



Sepsis Detection using Patient Clinical Data with Multi-Layer Perceptron- A Review

Rakesh Kumar Yadav, Research Scholar, School of Computer Science and Engineering, Sandip University, Sijoul, Madhubani (Bihar)
Shambhu Kumar Singh, Research Supervisor, School of Computer Science and Engineering, Sandip University, Sijoul, Madhubani (Bihar)

Introduction:

Sepsis is a real-life threat for humanity as it is one of the serious problems among the medical field. It is a lifethreatening condition and increases with the severity without detection. As per WHO, it kills more than 6 million people a year. The report says that every year 3 million newborns and 1.2 million children suffer from sepsis globally. Due to the resistant pathogens, death rate for neonatal sepsis is estimated as three out of every ten deaths. Maternal sepsis cause deaths associated with pregnancy and childbirth. More than 95% of deaths happen in low and middle income countries due to maternal sepsis. Maternal sepsis causes one million newborn deaths in every year [1].

Early detection of sepsis can be treated using antibiotics and completely curable and save millions of people. In this scenario the early detection or prediction of sepsis using Machine Learning is a hot area for research. Clinical values or criteria are essential for achieving this type of research. Real values are more important to diagnose Sepsis but it is very difficult to get. Normally Systemic Inflammatory Response Syndrome (SIRS) criteria are used to predict or diagnose sepsis. Another criterion is qSOFA (quick Sequential Organ Failure Assessment) [2].

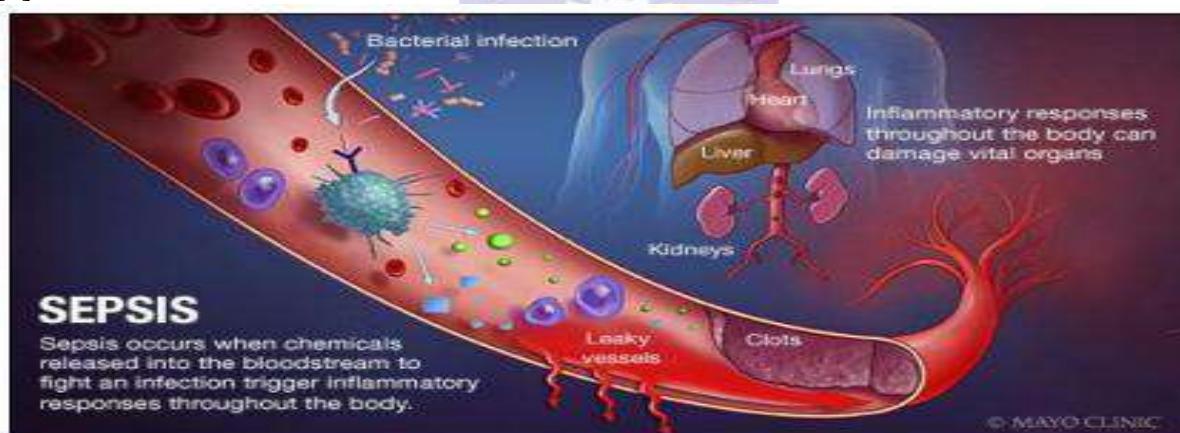


Figure 1: Images of Sepsis Condition.

Sepsis is a hazardous condition that happens when the body's reaction to contamination causes tissue harm, organ failure, or even demise of the person. Generally, the body releases natural synthetics into the circulation system in order to counterbalance the infection which is inside. Sepsis occurs when the body's response to these chemicals is out of balance; this can damage many organ systems. Sepsis is caused by infection and can happen to anyone. It is most common & dangerous for senior citizens, pregnant ladies, kids below one-year-old, persons suffering from chronic conditions, such as diabetes, kidney disease, lung disease, or even cancer, as they have

weak immune systems. This disease is a major health concern for the public in terms of morbidity, health care expenses and mortality. Detecting at early stages, with antibiotic treatment the outcomes can be improved. Though many professional care societies have proposed new methods in recognizing sepsis, the central requirement for early identification and treatment remains neglected. It can be treated if it can be recognized at early stages. Several examinations have demonstrated that delays in finding and treatment of sepsis can prompt high death rates. Our main aim is to detect sepsis as soon as the patient visits the



emergency department for the treatment.

