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Sepsis Prediction using Machine Learning and Deep Learning Algorithms

MSc Research Project
Data Analytics

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Sepsis Prediction using Machine Learning and Deep Learning Algorithms

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Abstract

This paper aims at presenting a methodology and comparing various machine learning (ML) and deep learning (DL) methods for predicting sepsis from clinical time-series data. Sepsis is among the most threatening condition that could occur during intensive care unit (ICU) treatment of a patient. Therefore, in this research, multiple models are applied to the data after they have been carefully cleaned and pre-processed to obtain the best results. In the research DL method such as long short-term memory (LSTM) is applied and ML method such as decision tree (DT), random forest (RF), extreme gradient boosting (XGB), adaptive boosting (AdaBoost) and k-nearest neighbours (KNN) to the data set which is provided from 2 hospitals via a challenge and has hourly data of more than 40,000 patients. Data were processed in two separate way and the best performing was used to apply all the models. Of which XGB performs the best with 0.98 of accuracy, 0.96 recall, 0.98 f1 score, and 0.99 precision followed by RF as the second-best model.

1 Introduction

Sepsis is by far the most common complication of trauma patients; Sepsis is a life-threatening disorder that occurs when tissue damage, organ failure, or death is caused by the body's response to infection. Every year around 5.8 million people worldwide die from trauma, 40% of deaths took place during hospitalization, 22% of which were caused by sepsis Fu et al. (2019). Sepsis is a major health problem with a significant health impact throughout the world Mohamed et al. (2020). Sepsis is an economically significant and severe disease in the Intensive Care Unit (ICU), costing hospitals about 6 billion pounds in the UK, costing more than 20 billion dollars in 2011 in the US around 5.2% of all hospital costs, with costs rising to over 23 billion dollars in 2013, 6.2% of all hospital bills in the US. Sepsis is defined as serious a "life-threatening dysfunction of the organ caused by a dysregulated response of the host to infection" (Li et al.; 2019) (Mohamed et al.; 2020).

Delayed treatment per hour is associated with an increase in mortality of approximately 4% - 8%. Sepsis detection can effectively decrease occurrence of post-traumatic complications and mortality (Fu et al.; 2019) (Mohamed et al.; 2020). It has been shown that early and targeted treatment greatly enhances the sepsis outcomes. In critical care settings, such as the ICU, predictive models were used to improve care, and can potentially be used for identification of patients at risk of becoming septic (Wang, Sun, Schroeder, Ameko, Moore and Barnes; 2018).

The sepsis diagnosis is currently based on clinical evaluation and analyses of vital signs or laboratory results that are often non-sensitive, non-specific, and non-rapid (Amiri et al.; 2019). More than 18.8 million electronic health record (EHR) data can be found in the ICU that provides a distinctive opportunity to generate new insights for improved care. EHRs are now an important information source and the big drive for modern medicine with the advances in ML (Li et al.; 2019) (Lin et al.; 2019). It can make more precise, robust, and personalised decisions. But a very little study has concentrated on predicting the severity of sepsis in EHR patients. Consequently, many studies suggest the end to end artificial intelligence models have enabled computer scientists to develop innovative decision support systems based on ICU (Li et al.; 2019). However, due to its sparse, irregular, and asynchronous nature, working with EHRs in their raw format is often very challenging (Lin et al.; 2019). But most early ICU analytic on sepsis data focuses primarily on the risk of mortality prediction and antibiotics improve survival (Li et al.; 2019).

Figure 1: Sepsis sign and symptoms

Given the growing evolution of modern biomedical technology, preterm infants remain highly vulnerable to the infection, particularly those of very low birth weight(Hu et al.; 2019). Neonatal sepsis is a condition which during the first thirty days of life presents signs of infection. Sepsis diagnosis can be defined as sepsis that is early-onset, late-onset, and very late-onset. Early neonatal sepsis is usually transmitted through the birth channel or during delivery, while late neonatal sepsis can be transmitted through the birth channel or in the hospital, environment, community, home. Sepsis is generally seen very late-onset in infants born with low birth weight and long-term hospital treatment, and rarely from the community (Tekin et al.; 2019).

The application of neural networks (NN) and ML models to clinical medicine have been studied by researchers since the early 1990s. Due to the availability of extensive computing power to perform deep ML, NN has been resurgent in recent years (Mohamed et al.; 2020). Recurrent neural networks (RNN) and particularly LSTM networks are presently a very powerful tool that is wildly used in many tasks, where information is a variable-length sequence, including signal classification, natural language processing (Vicar et al.; 2019).

In Section 2 all the related work in relation to sepsis has been discussed. In Section 3, the methodology followed for the project is explained in detail and the steps taken as well. In Section 4, the design of the project is given. In Section 5, the implementation of the models is explained. In Section 6, the evaluation matrix and model performance is compared. Section 7 is the conclusion and future work.

1.1 Motivation of this Research

Approximately 5.8 million people die of trauma worldwide, 40% of deaths occurred during hospitalization, 22% of which was sepsis. Detection of sepsis can effectively reduce the occurrence of post-traumatic complications and mortality (Fu et al.; 2019).

Survivors of sepsis can endure long-term physical as well as psychological problems that require more support for social and health services. Deaths largely consist of the elderly, neonates, and patients with impaired immune systems in critical care. A study by the world health organization in 2017 indicated that infectious diseases caused 50% of all deaths in children below 5 years of age (Shah et al.; 2019).

Premature infants are at higher risk of having life-threatening sepsis and multi-organ complication. Sepsis is a major concern for public health and greatly contributes to neonatal morbidity and mortality (Joshi et al.; 2020).

Since the people who are more susceptible to sepsis are babies and aged persons who do not have a healthy immune system, it is even more useful to identify sepsis accurately so that they can be diagnosed and treated on time.

1.2 Research Questions

The following is the research question that is answered by this research project:

- How can different ML and DL techniques be used to predict sepsis accurately?
- To what extend the patient's medical record can be used to enhance various models?

