Using Artificial Neural Networks to Extract Features for Heart Failure Prediction

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Heart failure is one of the most serious medical conditions affecting humans and potentially leading to death. It occurs when the heart muscle fails to pump blood adequately and effectively. Therefore, due to the seriousness of this disease, early prediction of patient outcomes is essential for enabling timely and appropriate treatment, which may reduce symptoms and increase longevity. This study aims to predict the survival status of heart failure patients and to identify the most influential clinical features affecting patient outcomes. A dataset of 299 heart failure patients was used, and artificial intelligence techniques were applied, specifically Artificial Neural Networks (ANN). In order to make this prediction, each feature was tested individually by feeding it into the ANN model to assess its impact on patient survival. The experimental results show that two features—serum creatinine and ejection fraction — were the most influential features and can independently be used to predict whether the patients with heart failure will survive or not.

Povzetek: Za zgodnje napovedovanje izida pri bolnikih s srčnim popuščanjem je razvit ANN-model, ki na osnovi 299 kliničnih zapisov izvaja ročno ekstrakcijo značilk in napoved preživetja. Rezultati kažejo, da serumski kreatinin in iztisni delež zadostujeta za 96 % napovedno natančnost.

1 Introduction

Heart failure, also known as congestive heart failure, is a serious condition that significantly affects human life [1]. It is a condition in which the heart muscle is unable to pump blood as efficiently as it should. When this occurs, blood and fluid return to the lungs, causing shortness of breath [2]. Cardiovascular diseases (CVDs), which are considered the most significant cause of death worldwide, are responsible for nearly 17.9 million deaths annually. The term "CVDs" refers to conditions that affect the "heart and blood vessels". Heart attacks and strokes account for more than four out of every five CVD deaths, with premature deaths accounting for one-third of these deaths in those under 70 [3]. Furthermore, according to the Centers for Disease Control and Prevention (CDC), more than 6 million people in the United States suffer from heart failure. In addition, heart failure is not limited to adults but includes children [4].

Clinically, heart failure is classified into two types based on the "ejection fraction (EF)", which refers to the percentage of blood pumped out of the heart with each contraction. Healthy EF values range from 50% to 75%. While heart failure with reduced ejection fraction (HFrEF), also known as systolic heart failure or left ventricular (LV) systolic dysfunction, is characterized by an ejection fraction that is less than 40%.

In addition, heart failure with preserved ejection fraction (HFpEF) is a kind of heart failure with a normal ejection fraction that is also referred to as diastolic heart failure or heart failure with normal EF [5].

In HFpEF, the left ventricle contracts normally during systole, but it is stiff and does not relax normally during diastole, causing filling problems [5].

Electronic health records (EHRs), also known as medical records are considered valuable resources because they uncover hidden patterns and relationships within patients' data, which can be helpful for clinical practice and research. EHRs are frequently used clinical data sources for making medical predictions [6].

It is important to know that clinical profiles can be used by researchers and medical professionals in the development and application for new treatments for this illness [7].

Moreover, because of the seriousness of the cardiovascular disease, it is essential to be detected as soon as possible.

Therefore, the aim of this research is:

1. To identify the most significant clinical features (or the risk factors) that contribute to the development of heart failure.
2. To predict survival status of heart failure patients by applying the ANNs algorithm to their medical records, with the goal of supporting treatment planning, early intervention, and clinical decision-making.

To the best of our knowledge, this is the first study in the field of heart failure prediction using this specific dataset with the ANN model aiming to identify the most important features that significantly impact a patient's condition by manually removing each individual feature and observing its impact on prediction accuracy, to identify which features most significantly affect patient survival.

2 Literature review

Numerous studies have been conducted in the field of heart failure prediction. Therefore, in this section, several studies that focused on predicting heart failure using machine-learning techniques and artificial neural networks are reviewed. Table 1 summarizes key previous studies on heart failure prediction using AI techniques. It compares their methods, dataset, and achieved accuracy.

The authors in [5] utilized a dataset of 299 heart failure patients. The dataset contains 13 clinical features such as high blood pressure, sex, and smoking. In this study, the authors applied various machine-learning models to predict whether the patient will survive or not. The experimental results revealed that serum creatinine and ejection fraction were the most impactful features that significantly affect the patient's state.

