ISSN PRINT 2319 1775 Online 2320 7876

Research paper Volume 11, Sp.Iss 6 , 2022

Deep Sequence Framework: Unravelling Mortality Patterns in ICU Patient Data

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DOI : 10.48047/IJFANS/11/S6/034

Abstract:

Accurate estimation of the physiologic limits of patients during their stay in the intensive care unit is critical for predicting mortality risk. However, patient populations in different ICUs may differ in age, severity of illness, and medication. Creating the models that are relevant for diverse populations poses a significant challenge. Existing models trained on data fromspecific ICUs may performpoorly in other settingsbecause of changes in the distribution of characteristics. To avoid those problems,we propose a deepsequence framework model topredictmortalityrisk based ontimeseries data received fromICUs.Weconductedexperimentsusingthepublic PhysioNet2012dataset,whichcontainsvitalsignsdatafrom6,000ICUpatientsfromfourdepartmentswith48 -timesteps.Ourmodelincludeslayersofconvolutional neural networks andlong-termmemoryto correctly predict mortality risk. We used two layers of convolutional and a hidden layer with 16 nodes, and a group of instances as 32 as batch. Ourexperimentalresultsshowedanimpressiveaccuracyof93.4%andalossof0.0008054.Futureworkcouldf ocusonexpandingvitalparameters,andvolume of the data set(acrossmultiplegeographicalregions)andensuringpatientdataconfidentiality.

Keywords: Deep Learning, ICU patient, mortality risk factors, Transfer learning,

I. Introduction

In intensive care units (ICUs), patient mortality is a foremost concern. Identifying mortality risk factors can help clinicians make informed decisions and improve patient outcomes. Machine learning (ML) techniques rapidly applied to ICU data analysis to create models that can predict patient outcomes with reliable accuracy. Effective management of drugs, care protocols, medical procedures, and other interventions is critical in determining the gravity of patient illness or injury. Physiological boundaries estimated during an ICU stay must be robust and discriminative across different patient populations. However, patients in different types of ICUs may differ in age, conditions, and medications, and models trained with patient data from a specific ICU may not perform well in other settings. Mortality rates

ISSN PRINT 2319 1775 Online 2320 7876
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appear to double during prolonged ICU stays. Accurately predicting mortality is necessary for medical care, as it provides an experimental risk estimate for assessing prognostic dynamics, guiding treatment decisions, and benchmarking hospitals. Precise prediction of mortality risk requires considering important clinical, physiologic, and demographic determinants. These variations can exist among various ICU patient populations.. In this research article, we propose a Deep Sequence Framework (DSF) to discover mortality causes for ICU patients using time-series data.

Keywords: Deep Learning, ICU patient, mortality risk factors, Transfer learning,

II. Survey of literature

In medical services, predicting mortality risk is crucial for prognosis dynamics, patient care, and benchmarking medical clinics. Traditional methods rely on a fixed set of ICU confirmation credits and generalized clinical information, which are prone to bias and require significant manual effort.[17]. In response to these limitations, there may be a demand for modernized methods that can really mitigate these deficiencies. Clinical observation notes, along with deep learning models, present opportunities to capture patient data and automatically identify related features..[4][11]

One promising approach is to record all patient features at specific times and use the previous state to make robust mortality predictions. PhysioBank, PhysioToolkit, and PhysioNet offer researchers access to complex physiological signals, such as electrocardiograms and electroencephalograms, to support biomedical engineering research.[6] In comparison, traditional models use cascaded SVM-GLM models, which consist of two stages: an SVM classifier trained to generate mortality predictions and a GLM trained managing the predicted probability and original features. This method achieved an AUC-ROC of 0.851 and an accuracy of 0.784, outperforming other state-of-the-art methods.[9]

To detect any deterioration of patients in the ICU or any unfavorable events, it is crucial to closely monitor them. Nonetheless, challenges arise in bed allocation due to the substantial demand for ICU services and restricted capacity. To tackle this issue, physicians must check the patientswith the lowest discharge risk to alleviate admission delays for incoming patients. Healthcare databases like MIMIC-III exhibit scoring systems and AI models for predicting patient mortality.[1] [2]. Although these models have demonstrated encouraging outcomes,

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the majority do not consider the evolving nature of patient conditions and provide a single score for the entire ICU stay.[22]

Several studies have explored the prediction of ICU length of stay using various techniques such as deep learning, Deep ANN, and fuzzy classifiers[19]. Predicting the length of stay can be beneficial for cost control and resource planning. Yet, there are challenges in obtaining useful information due to changing length, inadequate sampling, and missing data. Certain research activities have also employed semantic interpretations and logical operators to connect features and predictions.[24]

One successful tactic is the use of a powerful Support Vector Machine (SVM) classifier that trains six different SVMs to capture specific patterns that lead to patient outcomes. These SVMs are then combined using a linear model to predict patient survival[5]. More studies have proposed related approaches using a logistic regression classifier. These models use both broad and specific descriptors, including time-series features represented by measurement descriptors.[7]

Mobley et al. have completed another study on ICU prognosis, using 74 factors on 557 patients receiving coronary care. The research employed an Artificial Neural Network (ANN) and incorporated variables like patient characteristics, laboratory test outcomes, physiological data, vital signs, and diagnostic examinations.[2]

Vairavan et. al. employed calculated relapse classifiers in sequence with Hidden Markov Models to capture time-series data. [16]. They utilized a Markov Chain to estimate the transition probability from patients being alive to mortality. This model was used to predict patient's survival probability at each time interval, Later it was passed to the classifier along with the patient's general descriptors and selected feature. One noteworthy aspect of their model is that it does not require the entire 48-hour data to make a prediction, making it suitable for real-time monitoring. [13].