1.3 State of the Art

For the research, I have considered the research done by Mohamed et al. (2020) which was done in 2020. The research was done by comparing multiple models of ML and DL. This research will be following a similar pattern of working on multiple models and improve on the performance of few models used as in the State of the art (SOA) approach research and adding some additional models based on the literature review and comparing those papers in Section 2.1. Section 3.7 explains the models used for the research.

2 Related Work

The research involved using relevance vector machines (RVM) by Ribas et al. (2011) to provide an automated ranking of the mortality predictors. The database consists of severe sepsis patients from June 2007 through December 2010 of 354 patients. RVM through an embedded feature relevance determination process and has proved to be superior in terms of accuracy than other well-established methods with an AUC of 0.80.

The study by Marshall et al. (2012) focused on developing a discrete conditional survival model (DC-S) with a classification element to predict patient outcome and survival. The model DC-S consists of two main components; the conditional component that uses a tree of classification and the survival component that models the distribution of survival and gave an accuracy of 0.99.

The aim of Mani et al. (2013) is to develop a non-invasive prediction model from off-the-shelf medical data and EMR for late-onset neonatal sepsis. The data used in this study is from 299 infants. Naive Bayes (NB), support vector machine (SVM), RF, KNN,

classifiers classification and regression trees (CART), lazy bayesian rules (LBR), averaged one dependence estimators (AODE) and augmented naive Bayes (TAN) were applied to the data set. AODE had the best sensitivity with data set 1 at 0.88 while NB and RF had 0.95 and 0.94 respectively with data set 2.

The aim of the study by Guillén et al. (2015) is to explore a new framework for severe sepsis prediction. There are few models such as logistic regression (LR), SVM, and logistic model trees (LMT) that use vital signs, laboratory values, or a mixture of vital and laboratory values. The SVM model utilising lab and vital signs as predictors correctly identified 0.65 of the 3,446 patients as having severe sepsis.

The researchers Gunnarsdottir et al. (2016) built a generalized linear model (GLM) for the likelihood of sepsis in an ICU patient. Models were specifically trained on 29 patient records and evaluated on a different test set including 8 patient records. Using demographic measures as features, a classification accuracy of 62.5% was achieved. The addition of physiological time series features to the model increased the accuracy of the classification to 0.75.

The study endeavored to build a predictive sepsis model by Wang, Sun, Schroeder, Ameko, Moore and Barnes (2018). Using vital signs and blood culture results, LR, SVM, and LMT were used to predict sepsis onset in adult ICU patients. 19,358 patient's information was extracted from that 4,915 patients. LMT produced superior performance, the specificity of LMT was 0.83

An application was developed by Thakur et al. (2018) to calculate the likelihood of sepsis. The prediction model developed from non-invasive variables performed equally well in comparison with the invasive parameter prediction model. More than 58000 hospital admissions for 38645 adults and 7875 neonates are included in the data set. LR was used for 3 invasive and 3 non-invasive parameters for predicting. The AUROC was 0.777 and 0.824 for invasive and non-invasive prediction models, and 0.830 and 0.824 for validation data set respectively.

A great learning method is proposed to improve the performance of the extreme learning machine kernel, known as the optimisation of a chaotic fruit fly. Feature selection was done using the RF before the classification model was constructed. A total of 42 patients with sepsis were utilized for the research. RF-CFOA-KELM achieved results of 0.8160 accuracy, 0.7766 MCC, 0.8957 sensitivity, and 0.6577 specificity (Wang, Wang, Weng, Wen, Chen and Wang; 2018).

The goal by Gómez et al. (2019) was to develop a minimally invasive and cost-effective tool, based on heart rate variability (HRV) monitoring and ML algorithms, to predict sepsis risk in neonates within the first 48 hours. 79 newborns aged between 36 and 41 weeks with gestational age were recruited. The research has implemented adaptive boosting AdaBoost, bagged classification trees (BCT), RF, LR, SVM, NB, classification tree (CT), and KNN. They each have their own set of parameters that can be optimized for better performance. The AdaBoost AUC is best with 0.94 followed by BCT and RF.

The paper by Wang et al. (2019) presents 2 methods from the clinical data for the early prediction of sepsis. One is an LSTM and the other is based on the XGB method. The data set consists of 40 characteristics such as values of Demographics, Vital Signs, and Laboratory. There is a total of 40336 patient records. Along the timeline, the currently missing data were filled with the last non-missing data from previous data when data was found missing. In the LSTM-based method, the remaining missing data after the preceding step was filled with value 0. The utility score is 0.267 for the LSTM-based method, and 0.392 for the XGB based method.

The researchers Alnsour et al. (2019) aims to predict in-hospital mortality of patients with sepsis. The data set was composed of 1,048,575 sepsis patients hospitalised between 2008 and 2012. The following models were applied LR, RT, BN, NN, SVM, chi-square automatic interaction detection (CHAID), and Quest. The results showed that CHAID had the best accuracy of 82.08% invalidation followed by Quest. In phase 2, The authors added the attributes of the health care provider to the data used to construct the models and set the type of each attribute accordingly. CHAID model had the best with an accuracy of 0.853.

An early sepsis diagnostic model is suggested by Fu et al. (2019) using an improved deep forest (DF) cascade model. Electronic medical record (EMR) data with the first 24 hours of ICU admission for patients to be classified as sepsis. 3125 patient data were used. The models were SVM, RF, LR, KNN, GB, XGB. The researcher's model gave a better AUROC of 0.80 than the traditional models. The accuracy of the model was 73% which was the best along with GB which gave an accuracy of 0.73 as well.

The paper focuses on assessing the impact and relevance of 3 different patient metrics based on the similarity of a 1-year prediction of mortality when patients are related to the same diagnosis of sepsis. 16219 admissions were obtained; newborn patients with 16,080 admissions were excluded from these. Finally, only hospital admissions where 15751 patients were selected for more than one day. The best LR algorithm presented an AUROC of 0.73 (Garcia-Gallo et al.; 2019).

A method has been developed that focuses on identifying optimal HRV features in intensive pediatric care for early identification of sepsis. Four models of the classifiers viz KNN, DT, SVM, and Linear Discriminant Analysis (LDA) were used. Of all the models applied, DT had the best accuracy of 0.8636 (Amiri et al.; 2019).