Motivation:

Sepsis is an infection- chronic inflammatory disorder, typically results from the spread of a localized nidus to the systemic circulation, and both with very high deaths and morbidity levels correlated. It is one of the most critical factors of in-hospital deaths. However, a credible way to predict septic origins remains elusive. Early and reliable projections of sepsis will enable further agitation and tailored treatment while antimicrobial stewardship is preserved. Established detection approaches are badly implemented and need laboratory test tests, sometimes overtime. Recently, automated testing has proved to save lives. Tackling and researching enormous physiological observations continuously seen in ICU patients should immediately boost early position estimates, monitoring and essential disease treatment.

Under these conditions, beneficial local inflammatory processes, intervened by specific white platelets, for example, neutrophils and monocytes and the components they produce, and which are ordinarily present to control the spread of the irresistible centre, may grow their circles of movement into perilous fundamental irritation. The course by which a patient advances either to death or medical clinic release is notable and has been portrayed as a continuum from a state named foundational incendiary reaction disorder (SIRS) to progressive conditions of sepsis, serious sepsis, septic stun, numerous endorgan disappointment (MODS) and demise.

The goal of performing this dissertation was to the development of an algorithm for early prediction of Sepsis using routinely available clinical data. Early prediction particularly is potentially a lifesaving, while late or missed predictions are potentially life-threatening, and false algorithms might consume hospital resources and erode trust on the algorithm itself. The dataset seems a bit complicated, and hence we will first handle missingness and imbalance in the set as well try to come up with newer features before implementing the algorithm.

The algorithm will be designed at various levels and incorporating the clinical data, automatically identifying a patient's risk of conceiving Sepsis and also make a positive or negative prediction of at least by six hours and no more than twelve hours before the onset time of Sepsis. To evaluate the algorithm, we have for the time being selected to plot the precision- recall curve with an F1 score that can assess the algorithm and penalize them for wrongly classified data points.

Literature Review:

In 2012, a work is published by E.Gultepe et al. [3] about clustering technique used for extracting features of sepsis. They have done experiments using extracted features with and without lactate levels and evolved a relationship between this using Bayesian networks. They excluded an important parameter - heart rate - from their experiment. Respiratory Rate(RR), White Blood Cells (WBC), temperature, Mean Arterial Pressure (MAP), lactate, length of hospital stay in days (LOS) and sepsis occurrences (SO) are the features used for this study. Among 1492 patient's Electronic medical records, 233 cases of sepsis were used to construct Bayesian network. First network is constructed as BN1 having temperature, RR, WBC, lactate, LOS, SO as parameters and BN2 is the second network with addition of MAP test to the above parameters. Because of the lowest loss function value, BGE scoring criterion was chosen for the learning method of first network BN1. BN2 is learned using BIC and BGE. Having a lower loss function value BIC is used for the final network. BN1 had lower estimated goodness of fit compared with BN2. The relationship between lactate levels and sepsis were obtained for the sepsis patients using Bayesian network. It was shown that lactate levels may be predictive of the SIRS criteria.



Y.Jiang et al. proposed a graphical computational model used for the pathological presentation of the sepsis in their paper 2016 called AdapDBN [4]. This computational model captures risk factors of sepsis using dynamic Bayesian network using some screening mechanisms. Physician's knowledge, published clinical research, epidemiological status and patient's data are the input measures used for the construction of AdapDBN. Three conditions were considered for the confirmation of sepsis as initial sepsis, severe sepsis and septic shock. An automaton is constructed with a threshold of onset probability detection and mortality rate monitoring. Each state DBN is attached with the dependency relation with vital signs. When threshold crosses, sepsis is confirmed. Later one is used for AdapDBN model and for screening the system. This helped in shortening the time for syndrome detection and helped to improve the effectiveness of the treatment.