Davoudi, Anis, et.al .utilized a combination of wearable sensors, light and sound sensors, and cameras to collect patient and environmental data. It was used to develop an intelligent intensive care unit (ICU) system.[20] This system employs pervasive sensing and deep learning algorithms to automatically monitor patient health status and forecast adverse events. Using the saved data from various sources, including electronic medical records, wearable

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sensors, and medical devices, deep learning algorithms analyze the information and generate real-time predictions of patient outcomes. This innovative ICU system has the ability to enhance patient outcomes by providing continuous monitoring and early detection of adverse events, enabling timely intervention. The outcomes of this study demonstrate the promise of using intelligence system and machine learning to improve patient care in the ICU. [20].

In their study, B Shickel et al. proposed a novel DeepSOFA[15] score framework that utilizes quick assessments and interpretable deep learning models to assess disease severity at any point during an ICU stay. They compared DeepSOFA with Sequential Organ Failure Assessment (SOFA) prediction models using the same input data and found that DeepSOFA offers significantly enhanced predictive accuracy of in-hospital mortality at any point during an ICU admission. A DeepSOFA model developed in an open database and validated in a single institutional partner showed a mean AUC for the total ICU stay of 0.90 (95% CI 0.90-0.91), compared to standard SOFA models with a mean AUC of 0.79 (95% CI 0.79-0.80) and 0.85 (95% CI 0.85-0.86).

Christopher Rugg et al conducted a a research study to explore the correlation between hyperphosphatemia (high levels of phosphate in the blood) and injury severity, Additionally, it pertains to the mortality rates of poly-trauma patients joined to the intensive care unit (ICU). The researchers analyzed data from 61 patients who suffered from polytrauma and were joined to the ICU between 2013 and 2017. The findings revealed that hyperphosphatemia was significantly linked to shock, tissue damage, injury severity, and death in polytrauma patients. The study also explained that patients with hyperphosphatemia had longer stays in the ICU and better rates of mechanical ventilation.[23]

F. Shann et al. developed and assessed the efficacy of the Paediatric Index of Mortality (PIM), which is a mortality estimate model for children receiving intensive care. The primary goal of PIM is to help healthcare practitioners estimate the stake of mortality in critically ill children and identify patients who might require more intensive treatment [29]. he PIM is presently utilized as a widely adopted instrument in pediatric intensive care units worldwide for the purpose of forecasting mortality risk and providing guidance for clinical decision-making.[29]

In their article, Shickel et al. present aanalysis of recent improvements in deep learning techniques used for analyzing electronic health records (EHRs) [25]. They highlight the prospective advantages of employing deep learning models for analyzing EHRs, which can specify valuable perceptions into patient health and medical history. The authors describe

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different types of deep learning models that have been used for EHR analysis, including convolutional neural networks (CNNs), recurrent neural networks (RNNs), and deep belief networks (DBNs). They also discuss various applications of deep learning in EHR analysis, such as predicting patient outcomes, recognizing risk factors for diseases, and developing personalized treatment plans. The authors also address the challenges and limitations associated with utilizing deep learning techniques for EHR analysis.

Komorowski et al. (2018) reviewed 26 research endeavours employing deep learning techniques to predict mortality in ICU patients. The authors found that deep learning models had higher accuracy in predicting mortality compared to traditional scoring systems such as APACHE and SAPS.

After examining various research studies, it was observed that predicting the mortality rate of ICU patients encounters various obstacles, including the intricacy of patient cases, the absence of uniform data, the urgency of time, the limited number of patients, the interplay of variables, the quality and consistency of data, selection bias, and overfitting as a result of the restricted size of ICU datasets. It was discovered that by capturing abstract patient information and utilizing deep learning models, researchers can enhance mortality predictions and provide improved patient care.

III Methodology:

3.1 Data Collection and Pre-processing

The Physio Net 2012 database was used to collect data utilized in this work. The database contains vital information sequences collected from four ICU units of 6,000 patients. We extracted data from the first 48 hours of ICU admission, incorporating vital signs, laboratory results, demographics, and diagnosis codes.

The details include patient age, gender, height, and weight as overall group descriptors. Around the time of admission into the ICU, the patient details - the group descriptors are recorded. Details of these six group descriptors are recorded in Table 1.

Table 1. Group descriptors.

Descriptor	Remarks	Data type
RecordID	-Id gave to the patient	Integer

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Gender	0: Male, 1:Female	Boolean
Age	In years	Integer
Height	In cm	Integer
Type of the ICU	1: Coronary Care Unit 2: Cardiac Surgery Recovery 3: Medical ICU Unit 4: Surgical ICU)	Integer
Weight	In kgs	Integer

It included 37 essential time-series physiological parameters that were monitored over the course of 48 hours in the ICU.Table 2 shows the particulars of the vital parameters given in the Physionet challenge[15].

Table 2. Vital time-series parameters of patients were recorded in each hour.

Albumin(gIdL)	HCT[Hematocrit(%)]	PaCO2 [partial pressure of arterial CO2(mmHg)]
ALP[Alkaline phosphatase (IU/L)]	HR[Heart rate (bpm)]	PaO2 [Partial pressure of arterial O2(mmHg)]
ALT[Alanine transaminase (IU/L/L)]	K[Senun potassium (mEq/L)]	pH[Arterial pH (0-14)]
ALT[Aspartate transaminase (IU/L)]	Lactate(mmol)	Platelets(cells/nL)
Bilrubin(mg/dL)	Mg[Serum magnesium (mmol/L)]	RespRate Respiration rate (brat)]
BUN[Blood urea nitrogen (mg/dL)]	MAP[Invasive mean arterial blood pressure (mmHg)]	Sa02[O2 saturation in hemoglobin (°/0)]
Cholesterol(mg/dL)	Mach Vent[Mechanical ventilation respiration	SysABP[Invasive systolic arterial blood pressure