A method has been developed which predicts the onset of sepsis early by observing the lack of physiological variables and comparing them with general patterns of data. XGB model has been applied to that data set. The "best model" described in the XGB-W paper, and a larger vector of the masking. The best model yielded a 0.8406 AUROC score (Singh et al.; 2019).

The paper developed a bagged decision trees (BDT) ensemble with a highly unbalanced misclassification cost to predict the sepsis for each sample of patient features. A three-bagger classifier was trained using the training data set, and the appropriate features and hyperparameters were chosen in an iterative process until the best score was reached. A group of DTs was developed using binary outputs: sepsis or no sepsis. The accuracy of the model was 0.871 and 0.912 on the two data sets (Firoozabadi and Babaeizadeh; 2019).

A general framework is proposed by Lin et al. (2019) that represents, in a unified and systematic way, the extracted temporal relationships and local patterns through facial representations that have evolving emotional expressions based on patient health conditions.2D CNNs are used to extract high-level facial characteristics from the images produced and then fed the facial representations extracted into LSTM-based models to predict. The best accuracy is by the proposed model dyn+ img.2D CNN.LSTM + sta of 0.9037.

The research is on neonatal sepsis data set analysis using DM techniques. This study aims to tackle the relationship between data mining methods and health services. 13 variables are present in the data set. KNN and NB algorithms are applied to the data set. KNN algorithm gave an 0.9453 accuracy while NB algorithm produced a 0.9375 accuracy (Tekin et al.; 2019).

An attention-based model in sepsis prediction that provides more details on the amount of contribution to the final prediction of each of the medical measurements is explored. More than 53,000 adult patient's records were used. In total there are 11,791 patients in the cohort under study. A total of 39 features were selected. The research is utilising RNN as specific bidirectional RNNs. The model gives a precision of 0.75 (Baghaei and Rahimi; 2019).

The paper by Hu et al. (2019) focuses on creating an application for preterm newborns which predicts sepsis using CNN at an early stage. The data set is composed of 146 newborns. Data chunks were used which are sequences of data cut and transformed to a certain length. The study used a 14-layer deep CNN. The proposed model had an AUC 0.79 and precision is 0.76.

Bidirectional LSTM Networks for predicting the severity of sepsis in ICU patients as most previous severity prediction models rely on multi-task recurrent NN. It proposes an end to end recurrent neural model that simultaneously analyses different organ systems and intuitively reflects patients' condition in a timely manner. For the prediction 48 features were used from the data set. Bidirectional LSTM network consists of the sub-LSTM, both forward and backward. Attention mechanism for selectively learning important features and for creating short direct connections between target and source. The proposed model achieves an F1 score of 0.9472 (Li et al.; 2019).

The study focuses on sepsis patient identification based on EMR in the emergency department. DT, Discriminant Analysis (DA), LR, KNN, Ensemble Classification (EC), SVM, and NN are the techniques used in ML. Also includes a novel rule-based genetic-algorithm-optimized system. The data set consists of 912 sepsis and 975 non-sepsis patients. The NN model yielded the best results. 65 hidden neurons with 0.9208 sensitivity and 0.9233 specificity were the best performing NN model (Mohamed et al.; 2020).

The study compares the performance of several major ML techniques to identify patients with sepsis in the Emergency Department (ED). The following models were applied to compare DT, DA, LR, KNN, Ensemble Classification, SVM and NN are the techniques used in ML. A novel, genetic-algorithm-optimised rule-based system developed by the authors is also used. The data set had 1,887 unique cases. The NN model yielded high performance with sensitivity of 0.9208, specificity of 0.9233, PPV of 0.9178, and accuracy of 0.9221 (Mohamed et al.; 2020).

The research presents a model for overcoming these deficiencies using a DL approach to a diverse multicenter set of data. The research had three main approaches for early detection of sepsis: a GB-Vital system based on vital sign characteristics; a non-sequential MLP model of thousands of characteristics, including those used for the GB-Vital model; and a sequential CNN-LSTM model with an equal number of functions. GB-Vital model had reasonable performance, with an AUROC of 0.786 3 hours before sepsis onset. CNN-LSTM model achieved an AUROC of 0.856 when evaluated for 3h(Lauritsen et al.; 2020).

2.1 Approach comparison

This section compares the different important papers and including the models applied, aim and objective. the data set. This papers are the primary papers considered while applying the model in the research.

Author(s) and Title	Aims and objective	Models Applied	Dataset	Findings relevant to the review
Mani et al. (2013) - "Medical decision support using machine learning for early detection of late-onset neonatal sepsis"	"To develop non-invasive predictive models for late-onset neonatal sepsis from off-the-shelf medical data and electronic medical records"	NB, SVM, RF, KNN, CART, LBR, AODE, and TAN	Infants admitted to the NICU over a period of 18 months starting from 1 January 2006 with 299 infants	AODE had sensitivity of 0.88 with data set 1 and with data set NB and RF had 0.95 and 0.94 sensitivity respectively.
Wang et al. (2019) - "Prediction of Sepsis from Clinical Data Using Long Short-Term Memory and eXtreme Gradient Boosting"	"To develop an objective and efficient computer-aided tool for early detection of sepsis"	LSTM and XGB	Data of two independent hospitals were used. A total of 40,336 records.	The utility score is 0.267 for the LSTM-based method, and 0.392 for the XGB based method.
Amiri et al. (2019) - "Identifying Optimal Features from Heart Rate Variability for Early Detection of Sepsis in Pediatric Intensive Care"	Early diagnosis of sepsis before clinical signs are developed to give physicians enough time for antibiotic therapy of these patients	SVM, LDA, KNN, and DT	Data was of two PICU hospital and the patients were between 2016 and 2018 and had about 500 records	DT had the best accuracy of 0.8636.
Singh et al. (2019) - "Utilizing Informative Missingness for Early Prediction of Sepsis"	"To predict the occurrence of sepsis early by studying the missingness of physiological variables and using it with the overall trends in data"	XGB with multiple variations	Data comprised of three distinct hospitals in the United States with ICU stay records of 40,336 patients	Best Model of XGB got a 0.8406 AUROC score.
Tekin et al. (2019) - "Analysis of the Neonatal Sepsis Data Set with Data Mining Methods"	"To address the relationship between data mining methods and health services."	KNN and NB	Data set used is from the Department of Pediatrics of Fırat University Hospital between May 2013 and January 2014	KNN algorithm made 0.9453 accuracy.
Gómez et al. (2019) - "Development of a Non-Invasive Procedure to Early Detect Neonatal Sepsis using HRV Monitoring and Machine Learning Algorithms"	"To develop a minimally invasive and cost-effective tool, based on HRV monitoring and ML algorithms, to predict sepsis risk in neonates within the first 48 hours of life."	AdaBoost, BCT, RF, LR, SVM, NB, CT, and KNN	79 new-borns with age between 36 and 41 weeks data was recorded	AdaBoost AUC is best with 0.94.
Mohamed et al. (2020) - "Electronic-Medical-Record-Based Identification of Sepsis Patients in Emergency Department: A Machine Learning Perspective"	"To compare the performance of several major machine learning techniques to identify emergency department sepsis patients during their first 6 hours of care."	DT, DA, LR, KNN, EC, SVM, NN, and genetic algorithm optimised system	1887 patients from ED of the Detroit Medical Center in Michigan, USA	NN model achieved 0.9208 sensitivity, 0.9233 specificity, and 0.9178 PPV.