In [8], the authors proposed a heart failure prediction method using an ANN model. They also introduced a unique wrapper-based feature selection method using a Grey Wolf Optimization (GWO) to reduce the number of necessary input attributes. The results demonstrate that fewer features were required to achieve higher prediction accuracy, reaching approximately 87%.

In [9] the authors employed data from the Faisalabad Institute of Cardiology and Faisalabad United Hospital to develop a Multilayer Perceptron (MLP) neural network model for predicting heart failure. Their model achieved an accuracy of 88%, outperforming previous models.

In [10] a dataset of 299 heart failure patients were recorded in the EHR of the Faisalabad Institute of Cardiology and the Allied Hospital in Faisalabad was used. In order to address the class imbalance problem, the authors applied the Synthetic Minority Over-sampling Technique (SMOTE) for the augmentation of minority classes. SMOTE was used to oversample the EHR data for more accurate prediction of death risk among heart failure patients. Finally, they used the Random Forest (RF) algorithm for classification, which enhanced the accuracy of death risk prediction.

3 Artificial Neural Networks (ANNs)

The Artificial Neural Network (ANN), which simulates the structure and learning mechanism of biological neural networks, is considered one of the most widely used prediction techniques [11]. Neural Networks are a biological structure inspired by human nervous systems due to their powerful learning capabilities. They can extract patterns, learn from data, and generate a network model that can be used for classification, pattern recognition, and predictive analytics.

Neural networks are widely used in various applications. One of their most promising characteristics—unlike other classification techniques—is their ability in the simulation of the network and creating a model capable of making predictions on new, unseen data [12].

As illustrated in Figure 1, a neural network consists of several interconnected processing units known as neurons or nodes.

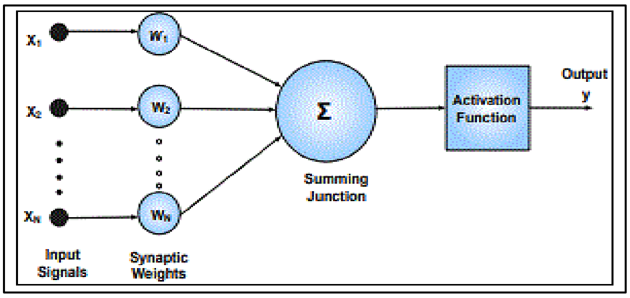

Figure 1: A processing unit [13].

The nodes are logically arranged into multiple layers, interconnected through weighted connections. These scalar weights determine the effect's nature and strength between connecting nodes[13].

The learning procedure's primary goal is finding the best weights for the supplied inputs. The output of the network is compared to the desired response. Neural networks can be implemented using many architectural structures, that depends on the task complexity [14].

The ANN consists of a set of artificial neurons called nodes that receive inputs in the form of a feature vector [15]. Each node in the following layer is connected to all nodes in the previous layer. The network includes an input layer that feeds data to the neural network (into the model), and an output layer for storing the network's response to the input (that captures the final prediction). Between them, there is the intermediary layers, also known as hidden layers, which enable the network to represent complex, non-linear relationships. Each hidden and output node multiplies each input by its weight, sums the results, and then passes the sum through a nonlinear activation function to generate its output [16]. The architecture of ANN, including the input, hidden and output layers with weighted connections is illustrated in Figure 2.

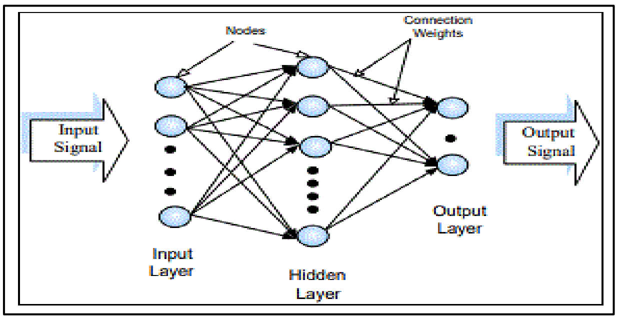

Figure 2: Architecture of Neural Network [13].

Table 1: Comparative summary of previous studies on heart failure prediction, including classifiers and reported accuracy.