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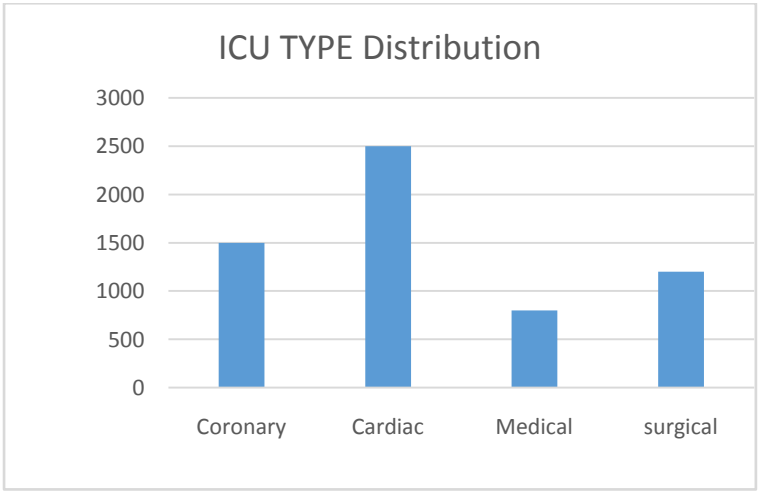
	(0:false, or 1 :true)]	(mmHg)]
Creatinine [Serum creatinine (mg/dL)]	Na [Serum sodium (mEq/L)]	Temp [Temperature (°C)]
DiasABP[Invasive diastolic arterial blood pressure (mmHg)]	DiasABP[Non-invasive diastolic arterial blood pressure (mmHg)]	Tropl[Troponin-I (ug/L)]
FiO2 [Fractional inspired O2(0- 1)]	NIMAP[Ision-invasive mean arterial blood reassure (mmHg)]	TropT[Troponin-T(g/L)]
GCS[Glasgow Coma Score (3-15)]	NisysABP[Non-invasive systolic arterial blood pressure (mmHg)]	Urine [Urine output (mL)]
Glucose [Serum glucose (mg/dl)]	HCT[Hematocrit(%)]	WBC[Arliite blood cell count (cells/nL)]
HCO3 [Serum bicarbonate (mmol/L)]		Weight(kg)*
Albumin(gIdL)		PaCO2 [partial pressure of arterial CO2(mmHg)]

The data distribution, according to the ICU type, is identified for further analysis, as depicted in Figure 1. The Cardiac ICU has more patients compared to the Medical, Surgical and Coronary Units.



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We then processed the data to remove missing values and standardized the numerical features.The vital information collected for each hour might not be recorded for all vital parameters. For example, at a point, i.e., at 2 hours 18 minutes, only nine vital information of the patient has been recorded, as explained in Figure 2. So handling missing values among the 37 vital information for each hour is a very complex task.

```
02:18,HR,93
02:18,NIDiasABP,41
02:18,NIMAP,75.33
02:18,NISysABP,144
02:18,RespRate,24
02:18,Temp,37.8
02:18,Urine,140
02:33,GCS,15
02:33,HR,84
```

Figure 2. Vital information of a patient.

The missing data points within the provided dataset are depicted in the following Figure 3.And observed that height is missing for 1894 patients.

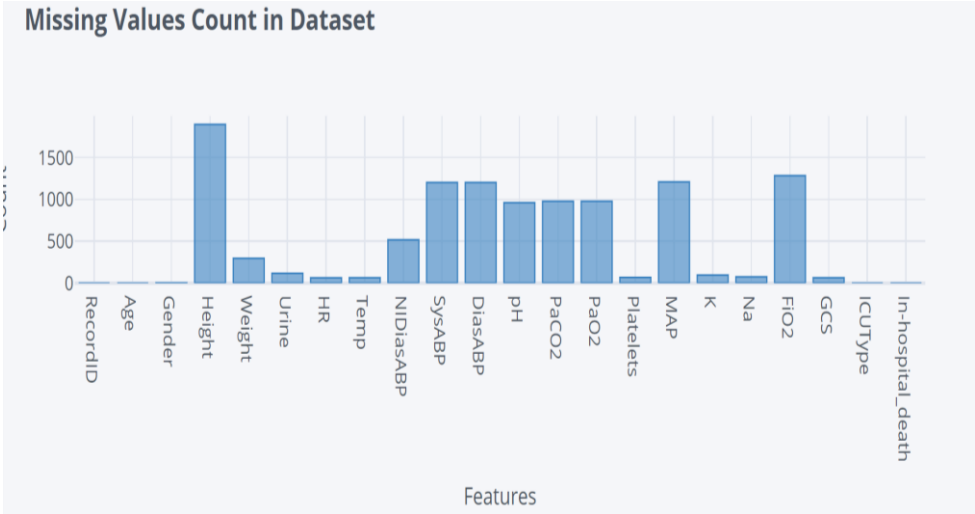

Figure 3. Missing values count in the dataset.

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The data parameters recorded at 48 timestamps are displayed in Figure 4, illustrating the observations of heart rate (HR) and respiratory rate for each timestamp. However, temperature and platelet readings were not consistently recorded, resulting in missing data. In response to this concern, we substituted the missing values with the average value of the corresponding parameter.