Table 1: Important Paper Comparison

3 Methodology

For this research project, Knowledge Discovery in Databases(KDD) was used. KDD is an incremental method where measurements for assessment can be improved, mining can be refined, the latest data is integrated and converted to obtain different and more appropriate results[1].

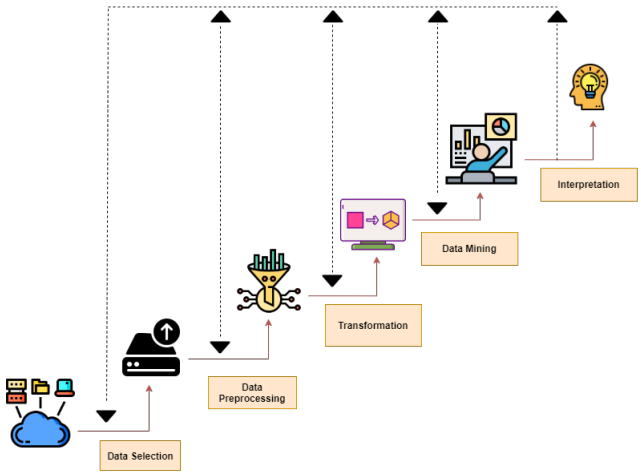

Figure 2: Knowledge Discovery in Databases

KDD has 5 important phases as shown in figure 2. Phase one is Data selection where the data for the research is selected. The second phase is prepossessing of the data. Prepossessing involves cleaning data, deleting unnecessary data, imputing missing data. The third phase is called transformation which transforms data from one type to another, as per the algorithm or model. This also involves converting data from a complicated format into one that is simple. Phase four is called DM. This is where the proposed ML model or algorithm is implemented. The data set is split into test and train. The model is trained using the train data. Upon completion of the training, the model runs on a new data called the test data. The fifth phase is termed as interpretation. That, too, is a critical point. From this stage, knowledge is acquired and insights learned.

3.1 Data set

Type	Features								
Demographics	Age	Gender	Unit 1	Unit 2	HospAdmTime	ICULOS			
Vital Signs	HR	O2Sat	Temp	SBP	MAP	DBP	Resp	EtCO2	
	BaseExcess	HCO3	FiO2	pH	PaCO2	SaO2	AST	BUN	Alkalinephos
Laboratory Values	Calcium	Chloride	Creatinine	Bilirubin_direct	Bilirubin_direct	Glucose	Lactate	Magnesium	Phosphate
	Potassium	Bilirubin_total	TroponinI	Hct	Hgb	PTT	WBC	Fibrinogen	Platelets

Figure 3: Data set Variables

Figure 3 shows us the data set variables. Data used for the research is obtained from ICU patients of two separate hospitals. The data set was part of a challenge and openly

[1]https://www.geeksforgeeks.org/kdd-process-in-data-mining/

available on https:/physionet.org/content/challenge-2019/1.0.0/. Each file has the same header and each row represents the value of a single hour of data. Data available for patients are Demographics, Vital Signs, and Laboratory values. The data set contains 20,336 and 20,000 patient records. Each table column provides a sequence of measurements over time, in which the column header explains the observation. There are 40 variables that depend on time. SepsisLabel, indicates sepsis where 1 shows sepsis and 0 shows no sepsis. NaN indicates that no measurement of a variable was recorded at the time interval.

3.2 Exploratory Data analysis

In this section, the data is explored and checked before data preprocessing is done. When the records are merged the hourly data sums up to 1552210 rows.

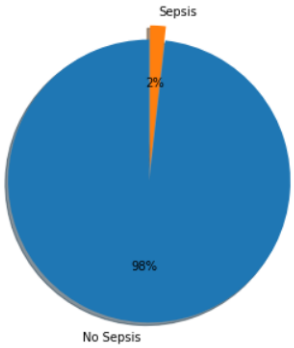

Figure 4: Sepsis records

As seen in figure 4 only 2% of the total patient records shows sign of sepsis. Of 40336 patients in 2932 patients had sepsis. This shows how the data set is highly imbalanced for the predicting/dependent variable.

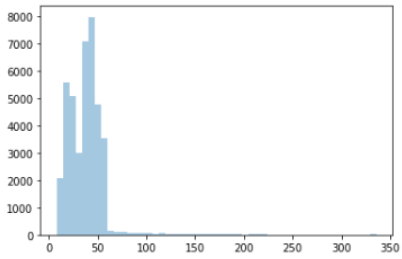

Figure 5: Hourly graph of patients admitted

Figure 5 shows the trend of how long the patients were admitted to the hospital. It can be seen that post 60 hours the number of patients is very less.

