and mortality

In Figure 3, outliers can be identified in the characteristic "serum_creatinine." These unusual values deviate significantly from the majority of the data in that variable and may be the result of measurement errors or simply represent unusual cases in the study population.

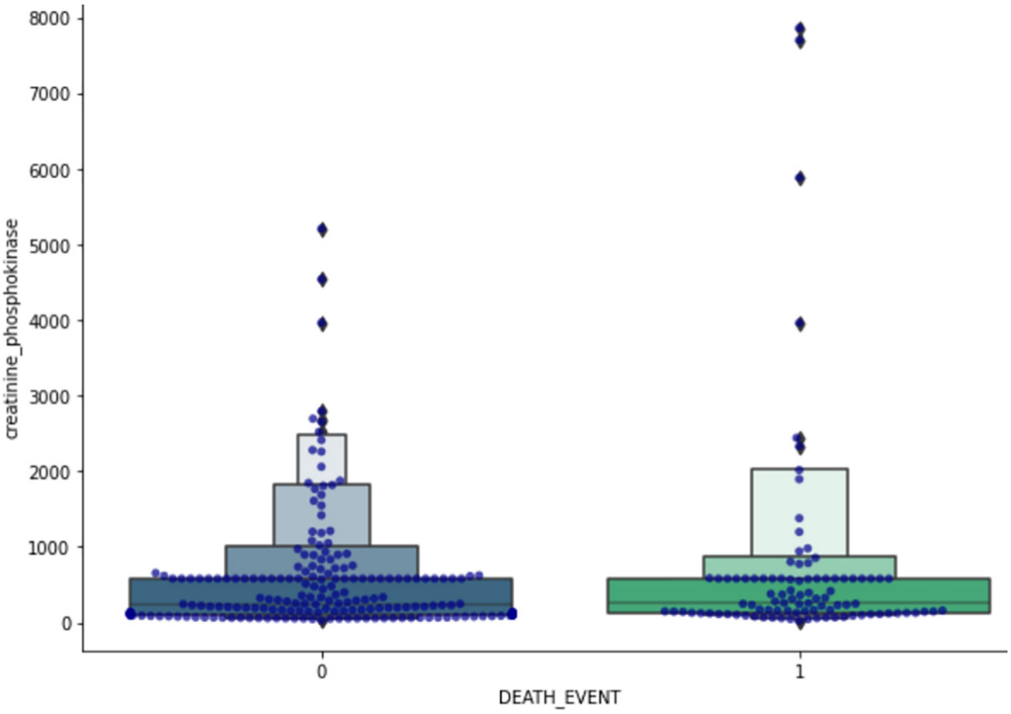

Fig. 4. Outliers in the variables

Figure 4 shows a remarkable trend in the relationship between age and mortality rate. In particular, it is notable that at the age of 60 years, as well as at 50 and 55 years, a significant increase in mortality rates is observed. These points suggest that these ages may be critical points in the health of individuals, which could be related to specific risk factors or physiological changes that increase vulnerability to serious health problems. These findings underline the importance of closely considering the impact of age on mortality and the need for specific preventive measures and medical care in these age groups.