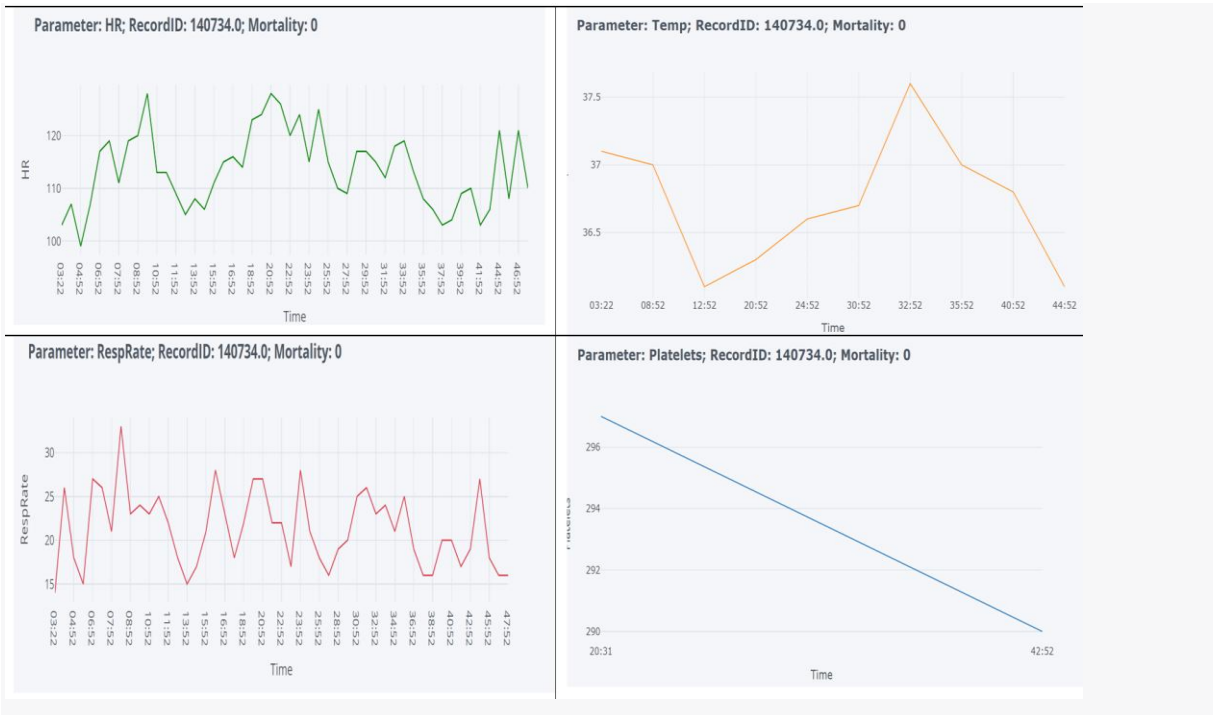

Figure 4. Parameter values were recorded in 47 timestamps.

3.2 Deep Sequence Framework

The proposed DSF consists of three main components: a feature extraction module, a sequence modeling module, and a mortality prediction module. The attribute extraction module is responsible for extracting relevant vital features from the recorded 37 features within 48 hours' time-step. In this prediction work , we used a combination of convolutional neural networks (CNN) and long short-term memory (LSTM) networks to extract temporal and spatial attributes from the data. The sequence modeling module takes the unearthed features as input and learns the temporal dependencies between the features using an LSTM network. The mortality prediction module takes the output from the sequence modeling

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module as input and estimates the likelihood of patient mortality using a connected neural network.

3.2.1 Feature extraction module:

The first part of the DSF is the attribute extraction module. This module is responsible for identifying relevant vital features from the recorded 37 features with a 48-hour time-step. The feature extraction module uses a combination of convolutional neural networks (CNN) and long short-term memory (LSTM) networks to extract both temporal and spatial attributes from the data.

The algorithm to extract attributes using CNNLSTM model is

Let X be the input data, where X = {x1, x2, ..., xn} represents a sequence of n samples.

Convolutional Neural Networks (CNN) (X):

The CNN layer is used to get spatial attributes from the input sequence. The input X is passed through a set of convolutional filters, which detect various spatial features available in the data. Each filter produces a feature map, which is a 2D matrix of values that highlights the presence of a specific feature in the data. The output of the CNN layer can be represented as follows:

Step 1: F = CNN(X)

where F = {f1, f2, ..., fm} represents a set of m feature maps, each of size h x w.

Step 2: Long Short-Term Memory (LSTM) Networks:

The LSTM layer is used to extract temporal features from the input sequence. The end value of the CNN layer is fed as input to the LSTM layer, which is responsible for capturing the temporal dependencies between the different feature maps. The LSTM layer uses a set of gates to manage the flow of information and selectively store or discard information from the preceding time step. The output of the LSTM layer can be denoted as follows:

H = LSTM(F)

where H = {h1, h2, ..., hn} represents a sequence of n hidden states, each of size d.

Step 3: Feature Fusion:

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The final step is to fuse the spatial and temporal features obtained from the CNN and LSTM layers, respectively. This is done by adding the final hidden state of the LSTM layer with each of the feature maps produced by the CNN layer. The resulting feature vector can be symbolized as follows:

V = [h_n, f_1, f_2, ..., f_m]

where V is a feature vector of size (d + m*h*w).