3.3 Data Pre-processing

Pre-processing of data is performed to make sure no inconsistencies were found in the data. Irrelevant and redundant present or noisy and unreliable information is removed

from the data set. First, the most important thing was to check how much of the data is missing from the entire data set.

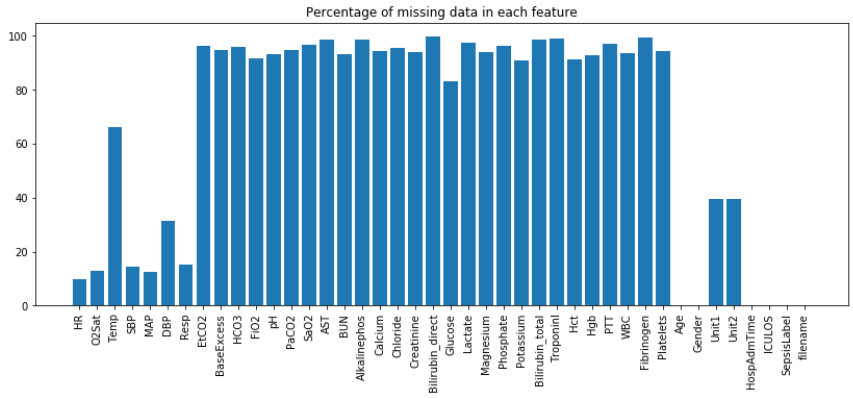

Figure 6: Missing data from the data set

Figure 6 gives overall information on the missing data. EtCO2, BaseExcess, HCO3, FiO2, pH, PaCO2, SaO2, AST, BUN, Alkalinephos, Calcium, Chloride, Creatinine, Bilirubin_direct, Glucose, Lactate, Magnesium, Phosphate, Potassium, Bilirubin_total, TroponinI, Hct, Hgb, PTT, WBC, Fibrinogen and Platelets had more than 80% of the data missing. Hence the columns/features were dropped. Temp had more than 60% of the data missing while Unit1 and Unit2 had more than 40% of the data missing. Temp, Unit1, and Unit2 were also dropped.

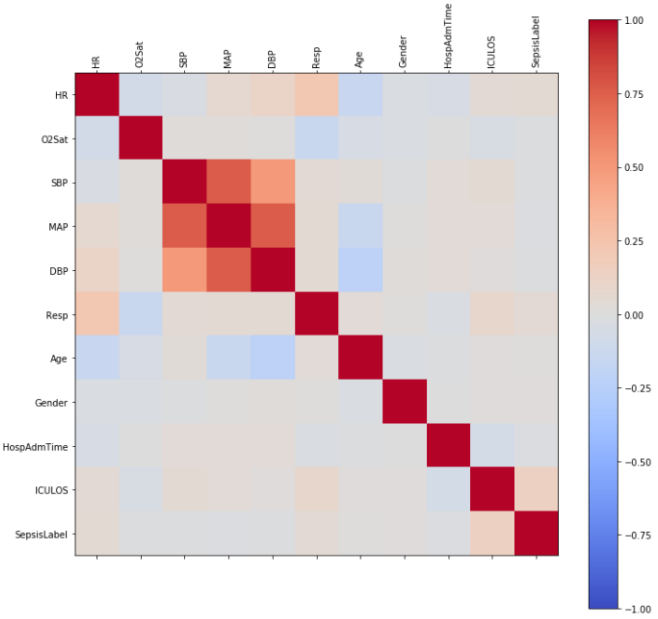

Figure 7: Correlation matrix

Figure 7 shows the correlation of the variables with each other. The correlation matrix shows the degree to which a pair of variables are linearly related. The variables can be correlated positively or negatively. If they are positively correlated then the color is towards red/maroon. The more they are correlated the darker the color gets. Similarly, if the variables are negatively correlated then they are marked with blue color. From

the image it is SBP and MAP are strongly correlated positively while SBP and DBP are slightly correlated positively. All the other variables are loosely correlated and the correlation value is almost zero.

The next step is data imputing. This is the process of substituting missing data with replaced values. For this research, median substitution is used for data imputation. This involves calculating the median of the non-missing values in a column and then substituting the missing values. Some of the benefits of this type of imputation are that it is easy and fast, working well with numerical data sets[2].

3.4 Feature Extraction and Encoding

Feature Extraction helps to reduce the number of features in a data set by creating new features from existing features. This makes it possible to create a summarized version of the original features from a combination of the original set[3]. In the research, there were 11 features left post data cleaning and data imputation. Of which 10 being independent feature while 1 being the dependent feature. SBP stands for Systolic blood pressure which is upper number while measuring Blood pressure while DBP stands for Diastolic blood pressure, It is the lower number while measuring Blood pressure. In this research, we combined both the features to get blood pressure as low, normal, elevated, high, and missing (which does not fall in any categories). This missing value had to be filled with median imputation. Other features/variables which were changed were Age, O2Sat, Respiration, MAP, and heart rate where the values were converted to a range and if there were any missing values then it had to be imputed as well. Also, Values of the data set were converted into fixed values based on the medical information also called as encoding.

3.5 Under Sampling

If a data class is the over-represented majority class, this can be used to balance it with the minority class under-sampling. Under-sampling is used when the amount of data collected is sufficient. Trying to reduce the bias associated with imbalanced data classes under-sampling. Overall the majority class works best for large data sets under-sampling. In the research, NearMiss library is used for under-sampling.

3.6 Data Splitting

There are 2 different data splitting in the research. The first one with the data into train and test data set of the data after feature extraction and under-sampling done. The second data splitting was to the data without applying feature extraction but using under-sampling. In both, the scenario the actual data was split into train data which was 75% of the data while the test data was the remaining 25% of the data.