Research	Year	Classifiers for heart failure prediction	Best Accuracy
[5]	2020	Employed many machine learning classifiers to rank the characteristics related to the most significant risk variables and forecast the patients' survival. including neural network, Support Vector Machine, k-Nearest Neighbors, Random Forests, One Rule, Linear Regression, Naïve Bayes, and Decision Tree.	0.74%
[8]	2021	They used an artificial neural network (ANN) to predict heart failure. They also proposed a novel wrapper-based feature selection by the GWO to reduce the number of features.	87%
[9]	2020	In this study, they want to predict an early heart failure by using multilayer perceptron neural network (MLP)	88%
[10]	2020	This study performed a comparative analysis of renowned oversampling methods like (SMOTE) (SMOTE), borderline-SMOTE, and adaptive synthetic (ADASYN) sampling techniques. The classification done by the Random Forest model	F1-score = 0.63

The ANN model operates based on three main steps: multiplication, summation, and activation. First, each input is multiplied at the input of the artificial neuron, meaning each input value is multiplied by a corresponding weight. Then, a summation function adds all weighted inputs along with the bias inside the artificial neuron. Finally, the total of these weighted inputs and bias is passed through an activation function—also known as a transfer function— to produce the neuron's output.
Equation (1) [17] represents the output of a typical ANN with K input components:

$$\boldsymbol{y(x) = \sum_{i=1}^{k} w_i y_i(x)} \qquad (1)$$

Where $\boldsymbol{yi}$ is the output of net $\boldsymbol{i}$ and $\boldsymbol{wi}$ is the weight linked with the net.

Different ANN architectures can be used. In this study, the Multilayer Perceptron model (MLP) was employed [17]. The MLP consists of multiple layers, where each node in a given layer receives input from the connected nodes in the preceding layer, then computes a weighted sum followed by an activation function, and then sends the result to the corresponding nodes in the next layer

An ANN model consists of three types of layers: the input layer, hidden layers (one or more), and the output layer. Hidden layers are intermediate layers that do not directly connect with external input or output. Each neuron in the hidden layers and output layer computes a weighted summation of the inputs it receives, and then passes the result through an activation function to generate its output [17].

The proposed architecture consists of three layers: an input layer, multiple hidden layers, and output layer. The input layer represents the dataset used in this study. The hidden layers include five fully connected layers, each containing a different number of neurons, as illustrated in Table 2.
For each hidden layer, a ReLU (Rectified Linear Unit) activation function is applied.

The output layer consists of a single neuron that produces the final decision, representing the patient's survival status. In addition, in the output layer a sigmoid activation function was used to produce a probability score between 0 and 1.

During training, the model was optimized using the Adam optimizer. In addition, Binary cross-entropy was used as the loss function, and accuracy as the evaluating metrics. It is important to mention that the proposed model was trained using a batch size of 5, 100 epochs and a learning rate of 0.001.

Table 2: The numbers of neurons in each hidden layer.

The hidden layers	Numbers of neurons in each layer
First hidden layer	7
Second hidden layer	7
Third hidden layer	14
Forth hidden layer	4
Fifth hidden layer	7

4 Evaluating metrics

In this paper, several evaluating metrics were used to assess model performance, and these metrics are explained as follows:

4.1 Confusion matrix

The confusion matrix is a table that summarizes the classification results, indicating whether the instances were classified correctly or incorrectly. For binary classification, a (2×2) matrix is typically employed [18]. Table 3 presents an example of a binary classification confusion matrix.

Table 3: The confusion matrix.

Confusion Matrix		Actual Class	
		Positive (p)	Negative (N)
Predicted Class	Positive (p)	True Positive (TP)	False Positive (FP)
	Negative (N)	False Negative (FN)	True Negative (TN)

- True Positive (TP): The model identified positive instance correctly.
- False Negative (FN): A positive instance wrongly classified by the model.
- False Positive (FP): A negative instance mistakenly classified by the model.
- True Negative (TN): The model classified negative instance correctly.