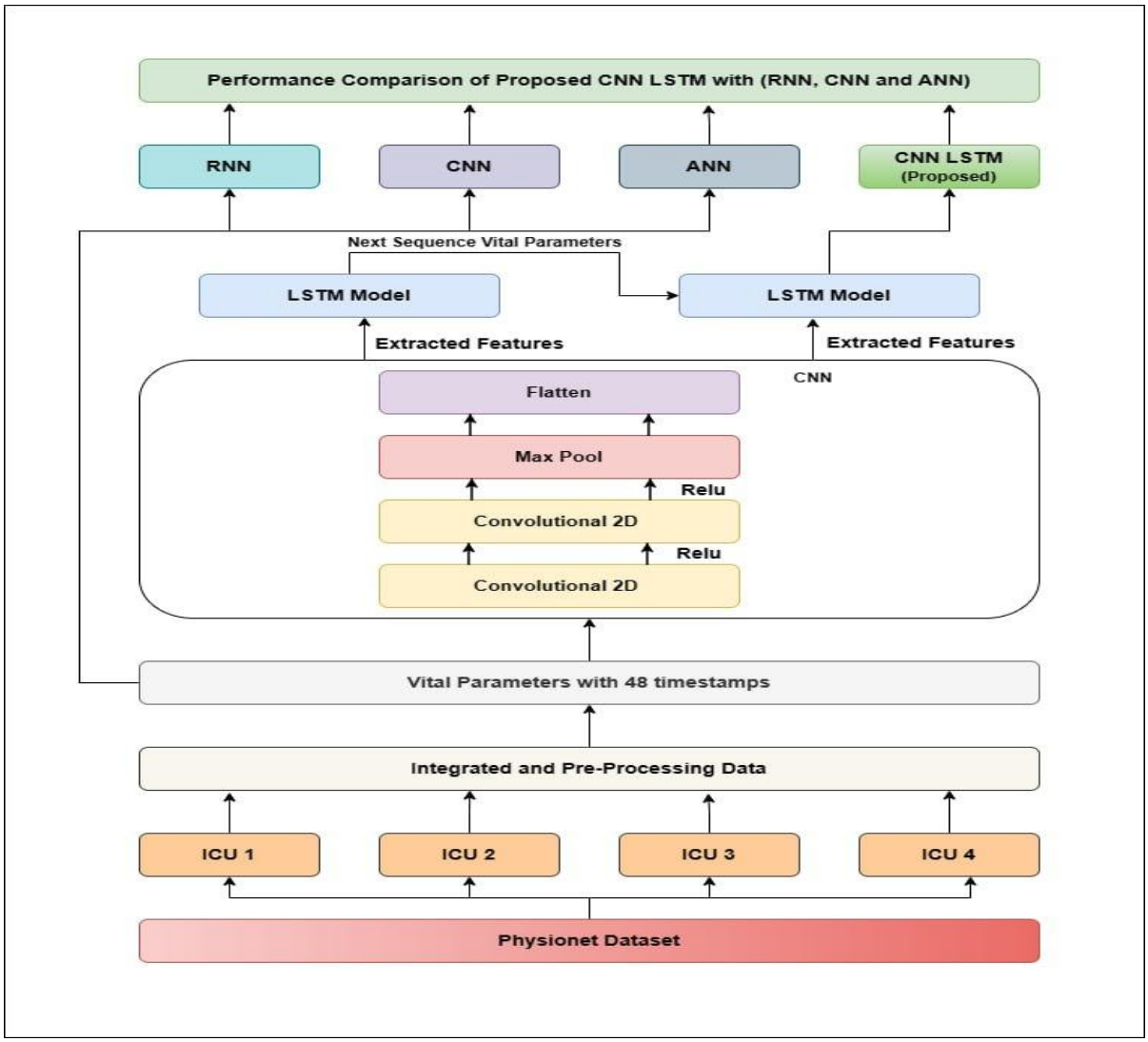

Figure 6. Deep sequence framework model.

3.2.2 Sequence model and predicting the mortality :

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We used LSTM to learn the temporal dependencies between the features. The LSTM takes as input the sequence of spatial features ‘ V’ extracted by the CNN and outputs a prediction for the mortality of the patient. The outcome of sequence modeling primarily consists of a series of feature representations that effectively capture the temporal relationships among the essential features. Let h_t be the hidden state of the LSTM at time step t, and let p(y_i|f(x_i)) be the predicted probability of mortality for patient i given the sequence of spatial features extracted by the CNN. *The LSTM can be defined as:*

$$h_t = LSTM(h_{t-1}, f(x_i))$$

$$p(y_i|f(x_i)) = sigmoid(W_h*h_t + b)$$

where LSTM represents the long short-term memory cell, W_h represents the learnable weights of the output layer, and sigmoid represents the sigmoid activation function.

During training, we can minimize the binary cross-entropy loss between the predicted probability of mortality and the true label using gradient descent:

$$L = -y_i * log(p(y_i|f(x_i))) - (1 - y_i) * log(1 - p(y_i|f(x_i)))$$

The model can undergo end-to-end training using backpropagation through time to modify the weights of both the CNN and the LSTM. Once the model is trained, it can be used to predict the mortality of new patients based on their vital feature data.

3.3. Evaluation Metrics

We evaluated the performance of the DSF using the area under the receiver operating characteristic curve (AUC-ROC) and accuracy. We also conducted a feature importance analysis to identify the most important features for mortality prediction.

IV . Results

The vital parameter is given as response to this LSTM model, and the time's steps are considered as 48. For example, if x is a BP parameter, then the recorded BP values recorded during the stay in ICU in 48 hours are considered for a time slot. Using the Data Generator in

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KERAS, we transformed all the parameter values into 48-time steps. The HR and Urine vital parameters readings of a patient are represented in the following diagram Figure 8. The heart is observed stable compared to the urine reading in the 48 hours.

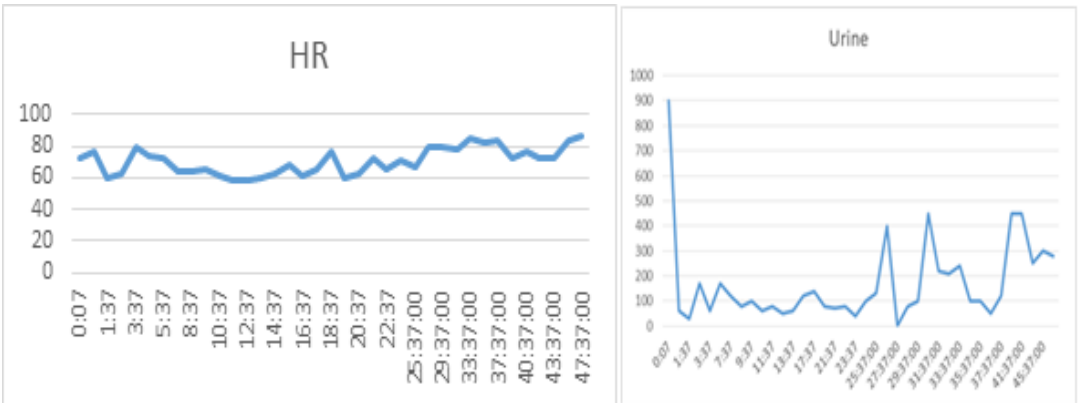

Figure 8 The vital parameters HR, Urine with time steps.