3.7 Models

- **Long Short-Term Memory**: It is a kind of artificial NN designed for recognizing patterns in data sequences. LSTM help preserves the error that can be over time and

[2]https://towardsdatascience.com/6-different-ways-to-compensate-for-missing-values-data-imputation-with-examples-6022d9ca0779

[3]https://towardsdatascience.com/feature-extraction-techniques-d619b56e31be

layers propagated backward. By keeping a more constant error, they allow recurrent networks to continue learning over many time steps, thus opening a channel to remotely link causes and effects[4]. As shown in the research of Wang et al. (2019) LSTM works well and gives good results.

- **Random Forest**: It is an ensemble method that integrates more than one method of the same or different sort for object classification. RF classifier helps to create a set of DT from randomly chosen training set sub-set. It then gathers the votes from different DT for the final class of the test object to be decided [5]. As shown in the research Mani et al. (2013) RF has a decent performance in 2 different data sets.

- **Decision Tree**: It is a predictive modeling tool with applications covering a variety of fields. In general, DT is constructed through an algorithmic approach that identifies ways of splitting a set of data based on various conditions. It is one of the methods of supervised learning that are most widely used and practice. DT is a non-parametrically supervised method of learning, used for classification and regression tasks. The aim is to create a model that predicts the value of a target variable by learning simple rules of decision inferred from the data characteristics [6]. Amiri et al. (2019) shows DT performs well for sepsis detection.

- **Extreme Gradient Boosting**: It utilises the mentioned techniques with boosting and is wrapped in a library that is easy to use.Some of XGBoost's major advantages are that its highly scalable / parallel, quick to implement and usually outperforms other algorithms [7] also shown is research done by (Wang et al.; 2019), (Singh et al.; 2019).

- **Adaptive Boosting**: Ii is a meta-estimator that starts by fitting the classifier to the original data set and then fits additional copies of the classifier to the same data set but adjusts the weights of the incorrectly classified instances so that subsequent classifiers focus more on difficult cases [8]. Sepsis detection is done with good results as shown by Gómez et al. (2019) in their research.

- **K-Nearest neighbors**: It uses 'feature similarity' to forecast the values of new data points, meaning that the new data point will be allocated a value based on how closely it fits the training points[9]. KNN performs well with text data and was used by Tekin et al. (2019) for the research.

4 Design Specification

As mentioned in Section 3, the research follows a KDD approach for the execution. The local system of processor i7 8th generation with 1TB hard drive, 16 GB RAM, and 8

[4]https://pathmind.com/wiki/lstm

[5]https://medium.com/machine-learning-101/chapter-5-random-forest-classifier-56dc7425c3e1

[6]https://www.hackerearth.com/practice/machine-learning/machine-learning-algorithms/ml-decision-tree/tutorial/

[7]https://www.aitimejournal.com/@jonathan.hirko/intro-to-classification-and-feature-selection-with-xgboost

[8]https://scikit-learn.org/stable/modules/generated/sklearn.ensemble.AdaBoostClassifier.html

[9]https://www.tutorialspoint.com/machine$_l earning_w ith_p ython/machine_l earning_w ith_p ython_k nn_a lgorithm_f inding_n e$c

GB of the graphic card was used to execute the project code. The code ran on python version 3.7.3 on the jupyter notebook. Multiple python packages had to be imported for the execution of the project.

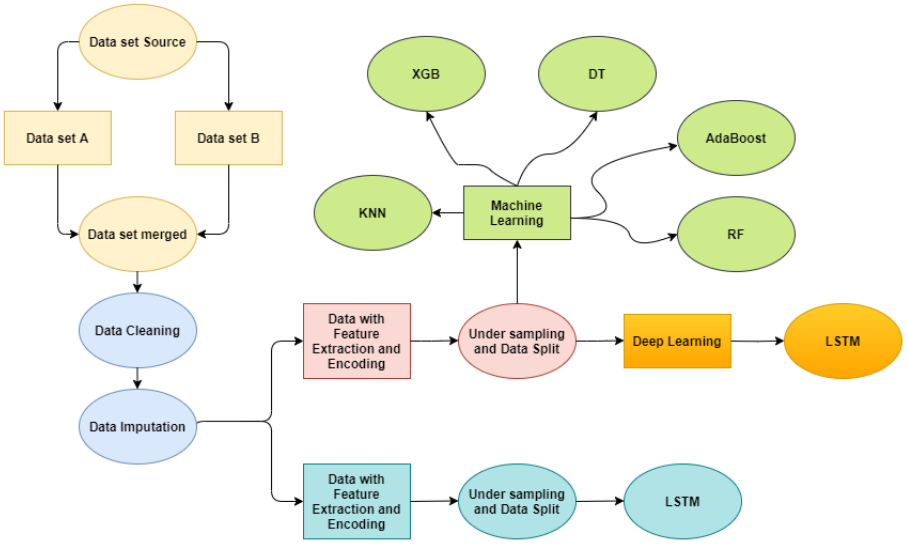

Figure 8: Design Architecture

Figure 8 shows the detailed full process flow and design of the research approach. The downloaded data from the website consists of 2 separate data set viz training set A and training set B. Both the data set are loaded in data frames in python and them combined. An alternate way was to download the 2 data set and combine the 2 data set on the excel folder and use that to load in python. Now the data pre-processing part starts as shown in Section 3.3.

After the pre-processing, there are 2 different scenarios. Scenario 1 is when feature extraction and encoding are applied to the data set as mentioned in section 3.4. Once the imputation was done data under-sampled to compensate for the data imbalance. To overcome the imbalanced data set, under-sampling was applied to get 55,832 rows which involve making the data set of equal sepsis and non-sepsis case. Now the data was divided into the train (75% of data) and test (25%) of the remaining data. LSTM was applied to this data set and had accuracy of which was less than the data set which did no undergo Feature Extraction and Encoding. Hence, it was not considered for other models.

Scenario 2 is when no feature extraction or encoding is applied to the data set. Hence directly undersampling is done. Then data is split into training and test data set. Now multiple models are applied on this data set including LSTM, RF, Adaboost, XGB, KNN, and DT.

5 Implementation

5.1 Deep Learning

- **Long Short-Term Memory**: The data had to be converted from a 2 dimension to a 3 dimension in order to feed it into for LSTM. The input shape was (1,9) for data set with feature extraction and encoding while it was (1,10) for the data set

without feature extraction and encoding. The input shape is by the number of input variables to the output variables.