4.2 Accuracy

It is one of the most widely used evaluation metrics. It is the ratio of correctly classified instances to the total number of instances for a given test dataset [18], and it is calculated as:

$$\textbf{Accuracy} = \frac{\textbf{TP+TN}}{\textbf{TP+TN+FP+FN}} \qquad (2)$$

4.3 Precision

Precision is the ratio of all correctly predicted positive instances to the total predicted positive [18]. Mathematically, it is defined as:

$$\textbf{Precision} = \frac{\textbf{TP}}{(\textbf{TP+FP})} \qquad (3)$$

4.4 Recall

It is also known as True Positive Rate (TPR) is the ratio of successfully predicted positive instances to the total number of positive instances in the dataset [19]. It is given by:

$$\textbf{Recall} = \frac{\textbf{TP}}{(\textbf{TP+FN})} \qquad (4)$$

4.5 F1-score

It is the harmonic mean of precision and recall. It provides a balance between the two measurements, particularly when the data is unbalanced. [18], [20]. It is computed as [21]:

$$\textbf{F1} = 2 * \frac{1}{\frac{1}{\textbf{precision}} + \frac{1}{\textbf{recall}}} \qquad (5)$$

5 The proposed system

This section introduces the proposed system, which aims to predict the survival status of patients diagnosed with heart failure. The proposed system is composed of four main stages: The first stage is data collection; the second is data preprocessing, which involves data splitting and feature scaling; the third is feature extraction; and the final stage is prediction, which determines whether a patient with heart failure is likely to survive. Each stage is described in detail in the subsequent paragraphs. An overview of the proposed system for heart failure prediction is illustrated in **Figure 3**.

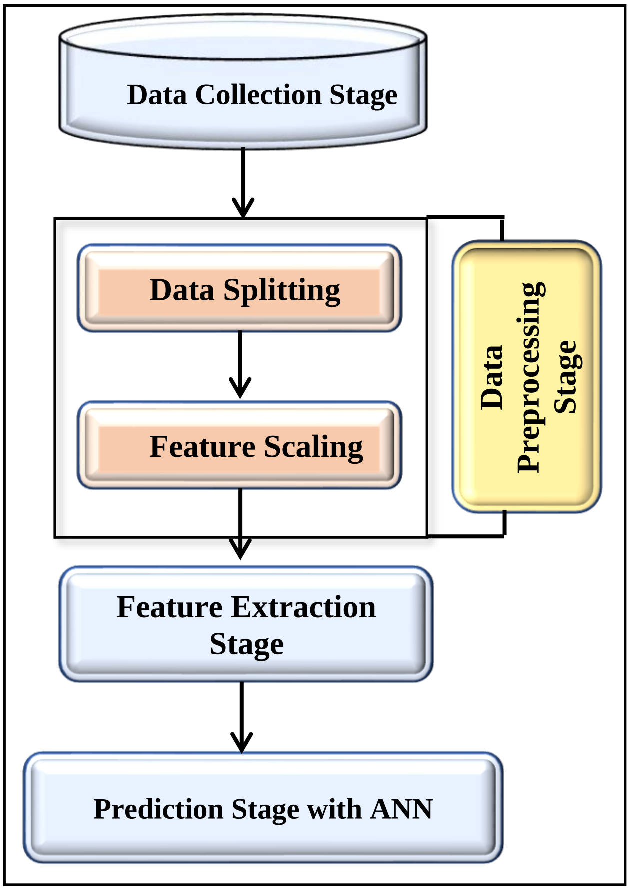

Figure 3: The proposed system for heart failure prediction.

5.1 Data Collection Step

In this step, the dataset used in this study is described.

5.1.1 Dataset description

The dataset includes medical health records of 299 heart failure patients collected between April and December 2015 at the Faisalabad Institute of Cardiology and the Allied Hospital in Faisalabad, Punjab, Pakistan. The patients' ages range from 40 to 95 years, with 105 females and 194 males. In addition, the dataset contains 13 features that represent clinical, physiological, and lifestyle-related information. It is important to note that the dataset is imbalanced as it contains 203 alive patients (death event = 0) and 96 dead patients (death event = 1), which corresponds to 67.89% negatives and 32.11 % positives. The key features of the heart failure dataset used in this study are summarized in Table 4, including their descriptions, measurement units, and value ranges.

Table 4: Describes the elements in the dataset.