4.1. Training Data

First, the CNN model extracts important features and converts them into a vector format. Then, using data generator sequences, two LSTM models are learned with the extracted features over 48 time steps. The CNN model uses a kernel size of (3,3) with 32 nodes in the first convolution layer, followed by a second convolution layer with 64 nodes, and a third convolution layer with 16 nodes. The output of the third convolution layer is fed into the LSTM layer. Figure 9 provides a detailed description of the model.

```
model = Sequential()
model.add(Conv2D(32, kernel_size=(3, 3),
                 activation='relu',
                 input_shape=input_shape))
model.add(MaxPool2D(pool_size=(2, 2)))
model.add(Conv2D(64, (3, 3), activation='relu'))
model.add(Conv2D(16, (3, 3), activation='relu'))
model.add(MaxPool2D(pool_size=(2, 2)))
model.add(Flatten)
```

Figure 9. The CNN LSTM model for extracting the features

To predict critical ratings and mortality risk, we utilized an LSTM many-to-one model that was taught using 48-time steps of available historical data, with a batch size of 32. The model's architecture is depicted in the diagram below, where each rectangle represents a layer. Figure 10 displays the convolution layers and their corresponding feature size. Initially,

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the model receives 37 vital parameters, which are reduced to 24 features after feature extraction using the CNN layers. These features are then inputted into the LSTM layer, and the final output layer is used to predict the patient's mortality using the 24 vital parameters. We randomly split the dataset into training (70%), validation (10%), and testing (20%) sets.

The convolutional layers of the CNN are responsible for gettingattributes from the input data. Each convolutional layer consists of a set of learnable filters or kernels, which are applied to the input data to produce a set of characteristic maps.It is represented in Figure 10.

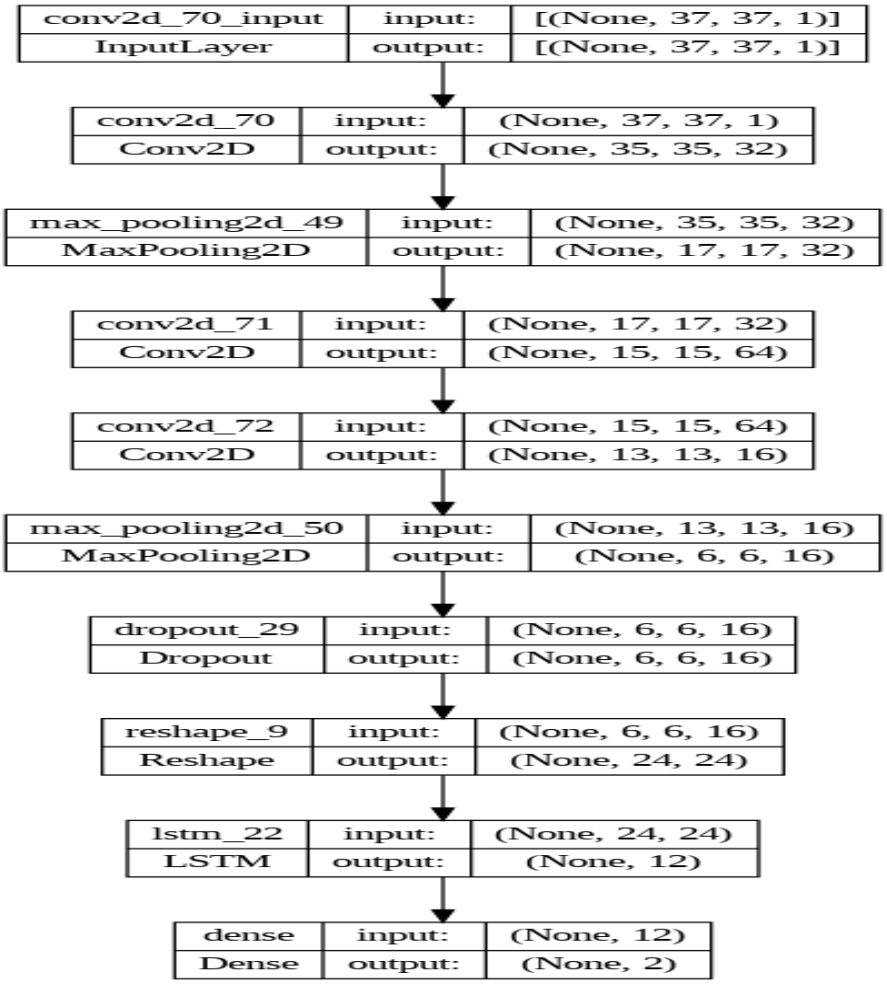

Figure 10. The CNN and LSTM model with the details of each layer

Figure 11 displays the loss for every epoch during the testing of the model with the test data. The model parameters are trained and the weights are updated using gradient descent. The cost/loss function is evaluated using the error during training. Model performance is