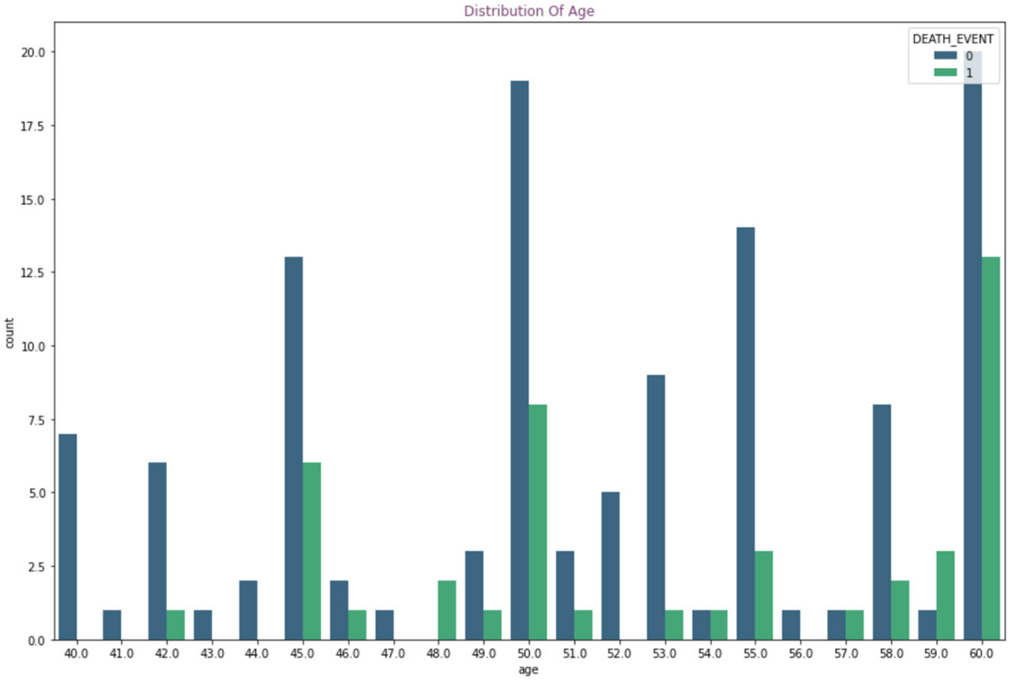

Fig. 5. Age-based mortality

Figure 5 shows that certain characteristics have a significant impact on the target variable, which is associated with mortality. The analysis highlights that the variable "time" is the most relevant characteristic, indicating that early diagnosis of cardiovascular problems is crucial for the reduction of mortality rates. This importance is reflected in the inverse relationship between time and mortality, where a longer time to diagnosis is associated with lower mortality. Likewise, "serum_creatinine" is identified as an influential characteristic due to its essential role in cardiac function. Ejection_fraction" also plays a significant role, which is consistent, as it represents the efficiency of the heart. In addition, a pattern of inverse relationship is observed that points to a deterioration in heart performance with increasing age. These findings are essential for understanding how these variables affect mortality rates and can guide medical decisions in the early identification and treatment of cardiac problems.

3.6 Data processing

In the data processing stage, several essential tasks are carried out. First, independent attributes (predictor variables) and dependent attributes (the target variable) are defined and distinguished in the training and test sets, thus establishing which information will be used to predict the HF. Next, a standard scaler is set up for the features, which involves normalizing or standardizing the variables so that they have a similar scale and are more easily comparable. Finally, the dataset is divided into two groups: the training set, which is used to train the model, and the test set, which is reserved for evaluating its performance, thus ensuring that the model undergoes an unbiased evaluation of previously unseen data.

4 RESULTS

In this study, the analysis and training of two ML models, such as SVM and ANN, were carried out. The focus was on predicting the presence of HF. A dataset consisting of 13 variables and 299 patient records, obtained from the Kaggle platform, was used. This dataset underwent a process of analysis and preparation before training the ML models. The results of these trainings are detailed in Table 3.

Table 3. Training results

	Precision (%)	Recall (%)	F1-Score (%)	Support
SVM				
0	0.84	0.85	0.84	60
1	0.69	0.67	0.68	30
Accuracy			0.79	90
Macro avg	0.76	0.76	0.76	90
Weighted avg	0.79	0.79	0.79	90
ANN				
0	0.85	0.78	0.82	60
1	0.63	0.73	0.68	30
Accuracy			0.77	90
Macro avg	0.74	0.76	0.75	90
Weighted avg	0.78	0.77	0.77	90

After finishing the training process for the SVM and ANN models. The results show that these models managed to achieve an accuracy of 79% and 77%, respectively.

It can be seen that the SVM model stands out in terms of accuracy, sensitivity, and F1 score, obtaining Figs of 79%, 79%, and 79%, respectively. This places it as the most effective predictor in the identification of HF. However, ANN should not be underestimated, as it achieves values of 77% in accuracy, 77% in sensitivity, and 77% in F1 score, placing it in a competitive position.

Figures 6a and b show the evolution of the loss during the model inter-validation. In Figure 6a, the x-axis shows the number of epochs, and the y-axis shows the loss, which is the degree of error in the model predictions. The figure shows two curves with dark and light red color; the light red color represents the training losses, and the dark red color represents the validation loss.

Both curves start with a high loss value, around 0.7, which is typical at the beginning of training, meaning that the model does not yet learn to predict correctly. However, from epoch 40 onwards, the training loss continues to remain at low values, around 0.3, indicating that the model is improving its accuracy.

With respect to Figure 6b, the accuracy in the validation set starts at around 0.82 and remains almost constant for the first 20 epochs. This may be because the model is overtrained and has not yet started to improve during validation. Also, it is evident that the accuracy starts very low at 0.65 but improves rapidly to reach values of 0.75. In the final phase, it can be seen that the accuracy keeps fluctuating, which indicates that the model has problems to generalize; mainly, after epoch 40, the validation accuracy drops and rises quite erratically. The training accuracy remains above 0.75, so overfitting could be suspected, as the model is achieving high accuracy rates in between-measurement but fails to maintain good validation accuracy.