Feature	Description	Measurement	Range
Age	Age of the patient	Years	[40, ….,95]
Anaemia	Decrease of red blood cells or hemoglobin	Boolean	0,1
High blood pressure	If the patient has hypertension	Boolean	0,1
creatinine phosphokinase (CPK)	The CPK enzyme Level in the blood	mcg/L	[23, ...,7861]
Diabetes	If the patient has diabetes	Boolean	0,1
Ejection fraction	Percentage of blood leaving the heart at each contraction	%	[14, ...,80]
Sex	Woman or man	Binary	0, 1
Platelets	Platelets in the blood	kiloplatelets/ Ml	[25.01, ...,850.00]
Serum creatinine	Level of creatinine in the blood	mg/Dl	[0.50, …9.40]
Serum sodium	Level of sodium in the blood	mEq/L	[114, ...,148]
Smoking	If the patient smokes	Boolean	0,1
Time	Follow-up period	Days	[4, ...,285]
[target] death event	If the patient died during the follow-up period	Boolean	0,1

5.2 Data pre-processing

This step includes two main stages as follows: Data Splitting and Feature Scaling.

5.2.1 Data splitting

In the splitting part, the dataset was partitioned into two subsets: a training set and a testing set. For this study, a split ratio of 70% for training and 30% for testing was adopted. As a result, 209 instances were used for training and 90 instances were used for testing.

5.2.2 Feature scaling

The feature scaling procedure represents the final stage in the preprocessing phase. The reason of applying this procedure is that the dataset contains input features with widely varying scales. As a result, this step ensures that all feature values are normalized to a range suitable for ANN algorithms.

In this study, StandardScaler normalization was applied, which transforms the data into a distribution with a mean of 0 and a standard deviation of 1. The transformation is mathematically represented in Equation (6):

$$\mathbf{Z} = \frac{\mathbf{x}-\boldsymbol{\mu}}{\boldsymbol{\sigma}} \qquad (6)$$

Where, $\boldsymbol{\mu}$ is the mean, $\boldsymbol{\sigma}$ is a standard deviation, $\boldsymbol{x}$ is an original value.

5.3 Feature extraction

In this stage, no statistical or automated feature selection techniques were applied. Instead, the feature extraction process was performed manually. As mentioned previously, the dataset used in this study contains 12 input features. The process starts by evaluating the ANN model using all 12 features to calculate its prediction accuracy. Then, each feature was removed individually, and the model was retrained to observe the impact of each feature on prediction accuracy.

It is worth mentioning that the feature whose removal causes the greatest reduction in ANN accuracy is considered the most influential feature in the dataset, as it significantly contributes to the model's predictive capability. These features can be used to determine whether the patient with heart failure will die or not.

5.4 Prediction

After completing the feature extraction stage, the most important features in the dataset were identified. In this stage, only these selected features were used to predict whether patients with heart failure will survive or not using the Artificial Neural Network (ANN) algorithm.

6 Experimental results

This section presents the results obtained from the ANN model after performing the feature extraction experiments. The performance of the ANN was evaluated using several metrics, including Accuracy, F1-score, Precision, and Recall. In addition, the confusion matrices are presented only for the most influential features in the dataset. Table 5 summarizes the ANN performance results based on the removal of each feature from the dataset.

Table 5: Accuracy of the ANN model after removing each feature individually to evaluate its contribution to heart failure prediction.

Removed Features	Accuracy	F1-score	Precision	Recall
Age	**76%**	**73%**	**73%**	**73%**
Anemia	**79%**	**76%**	**77%**	**76%**
high blood pressure	**79%**	**75%**	**74%**	**75%**
Creatinine phosphokinase(CPK)	**77%**	**72%**	**71%**	**73%**
Diabetes	**77%**	**72%**	**71%**	**73%**
Ejection fraction	**70%**	**65%**	**65%**	**66%**
Sex	**78%**	**75%**	**74%**	**77%**
Platelets	**77%**	**73%**	**72%**	**75%**
Serum creatinine	**73%**	**67%**	**68%**	**66%**
Serum sodium	**74%**	**72%**	**71%**	**74%**
Smoking	**78%**	**75%**	**74%**	**76%**
Time	**62%**	**58%**	**58%**	**59%**

- **The analysis of Confusion Matrices, which includes (Figures 4 –7)**

To further evaluate the ANN model performance, confusion matrices were generated using the four most essential features identified during the feature extraction stage, which are ejection fraction, serum creatinine, serum sodium, and time.