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calculated using the loss function, and to prevent overfitting and improve performance, a regularization term 'R' is included. The loss is calculated as $Loss = E(y,y') + \lambda R$, where y and y' represent the true and predicted values respectively, and λ is the regularization parameter.

```
Epoch 31/50
480/480 [==============================] - 4s 9ms/step - loss: 0.0996 - accuracy: 0.9631 - val_loss: 0.2142 - val_accuracy: 0.9341
Epoch 32/50
480/480 [==============================] - 4s 9ms/step - loss: 0.0959 - accuracy: 0.9644 - val_loss: 0.2182 - val_accuracy: 0.9308
Epoch 33/50
480/480 [==============================] - 4s 9ms/step - loss: 0.0951 - accuracy: 0.9644 - val_loss: 0.2695 - val_accuracy: 0.9198
Epoch 34/50
480/480 [==============================] - 4s 9ms/step - loss: 0.0899 - accuracy: 0.9676 - val_loss: 0.2205 - val_accuracy: 0.9348
Epoch 35/50
480/480 [==============================] - 4s 9ms/step - loss: 0.0886 - accuracy: 0.9671 - val_loss: 0.2315 - val_accuracy: 0.9313
Epoch 36/50
480/480 [==============================] - 4s 9ms/step - loss: 0.0902 - accuracy: 0.9672 - val_loss: 0.2139 - val_accuracy: 0.9333
Epoch 37/50
480/480 [==============================] - 4s 9ms/step - loss: 0.0870 - accuracy: 0.9681 - val_loss: 0.2209 - val_accuracy: 0.9328
Epoch 38/50
480/480 [==============================] - 4s 9ms/step - loss: 0.0839 - accuracy: 0.9687 - val_loss: 0.2233 - val_accuracy: 0.9345
Epoch 39/50
480/480 [==============================] - 4s 9ms/step - loss: 0.0814 - accuracy: 0.9701 - val_loss: 0.2326 - val_accuracy: 0.9345
Epoch 40/50
480/480 [==============================] - 4s 9ms/step - loss: 0.0815 - accuracy: 0.9699 - val_loss: 0.2452 - val_accuracy: 0.9295
Epoch 41/50
480/480 [==============================] - 4s 9ms/step - loss: 0.0773 - accuracy: 0.9711 - val_loss: 0.2371 - val_accuracy: 0.9335
Epoch 42/50
480/480 [==============================] - 4s 9ms/step - loss: 0.0777 - accuracy: 0.9711 - val_loss: 0.2457 - val_accuracy: 0.9294
Epoch 43/50
480/480 [==============================] - 4s 9ms/step - loss: 0.0779 - accuracy: 0.9707 - val_loss: 0.2311 - val_accuracy: 0.9323
Epoch 44/50
480/480 [==============================] - 4s 9ms/step - loss: 0.0741 - accuracy: 0.9716 - val_loss: 0.2412 - val_accuracy: 0.9337
Epoch 45/50
480/480 [==============================] - 4s 9ms/step - loss: 0.0710 - accuracy: 0.9741 - val_loss: 0.2455 - val_accuracy: 0.9314
Epoch 46/50
480/480 [==============================] - 4s 9ms/step - loss: 0.0709 - accuracy: 0.9743 - val_loss: 0.2379 - val_accuracy: 0.9323
Epoch 47/50
480/480 [==============================] - 4s 9ms/step - loss: 0.0663 - accuracy: 0.9750 - val_loss: 0.2455 - val_accuracy: 0.9323
Epoch 48/50
480/480 [==============================] - 4s 9ms/step - loss: 0.0695 - accuracy: 0.9741 - val_loss: 0.2435 - val_accuracy: 0.9326
Epoch 49/50
480/480 [==============================] - 4s 9ms/step - loss: 0.0672 - accuracy: 0.9749 - val_loss: 0.2379 - val_accuracy: 0.9333
Epoch 50/50
480/480 [==============================] - 4s 9ms/step - loss: 0.0638 - accuracy: 0.9761 - val_loss: 0.2402 - val_accuracy: 0.9334
<tensorflow.python.keras.callbacks.History at 0x7fc09575b3d0>
```

Figure 11. Generated loss from the model for 31 50 epochs

After testing the model with 4000 testing data points, the mortality and survival outcomes were determined and presented in Figure 12. The model attains an accuracy rate of 93.4%. The model successfully predicted both mortality and survival outcomes and Figure 12 provides a breakdown of the total number of predicted survivals and mortalities. Some of the most important characteristics for mortality prediction were age, mean arterial pressure, and serum creatinine levels.

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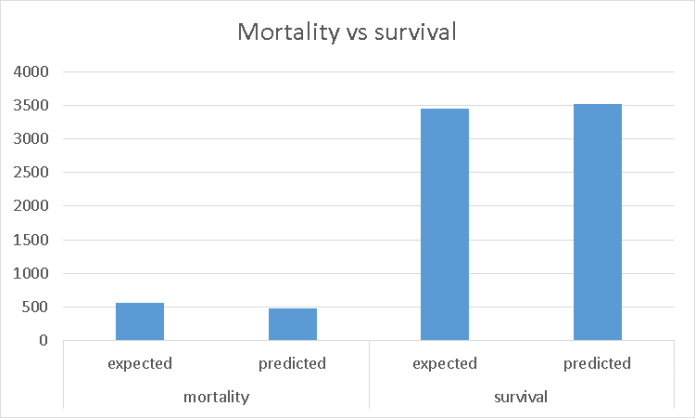

Figure 12 The model predictions.

Figure 13 shows the accuracy and loss of validation data and test data of the model. Compared to test data, validation data shows prominent results.