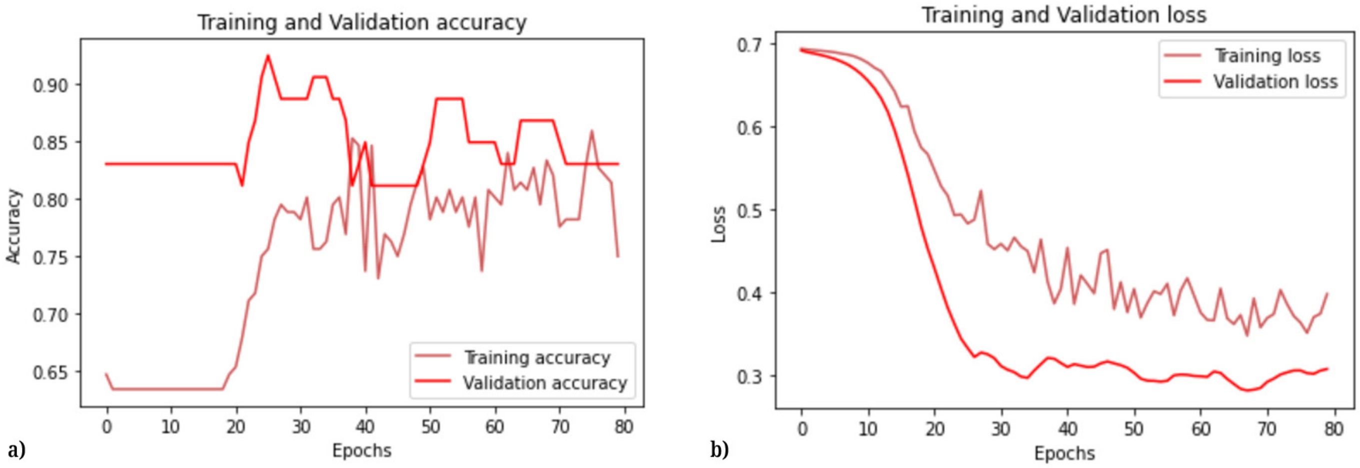

Fig. 6. (a) Training and validation loss; (b) Training and validation accuracy

5 DISCUSSION

Heart failure is one of the leading causes of death globally, claiming the lives of many people every year. Anticipating its progression becomes a key element in enhancing patients' quality of life by enabling preventive measures that can improve both treatment and survival rates. In this study, a comparative investigation was conducted to identify the most accurate model for HF prediction. After data processing and training, the SVM model stood out as achieving the most outstanding metrics, with an accuracy of 79%. This differs from studies [32] and [33] that concluded that the best predictor is RF with an accuracy of 97.78 and 83.15, respectively. On the other hand, [35] compared four ML classifiers, ranking SVM as the most outstanding with an accuracy of 96.67%. This is similar to this study that also positioned this model as the best predictor. In a different context, [36] combined several models, reaching an accuracy of 99.5%. These results exceeded those obtained in our research. In contrast with [37], where they developed a model using SVM and achieved an accuracy of 87.50%, which was higher than the results obtained in this study. On the other hand, in [38], they fused 10 classification algorithms, which were AdaBoost, CatBoost, DT, KNN, LR, Light GBM, NB, RF, SVM, and XGBoost, which obtained 85.2% accuracy. In the study [39] they compared seven ML classification algorithms. They performed a comparative performance analysis of these algorithms. NB, RF, and SVM models achieved an accuracy close to 85.86%. Also, in research [40], they combined an optimized ANN with an artificial bee colony and obtained an accuracy of 99.3%. One of the main differences with this study lies in the use of a larger dataset.

6 CONCLUSIONS

The use of ML models in healthcare is constantly expanding, highlighting the importance of creating models that ensure their effectiveness and efficiency in the training process. In this study, ML models were trained to predict HF and evaluate which of them provided the best performance. A Kaggle dataset, with a total of 299 records, was used to train the models. After completing the training, the results indicated that the SVM model stood out as the most effective, achieving an accuracy, sensitivity, and F1 score of 79%. It is relevant to note that the ANN model also showed similar results.

Certain characteristics have been identified as playing a significant role in the target variable related to mortality. The variable "time" stands out as the most relevant factor, underlining the importance of early diagnosis in reducing mortality rates. In addition, "serum_creatinine" and "ejection_fraction" emerge as influential factors due to their crucial role in cardiac performance. A pattern of inverse relationship between age and cardiac performance was observed, indicating the importance of considering age in risk assessment. These findings are fundamental to understanding how these variables affect mortality rates and, therefore, can guide medical decisions in the early identification and treatment of cardiac problems.

In the future, it will become essential to advance and train more ML models and use larger datasets. This will allow discerning and selecting those models that demonstrate optimal performance in the task of predicting heart failure.

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8 AUTHORS

José Luis Herrera Salazar is a professional in systems engineering with experience in planning, analysis, design and programming of computer systems and databases. Developer of equipment maintenance management systems, attendance control systems, warehouse control systems, production systems, academic systems. analysis, design and database administrator, management of human potential. strategic planning of business and social programs, strategic planning and objectives control using balanced scorecard and logical framework methodology. He has

self-learning capacity and facility to develop team work and under pressure. He can be contacted at luis.herrera@autonomadeica.edu.pe and jose210281@hotmail.com

Magdalena Talla Linderman is a Systems Engineer with a PhD in education and her academic interests are planning, designing, sizing, conceptualizing and evaluating the requirements of physical support (hardware) used for information treatment and automatic data processing. She is currently the academic vice-rector at the Autonomous University of Ica in Peru (E-mail: magdalena.talla@autonomadeica.edu.pe).

Orlando Iparraguirre-Villanueva is a Systems Engineer with a master's degree in information technology management, and has done PhD in Systems Engineering from Universidad Nacional Federico Villarreal-Peru. ITIL® Foundation Certificate in IT Service, Specialization in Business Continuity Management, Scrum Fundamentals Certification (SFC). National and international speaker/panelist (Panamá, Colombia, Ecuador, Venezuela, México) (E-mail: oiparraguirre@ieee.org).