In the work presented by C. Morales et al. [5] in 2016, one of the biggest available multi-centre sepsis database MEDAN is analysed using Conditional Independence Maps method. They explored potential causal relationships between the measured variables and the survival outcome. Then they validated the changes in the new definition of sepsis. Three different subsets are created from the pre-processing steps such as (i) the situation of patients at the time of admission, (ii) 24h later and (iii) 48h later. The authors mainly used the physiological parameters and personal information about the patients' profile. The Causal Independence Maps created by Causal Explorer is used for the experiments with the outcome variable and without the outcome variable. For the experimental setup three different scenarios were used as the time of admission at ICU, 24th and 48th hour after the admission in ICU. Three sets of results were collected using Causal Independence Maps. Authors proved that the peak time of the development of sepsis for the patient's situation is around 24 hours after being admitted at the ICU. The challenges addressed by this research were the remote collection and analysis of outpatient biometrics using commercially available technology. Considering this T.Bui et al. [6] presented a remote monitoring solution for early detection of sepsis for outpatients and published in 2016. In the proposed system, an additional sensor was attached for validating the device. This reduced readmissions in hospitals, mortality rates and improved the quality of outpatient care. Algorithm developed by the authors marked severe changes in the sepsis risk indicators including heart rate, respiratory rate, temperature, blood pressure and suspected infection. A daily report is generated and sent to the patient care coordinator who makes a better decision about the patient and gives the best response.

Diagnosis of sepsis was done using machine learning techniques. A new learning strategy called chaotic fruit fly optimization was proposed by X.Wang et al. [7] and published their paper in 2018 to increase the performance of kernel extreme learning machine (KELM). The chaotic population initialization and chaotic local search strategy were used as the new mechanisms to improve the performance. Random forest improved fruit fly optimization algorithm-kernel extreme learning machine (RF-CFOA-KELM), was introduced to diagnose sepsis effectively. Methods used for this can be divided into two separate sections such as feature selection and parameter optimization tasks. Using random forest, features are selected and using the parameters of KELM, optimization can be done through 5 fold cross validation by CFOA.

Gas chromatography mass spectrometry (GC-MS) was used for analysing human blood sample data from the hospital. Using sepsis patient's metabolic data, authors achieved a predictive accuracy of 81.6% [7] with the proposed method. For diagnosing sepsis they used SVM, BPN, ANN and nature-inspired algorithm based KELM model for comparison. The proposed RF-CFOA-KELM can achieve more competitive results than other counterparts.



The proposed RF- CFOA-KELM is new method consists of two stages as feature selection and parameter optimization. Feature selection is done by Random Forest and optimization of KELM parameters were done by proposed CFOA with five fold cross validation. Result of these two steps was the optimal feature subset and the parameters. The proposed method is used for the evaluation of classification performance. Ten-fold cross validation is done in the outer loop with inputs as optimal Bayesian network. It was shown that lactate levels may be predictive of the SIRS criteria.

Problem Statement:

The research for efficient and accurate method of early prediction of Sepsis is important to save lives. The goal of this research is to the development of an efficient and accurate algorithm for early prediction of Sepsis using routinely available clinical data with enhanced machine learning approach. Early prediction particularly is potentially a lifesaving, while late or missed predictions are potentially life-threatening, and false algorithms might consume hospital resources and erode trust on the algorithm itself. Moreover, improving limitations in existing approaches. [WIKIPEDIA](https://en.wikipedia.org/wiki/Early_sepsis_diagnosis) The Free Encyclopedia

Research Methodology:

The general architecture of the proposed model is shown below:

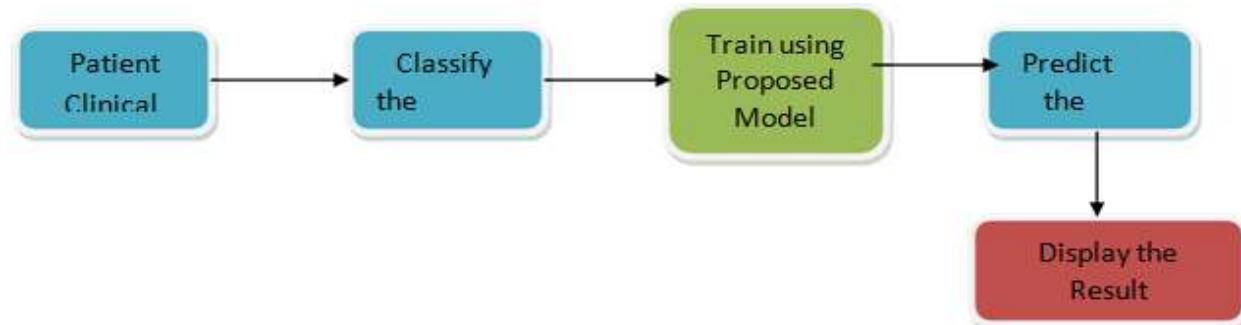


Figure 3.1: General architecture of Proposed Model.