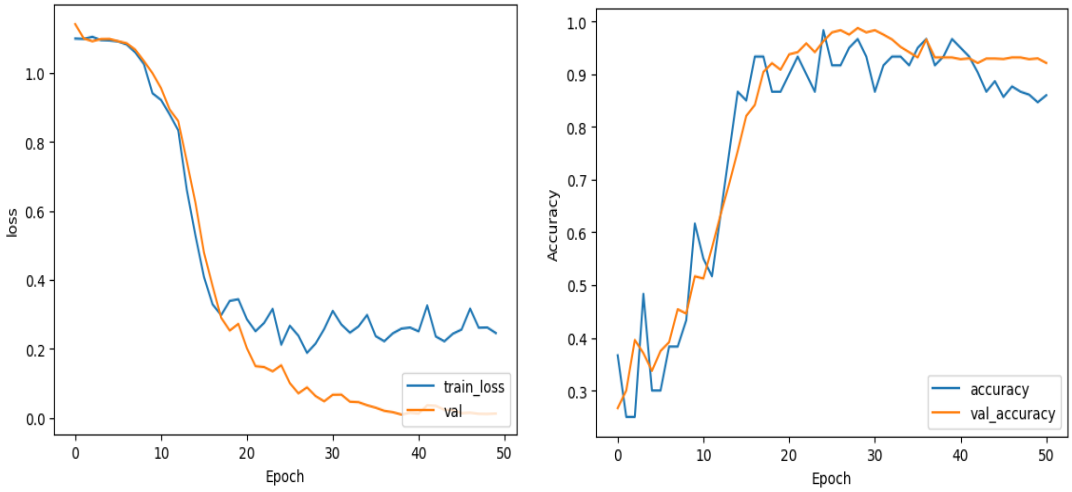

Figure 13. Accuracy and loss of model for training and validation data sets.

Statistical analysis We compared the performance of DSF with other standard deep learning algorithms, such as RNN [19], Convolution neural networks [12], and Deep ANN [20]. The evaluation of model performance was centered on discrimination, gauged through two commonly employed metrics: the area under the receiver operating characteristic curve (AUROC) and the area under the precision-recall curve (AUPRC). Additionally, positive predicted value (PPV), negative predicted value (NPV), and accuracy were assessed for all

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models and are presented in Table 3. When trained with the PhysioNet dataset, the RNN model predicted mortality with 90.2% accuracy, while the CNN model achieved 91.3% accuracy, and the ANN model achieved 88.2% accuracy.

Table 3. Evaluation of models.

Model	Accuracy	Precision
RNN	90.2	89.8
CNN	91.3	90.7
ANN	88.2	86.4
CNNLSTM	93.4	93.1

The proposed Deep sequence framework model with CNNLSTM layers predicts 93.4% accuracy which shows a significant improvement from the previous models.

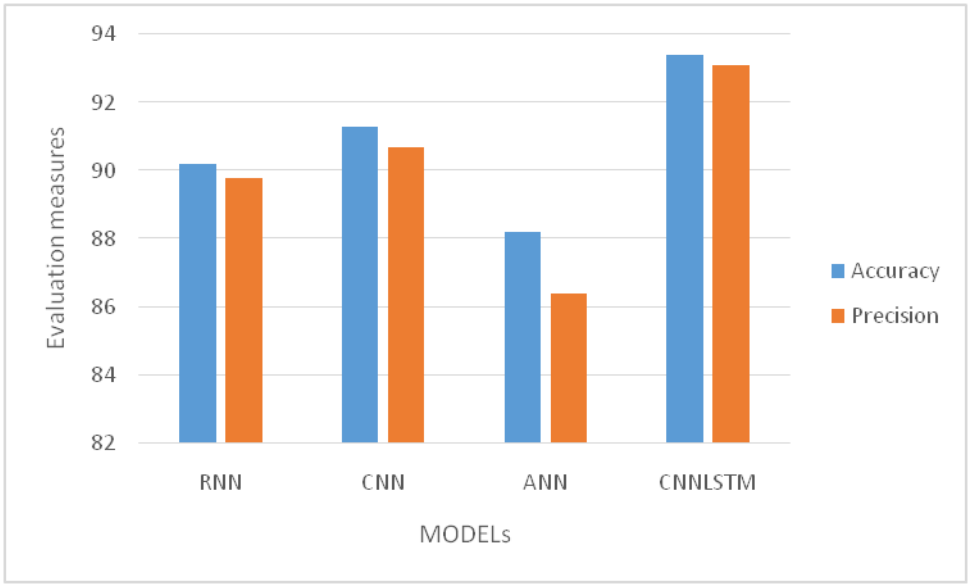

Figure 14. The comparison graph.

Figure 14 describes the comparison between the RNN, ANN, CNN, and CNNLSTM model's accuracy and precision. All the models are trained with the same PhysioNet data set.

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V . Discussion:

Our results indicate the efficacy of the deep sequence framework model for mortality prediction of ICU patients. The DSF model had a high level of accuracy indicating its potential for clinical use. The spatial and temporal features extracted from the model provided insights into features that contribute to mortality prediction, which could aid clinicians in decision-making.When deploying early warning systems (EWS) in ICU settings, it is imperative to consider both accuracy and false alarm rates. Our model can support generating warnings also. It was necessary in this instance sensitivity and specificity carefully evaluated and optimized.

First, the limited generalizability of our results may be because we only used data from one location. Future research could assess the model's performance using information from 28 hospitals in several areas. Further study is required to see whether it is effective at predicting mortality in other healthcare contexts because, second, we only considered mortality prediction in critical care settings.

VI Conclusion

In this study, we proposed a DSF for recognizing mortality risk factors for ICU patients. Our results established that the DSF can accurately predict patient mortality using time-series data. The discovered risk factors can help clinicians make informed decisions and improve patient outcomes. Experiments carried out in diverse ICUs indicate that our recently introduced deep sequence framework model outperforms existing benchmarks in predicting the risk of mortality.The model accomplished an accuracy of 93.4% and a loss of 0.0008054, demonstrating the potential of deep learning methods for predicting mortality in ICU patients. Subsequent research can delve into the application of the DSF in clinical environments and examine the model's interpretability.

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