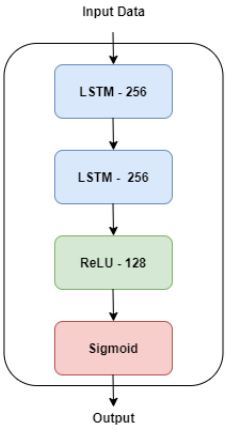

Figure 9: LSTM design

Figure 9 shows the LSTM design used for the research. There is 2 layer of LSTM 256 where 256 is the hidden nodes or the neurons. This is followed by a layer with ReLU and a dense layer with Sigmoid. The loss is checked using mean square error and adam optimiser is used. The batch size is set to 150 and the epoch is kept 50 and 45 for the 2 different training and testing data. The data with feature extraction and encoding gave a test accuracy of 0.9181, F1 score of 0.91, precision of 0.97, and recall value of 0.85 While the data set without feature engineering and encoding gave a test accuracy of 0.97, F1 score of 0.97, precision of 0.98, and recall value of 0.96. For LSTM the last epoch value is considered in the research.

5.2 Machine Learning

- **Random Forest**: The maximum depth which is the number of trees in the forest was set to 15 with n estimators set to 100 while the class weight was set to a balanced subsample. The rest of the parameters were kept to the default value. The accuracy of the model is 0.98, f1 score is 0.98, precision is 0.99 and recall is 0.96.

- **Decision Tree**: It works by splitting the data into binary values until the prediction can be done. The criterion is set to entropy which is for the information gain by measuring the quality of a split. Max depth is set to 5 and the random state is set 0. The accuracy of the model is 0.97, f1 score is 0.97, precision is 0.99 and recall is 0.95.

- **Extreme Gradient Boosting**: XGB parameter min child weight is set to 1,5 and 10 which specifies the minimum amount of the weights required for all observations. Gamma is set to 0.5, 1, 1.5, 2, and 5 which specifies the minimum reduction in losses required to make a split. The subsample is set to 0.6, 0.8, and 1.0 which signifies the fraction of observations per tree to be random samples. Colsample bytree is set to 0.6, 0.8, and 1.0 which signifies the portion of columns to be sampled at random within each tree. Finally, max depth is set to 1,2,3,4 and 5 which can be used to

control over-fitting. The accuracy of the model is 0.98, f1 score is 0.98, precision is 0.99 and recall is 0.96.

- **Adaptive Boosting**: Adaboost assists in combining multiple weak classifiers into a single powerful classifier. It works by placing more weight on instances that are difficult to classify and less on those already handled well. All the parameters are set to default in this model. The accuracy of the model is 0.97, f1 score is 0.97, precision is 0.99 and recall is 0.96.

- **K-Nearest neighbors**: Works on neighbors vote and for the research, all the parameters were set to default values. The accuracy of the model is 0.97, f1 score is 0.97, precision is 0.99 and recall is 0.95.

6 Evaluation

6.1 Evaluation matrix

For this research, four values have been considered of all the models viz Accuracy, F1 score, Precision, and Recall. These 4 values can be derived from a confusion matrix. The confusion matrix provides a matrix as output and explains the model's full performance.

There are 4 important terms in the confusion matrix:

- **True Positive (TP)**: To put it simply, the cases in which model predicted YES and the actual output were also YES.

- **True Negative (TN)**: Is a result of which model predicts the negative class correctly. That is to say, it is the cases where we predicted NO and the actual output was NO.

- **False Positive (FP)**: Is a result where the model wrongly predicts a positive class. In other words, where the model forecast, YES, and the actual output was NO.

- **False Negative (FN)**: Is a result where the negative class is incorrectly predicted by the model. In other words, where the model forecast NO and the actual output was YES.

6.1.1 Accuracy

It is the ratio of the number of predictions that are correct to the total number of input samples. It only works well when the number of samples belonging to each class is equal[10]. The formula is:

$$Accuracy = \frac{\mathrm{TP} + \mathrm{TN}}{\mathrm{TP} + \mathrm{TN} + \mathrm{FP} + \mathrm{FN}} \tag{1}$$

[10]https://towardsdatascience.com/metrics-to-evaluate-your-machine-learning-algorithm-f10ba6e38234

6.1.2 F1 Score

It tells how accurate the classifier is (how many instances it correctly classifies), and how robust it is (a significant number of instances are not missing). The formula is:

$$F1score = 2 \times \frac{1}{\frac{1}{\text{Precision}} + \frac{1}{\text{Recall}}} \tag{2}$$

6.1.3 Precision

It is the number of correct positive outcomes divided by the number of positive outcomes predicted by the qualifier. Precision attempts to respond to what proportion of positive identifiers was actually correct. The formula is:

$$Precision = \frac{\text{TP}}{\text{TP} + \text{FP}} \tag{3}$$

6.1.4 Recall

That is the number of correct positive results divided by the number of all relevant samples (all samples that were supposed to be positive). Recall tries to answer which proportion of positive actual was correctly identified. The formula is:

$$Recall = \frac{\text{TP}}{\text{TP} + \text{FN}} \tag{4}$$

6.2 Experiment

6.2.1 LSTM on data with and without feature extraction and encoding

The main reason for this experiment is to determine which data is to be selected. As mentioned in section 4 there are 2 scenarios for the data set. This experiment is of scenario 1.

Figure 10 shows that the test accuracy for data with feature engineering and encoding is between 0.90 and 0.92 while the test accuracy of the data without feature engineering lies between 0.96 to 0.98 other than the drop in one occasion to 0.95. Similarly, when compared F1 score, the value of data with feature extraction and encoding lies in between 0.89 and 0.91 to 0.94 and 0.98. When compared to the precision, the value of data with feature extraction and encoding lies in between 0.91 and 0.98 while data without feature extraction and encoding lie between 0.97 and 0.99. The Recall score of data with feature extraction and encoding is between 0.83 to 0.88 whereas recall of data without feature extraction and encoding is between 0.92 and 0.97.