The Detailed Architecture of proposed work is shown below:

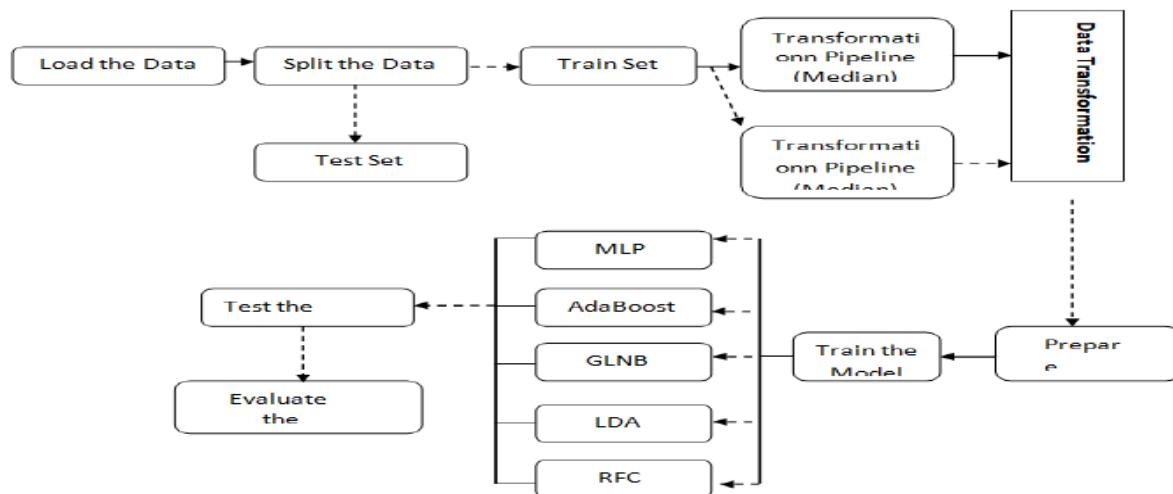


Figure 3.1: Proposed Model Architecture.

The selection of the model is a crucial factor, as we use machine learning algorithms to forecast the best outcomes. The supervised approach is used as a preparation for a collection



of input and output couples and to test the input and output association pattern. Supervised learning problems are grouped in two issues:

1. Regression analysis: Actual and Constant values in the target or output variable.
2. Classification: Problems not needed for filtering results.

We have a dataset of 40 Dependent variables (parameters or features) and an indie variable is the aim or performance variable, which determines whether or not patients become sepsis. Various classification algorithms are used in this dissertation which is described as follows:

MLP Classifier: It is also known as Multi-layer Perceptron classifier which itself suggests a Neural Network. MLPClassifier relies on an elemental Neural Network to perform the classification task. It comes under ANN. The phrase MLP is used ineptly, sometimes roughly to refer any feedforward ANN, occasionally strictly referring to networks consisting multiple layers of perceptrons (with threshold activation) Multilayer perceptrons now and then are vernacularly referred as "vanilla" neural networks, notably if they contain a single hidden layer, avoiding long time-taking lab [WIKIPEDIA](https://en.wikipedia.org/wiki/Multilayer_perceptron). It is very flexible and can be used generally to learn a mapping from inputs to outputs The Free Encyclopedia

The model that is being built using MLP Classifier, the data which is obtained after preprocessing is given to the model and the pre-processed data is divided such that eighty percent for training the model and twenty percent used for testing the trained model. With this MLP classifier we could achieve an accuracy of 94%, with a total of six layers in which one is input layer, four layers are considered as hidden layer and finally the last layer is the output layer, tanh as activation function and, max_iterations up to 5000.