1. In **Figure 4**, the confusion matrix shows that using only the ejection fraction feature the ANN model correctly classified 48 true negative instances (patients who survived), 15 true positives instances (patients who did not survive), 15 false positives, and 12 false negatives (which indicates misclassified instances). The high value of true negatives indicates the model's strong ability to correctly classify patients surviving. On the other hand, the equal values of true positives and false positives means that the model has limited sensitivity. As a result, ejection fraction feature contributes significantly to heart failure outcome prediction.
2. **Figure 5** illustrates the results when using the **s**erum creatinine feature. The ANN model was able to correctly classify 53 true negative instances (patients who survived) and 13 true positive (patients who did not survive), with 10 false positives and 14 false negatives. The high value of true negatives implies strong specificity; however, the higher value of false negatives relative to true positives shows low sensitivity. As a result, the "serum creatinine" feature Contributes extensively to heart failure outcome prediction, especially in identifying patients who are likely to survive.
3. As demonstrated in **Figure 6**, when only the "serum sodium" feature was used, the ANN model correctly classified 47 true negative instances and 20 true positive instances, with 16 false positives and 7 false negatives. The relatively high value of true positive indicates improved sensitivity, while the increase in false positives indicates reduced specificity. As a result, the "serum sodium" feature supports heart failure prediction, particularly in identifying patients who are at risk of death.
4. As illustrated **in Figure 7**, when the "time" feature was used, the ANN model correctly classified 42 true negative instances and 14 true positive instances, with 21 false positives and 13 false negatives.
   These results show that when depending just on this feature, the model's specificity and sensitivity were limited, as seen by the moderate number of true positives and comparatively large false positive rate. Although it might not be enough on its own for accurate classification, the "time" feature still contributes to heart failure prediction by capturing follow-up period dynamics.

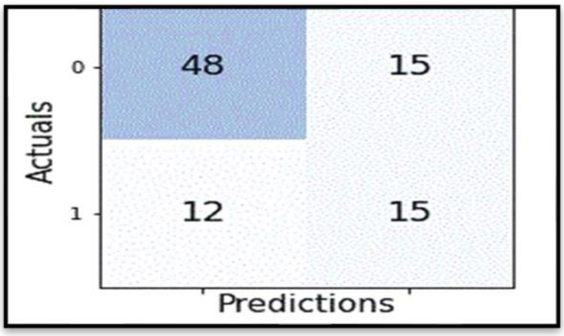

Figure 4: The confusion matrix for the proposed ANN model using only the ejection fraction feature.

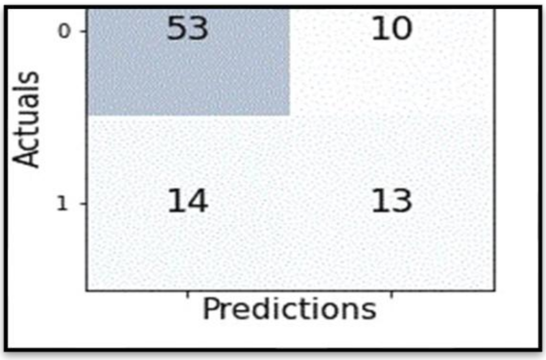

Figure 5: The confusion matrix for the proposed ANN model using only the serum creatinine feature.

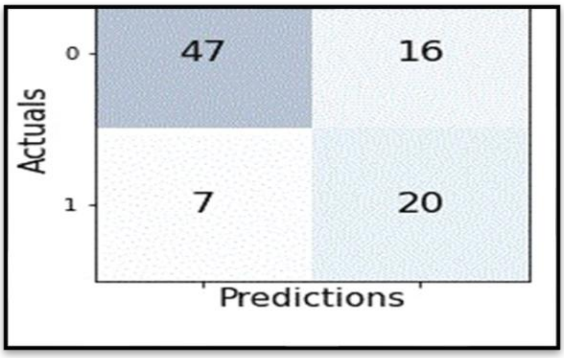

Figure 6: The confusion matrix for the proposed ANN model using only the serum sodium feature.