It is clearly seen that data without feature extraction and encoding has better performance for the LSTM model applied. Even the model loss is less when compared. Based on the results only data without feature extraction and encoding are considered further for the experiment where different models are applied. The data feature which was extracted did not perform better and then the further missing values meant again imputation which is not considered good as the data was already imputed earlier.

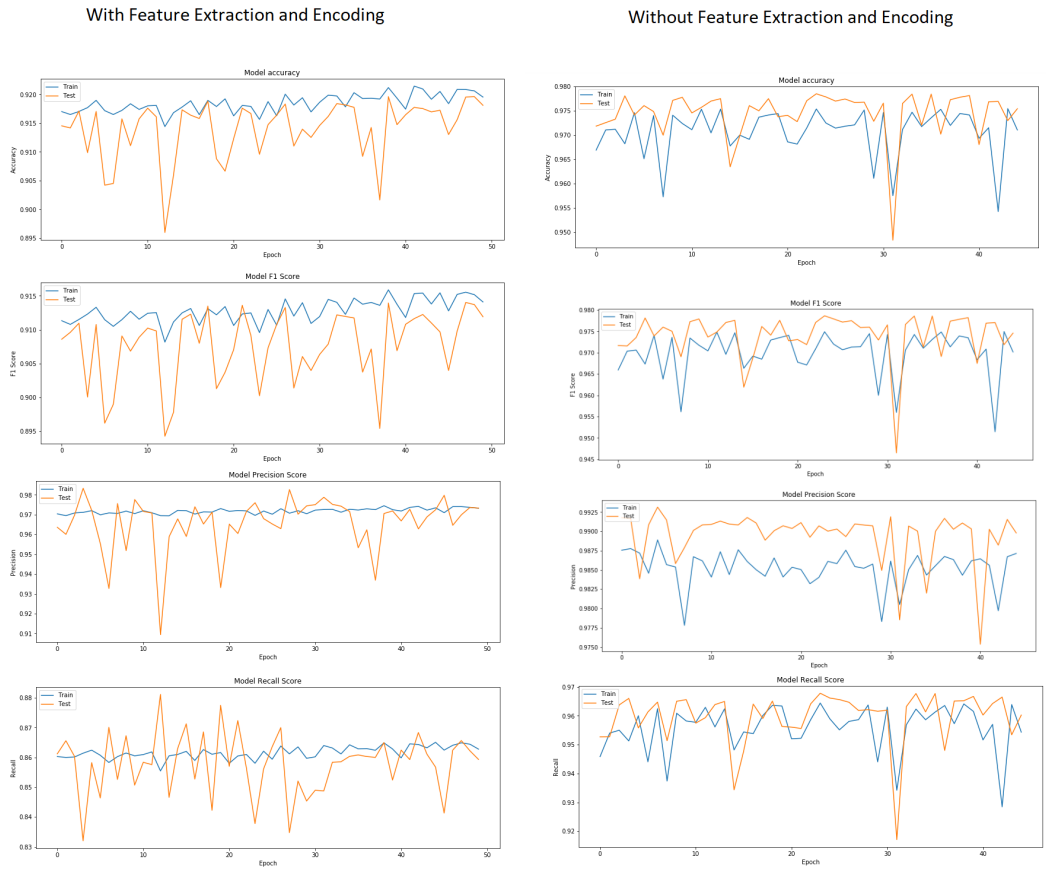

Figure 10: Long Short-Term Memory comparison

6.2.2 Deep Learning and Machine Learning models

In this experiment, DL models and ML models are applied to the data set which is cleaned and imputed. The objective of this experiment is to check the performance of various models. Figure 16 shows the table of the different model's performance using 4 parameters viz Accuracy, F1 score, Precision, and Recall.

Model	LSTM	RF	DT	XGB	AdaBoost	KNN
Accuracy	0.97	0.98	0.97	**0.98**	0.97	0.97
F1 Score	0.97	0.98	0.97	**0.98**	0.97	0.97
Precision	0.98	**0.99**	0.99	**0.99**	0.99	0.99
Recall	0.96	0.96	0.95	**0.96**	0.96	0.95

Table 2: Model comparison

Table 2 shows the complete performance of all the models applied. In terms of accuracy, XGB has the best with 0.98 followed by RF of 0.98. In terms of F1 score, again XGB has the best performance of 0.98 followed by RF with 0.98. XGB and RF perform the best in precision with 0.99 and for Recall XGB outperforms other models with 0.96 followed by RF with 0.96.

The SOA had its performance evaluated in terms of sensitivity, specificity, and PPV. Sensitivity is also called Recall and PPV is called precision. Since for the research, both Recall and Precision were calculated, will use those parameters to compare the research model against the SOA model.

	SOA - NN	Research - XGB
Precision	0.91	**0.99**
Recall	0.92	**0.96**

Table 3: SOA model vs Research model

From table 3 it can be seen that the best model of the research which is XGB outperformed the best model of the SOA model which was a NN model in both Precision and Recall.

7 Conclusion and Future Work

Predicting sepsis accurately was one of the objectives of the research and the experiment shows how multiple models do indeed help in predicting sepsis from the data. As discussed in section 6 XGB and RF are the two models that were the best of all the models applied with the accuracy of 0.98 and 0.98 respectively. Similarly, if we consider F1 score, Precision and Recall as well as XGB and RF outperform all the other models. The second objective of the research is to what extent the patient's medical record could be used to enhance the model. From this research, it can be seen that of the 40 variables that were measured for every patient only 10 were used. This was because the rest of the data had a lot of missing values. But of the 10 variables which had data with little imputation, the prediction could be made which is better than the paper reviewed.

However, considering that the research is done on medical records and even 0.98 - 0.99 accuracy may seem good when applied to large people the 0.01 or 0.02 where the model fails is significant and future work involves using a better model or combination of the model to check if the performance improves. The accuracy may improve if the data set did not have a high percentage of missing values and provided could use the other variables which were dropped. Then using variable importance or feature selection the best variables can be selected to improve the existing model or the new model.

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