Ada-boost or Adaptive Boosting: It associates multiple classifiers in order to increase the veracity of classifiers and is an iterative ensemble method. This classifier frames a robust classifier by associating multiple below par performing classifiers so that we get a high veracity robust classifier.

Guassian Naive Bayes: It is an uncomplicated procedure for building classifiers: models that designate class labels to problem instances, expressed as vectors of factor values, where these class labels are taken from some finite set. There isn't a sole algorithm for instructing such classifiers, but a tribe of algorithms based on a typical principle: all naive Bayes classifiers infer that a particular feature's value is sovereign of any other feature's value, given the class variable. **Linear Discriminant Analysis (LDA):** It is a technique of dimensionality reduction. As the name entails this technique reduces the total number of dimensions (i.e. variables) in a dataset while confining as much knowledge as possible.

Dataset Used: Data set is garnered from patients in ICU from separate hospitals. Each patient's clinical data contained likely 40 measurements of vital sign, laboratory, and demographics data. Each file has data separated with pipes in which each row represents a 1 hours' worth of data.

Extremely Imbalance data: The records are extremely imbalanced.

Missing Data: In the data set the percentage of data which is missing high (Shown in Fig 3). This is handled by ignoring the features with more than 80% of missing data.

Features Used: Respiratory rate, Temperature, Mean arterial Pressure etc. are Vital Signs. Platelet Count, Glucose, Calcium etc. are Laboratory Values. Age, Gender, Time in ICU, Hospital Admit time etc. are considered as Demographics.

The model that will be being built using proposed MLP Classifier, the data which is obtained after preprocessing is given to the model and the pre-processed data is divided such that eighty percent for training the model and twenty percent used for testing the trained model. With this MLP classifier we could achieve better accuracy, with a total of six layers in which one is input layer, four layers are considered as hidden layer and finally the last layer is the



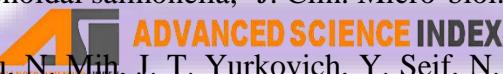
output layer.

Conclusion:

Sepsis is an infection- chronic inflammatory disorder, typically results from the spread of a localized nidus to the systemic circulation, and both with very high deaths and morbidity levels correlated. It is one of the most critical factors of in-hospital deaths. However, a credible way to predict septic origins remains elusive. Early and reliable projections of sepsis will enable further agitation and tailored treatment while antimicrobial stewardship is preserved. Established detection approaches are badly implemented and need laboratory test tests, sometimes overtime. Recently, automated testing has proved to save lives. Tackling and researching enormous physiological observations continuously seen in ICU patients should immediately boost early position estimates, monitoring and essential disease treatment.

References:

- [1] <https://www.who.int/news-room/WIKI-sheets/detail/Sepsis>.
- [2] Marik PE, Taeb AM. SIRS, "qSOFA and new sepsis definition", Journal of thoracic disease. 2017 Apr; 9(4):943.
- [3] E. Gultepe, H. Nguyen, T. Albertson, I. Tagkopoulos, "A Bayesian network for early diagnosis of sepsis patients: a basis for a clinical decision support system," 2nd international conference on Computational advances in bio and medical sciences (ICCABS), 2012, pp. 1-5.
- [4] Jiang Y, Tan P, Song H, Wan B, Hosseini M, Sha L, "A self-adaptively evolutionary screening approach for sepsis patient", 29th International Symposium on Computer-Based Medical Systems (CBMS) 2016 Jun 20, IEEE, (pp. 60-65).
- [5] Morales C, Ribas V, Vellido A, "Applying conditional independence maps to improve sepsis prognosis 16th International Conference on Data Mining Workshops (ICDMW) 2016 Dec 12, IEEE (pp. 254-260).
- [6] Bui, T., Grayson, M., Hofer, K., McGuire, K., Morrow, M., Rodammer, N., Farooque, A., Barnes, L.E. and Patek, S., "Remote patient monitoring for improving outpatient care of patients at risk for sepsis". Systems and Information Engineering Design Symposium (SIEDS), 2016, IEEE, (pp.136-141).
- [7] Wang X., Wang Z., Weng J., Wen C., Chen H, Wang X., "A new effective machine learning framework for Sepsis diagnosis", 2018, IEEE Access, 6, pp.48300-48310.
- [8] M. Nguyen, "Using machine learning to predict antimicrobial MICs and associated genomic features for nontyphoidal salmonella," J. Clin. Micro-biol., vol. 67, no. 2, 2019, Art. no. e01260.
- [9] E. S. Kavvas, E. Catoiu, N. Mih, J. T. Yurkovich, Y. Seif, N. Dillon, D. Heckmann, A. Anand, L. Yang, V. Nizet, J. M. Monk, and B. O. Palsson, "Machine learning and structural analysis of mycobacterium tuberculosis pan-genome identifies genetic signatures of antibiotic resistance," Nature Commun., vol. 9, no. 1, p. 4306, Dec. 2018.
- [10] M. W. Pesesky, T. Hussain, M. Wallace, S. Patel, S. Andleeb, C.-A.-D. Burnham, and G. Dantas, "Evaluation of machine learning and rules-based approaches for predicting antimicrobial resistance profiles in gram-negative bacilli from whole genome sequence data," FrontiersMicrobiol., vol. 7, p. 5, Nov. 2016.
- [11] M. Marschal, "Evaluation of the accelerate phenol system for fast identification and antimicrobial susceptibility testing from positive blood cultures in bloodstream infections caused by gram-negative pathogens," J. Clin. Microbiol, vol. 55, no. 7, p. 2116, 2017.
- [12] H. Yu, W. Jing, R. Iriya, Y. Yang, K. Syal, M. Mo, T. E. Grys, S. E. Haydel, S. Wang, and N. Tao, "Phenotypic antimicrobial susceptibility testing with deep learning video