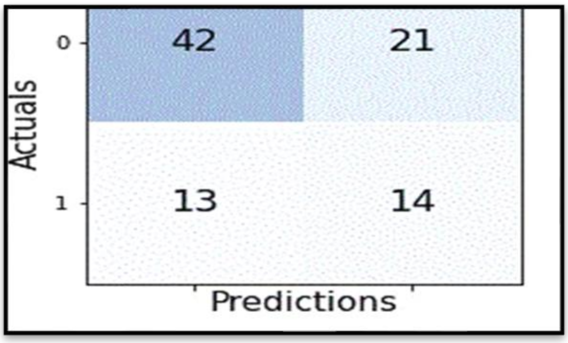

Figure 7: The confusion matrix for the proposed ANN model using only the time feature.

7 Discussion

This part discusses the experimental results of the proposed system.

After all the experiments, the findings show that several features, such as age, anemia, high blood pressure, creatinine phosphokinase (CPK), diabetes, sex, platelets, and smoking had minimal impact on the model's accuracy when removed individually. Therefore, these features can be excluded without significantly affecting the model's performance.

In contrast, some features cause a noticeable decrease in accuracy when removed, such as ejection fraction, serum creatinine, serum sodium, and time, confirming their critical importance in predicting heart failure outcomes.

It is important to mention that the time feature refers to the Follow-up period, and since not all patients were under the follow-up period, the time feature was excluded from the study.

Consequently, only two key features that significantly affect the prediction of heart failure patients in the dataset were identified. These features are ejection fraction and serum creatinine.

These results suggest that even in the absence of complete clinical or laboratory data, healthcare providers may still make reasonably accurate survival predictions using only these two key features extracted from the EHR.

Even though it is difficult to directly compare the manual feature selection method employed in this study with previous studies because of differences in methodology and general research concept, a deeper analysis reveals important insights. This study confirmed that serum creatinine and ejection fraction are the most influential predictors of heart failure survival, consistent with results in [5] , which used various machine learning models on a similar dataset. Unlike [8], which employed an automated GWO for feature selection for optimum accuracy, our manual feature removal approach focused on simplicity and clinical interpretation. In contrast to [9], which employed a MLP neural network to achieve greater accuracy, our simpler ANN model with manual feature selection highlights the clearer clinical relevance of selected features. Compared to [10], which addressed class imbalance with SMOTE while employing Random Forest classifiers to enhance performance, our strategy avoids data augmentation and ensemble methods to retain model transparency and ease of use in clinical settings.

It is important to note that the main limitation of our study is the relatively small dataset size, not the manual feature selection approach itself. Neural networks typically require large datasets for optimal performance, as demonstrated in [10] where data augmentation enhanced prediction accuracy. However, our goal in this study was to maintain the information in the dataset in its current state and contribute to the medical field by selecting just the most influential features.

8 Conclusion

Heart failure is a life-threatening condition and a leading cause of death. Early detection plays a crucial role in improving patient health and saving lives. Therefore, this study aimed to develop a predictive model that manually selects the most influential features from the dataset and uses them to predict patient survival. This prediction was made by using ANN model.

The dataset employed in this study consists of medical records of patients with heart failure, including 12 clinical features. Each feature was individually tested as entered manually into the ANN model and observing the impact on prediction accuracy. The time feature was taken into consideration separately, because it indicates the follow-up period, which was not consistently available for all patients.

The experimental results revealed that two features—serum creatinine and ejection fraction—had the most significant impact on model performance. These two features alone were adequate to produce reasonably accurate survival predictions, even in the absence of other clinical or laboratory data.

Based on these results, the proposed model could be integrated into clinical practice as a decision support tool that helps healthcare providers quickly assess the survival probability of heart failure patients based on only two key features. This simplified approach could reduce the burden of extensive data collection and facilitate timely interventions.

However, to ensure broader applicability and robustness of the model, future research should focus on validating the model using larger and more diverse datasets from multiple clinical settings. Additionally, exploring hybrid methods that combine manual and automated feature selection may contribute to improving prediction accuracy while maintaining interpretability.

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