microscopy," Anal. Chem., vol. 90, no. 10, pp. 6314_6322, May 2018.

[13] C.-S. Ho, N. Jean, C. A. Hogan, L. Blackmon, S. S. Jeffrey, M. Holodniy, N. Banaei, A.

[14] A. E. Saleh, S. Ermon, and J. Dionne, "Rapid identification of pathogenic bacteria using Raman spectroscopy and deep learning" ,Nature Commun., vol. 10, no. 1, p. 4927, Dec. 2019.

[15] Anuraag Shankar, MufaddalDiwan, Snigdha Singh, "Early Prediction of Sepsis using Machine Learning", 2021 11th International Conference on Cloud Computing, Data Science & Engineering (Confluence), | 978-1-6654-1451-7/20/\$31.00 ©2021 IEEE | DOI: 10.1109/Confluence51648.2021.9377090.

[16] A. Shankar, M. Diwan, S. Singh, H. Nahrpurawala and T. Bhowmick, "Early Prediction of Sepsis using Machine Learning," 2021 11th International Conference on Cloud Computing, Data Science & Engineering (Confluence), 2021, pp. 837-842, doi: 10.1109/Confluence51648.2021.9377090.

[17] G. Tsang and X. Xie, "Deep Learning-Based Sepsis Intervention: The Modelling and Prediction of Severe Sepsis Onset," 2020 25th International Conference on Pattern Recognition (ICPR), 2021, pp. 8671-8678, doi: 10.1109/ICPR48806.2021.9412058.

[18] Simon Meyer Lauritsen, MadsEllersgaardKalør, Emil Lund Kongsgaard, Katrine Meyer Lauritsen, Marianne Johansson Jørgensen, Jeppe Lange, Bo Thiesson, "Early detection of sepsis utilizing deep learning on electronic health record event sequences", Artificial Intelligence in Medicine, Volume 104, 2020, 101820, ISSN 0933-3657, <https://doi.org/10.1016/j.artmed.2020.101820>.

[19] Herry L. Kausch, J. Randall Moorman, Douglas E. Lake, Jessica Keim-Malpass, Physiological machine learning models for prediction of sepsis in hospitalized adults: An integrative review, Intensive and Critical Care Nursing, Volume 65, 2021, 103035, ISSN 0964- 3397, <https://doi.org/10.1016/j.iccn.2021.103035>.

[20] M. Chen, A. Hernández, Towards an Explainable Model for Sepsis Detection Based on Sensitivity Analysis, IRBM, Volume 43, Issue 1, 2022, Pages 75-86, ISSN 1959-0318,

SHRADHA EDUCATIONAL ACADEMY

