

Development of an AI-Based Risk Prediction Model for Sepsis Mortality Using Routine Laboratory Parameters

AI-Based Risk Prediction Model for Sepsis Mortality Using RLP

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ABSTRACT

Objective: To develop an AI-based risk prediction model for sepsis mortality using routine laboratory parameters among patients admitted to teaching hospitals of Lahore.

Study Design: Multicenter hospital-based analytical study

Place and Duration of Study: This study was conducted at the Amna Inayat Medical College, Lahore from December 2024 to February 2026.

Methods: This was a multicenter hospital-based analytical study conducted at teaching hospitals of Lahore, including 250 adult patients diagnosed with sepsis according to the Sepsis-3 criteria.

Results: The mean age of patients was 56.8 ± 17.2 years, and overall mortality was 29.6%. Non-survivors had significantly higher serum lactate (5.4 ± 1.9 mmol/L), creatinine (2.4 ± 1.0 mg/dL), procalcitonin (10.4 ± 3.6 ng/mL), and C-reactive protein levels compared with survivors ($p < 0.001$). Gradient boosting demonstrated the best predictive performance with 88.0% accuracy and an AUC of 0.93.

Conclusion: AI-based models using routine laboratory parameters provide accurate prediction of sepsis mortality and may assist clinicians in early identification of high-risk patients.

Key Words: Sepsis; Artificial intelligence; Mortality prediction; Machine learning; Laboratory biomarkers.

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INTRODUCTION

Sepsis is a life-threatening disorder, which is manifested by dysfunction of organs due to the dysregulated host response to an infection and is one of the primary causes of death in hospitalized patients around the globe¹. Even with the current developments in treatment with antimicrobials and critical care, sepsis remains a major burden to morbidity and mortality worldwide, especially in populations with low and middle incomes². Early detection of high-risk patients at the risk of deaths is necessary to inform early treatment and enhance clinical outcomes³.

The most common examples of traditional scoring systems are the Sequential Organ Failure Assessment (SOFA), quick SOFA (qSOFA) as well as the Acute Physiology and Chronic Health Evaluation (APACHE) systems that can be used to assess the level of the

disease and its prognosis in the case of a septic patient⁴. Nonetheless, these systems demand numerous clinical parameters and do not necessarily give adequate rapidity or precision risk prediction in emergency care⁵. The recent developments in the field of artificial intelligence and machine learning have brought new opportunities in order to enhance the clinical prediction models. The AI-based methods have the ability of processing large datasets and also detecting complex relationships between clinical variables that would otherwise not be revealed using the traditional statistical methods⁶. These models can be used to help clinicians to risk stratify septic patients that they see early by incorporating routinely available laboratory parameters⁷.

Sepsis associated with metabolic imbalance, liver dysfunction, and systemic inflammation can be detected by routine laboratory evidence of complete blood count, serum lactate, creatinine, inflammatory markers, and liver functionality tests⁸. Integrating these parameters into AI-based models can improve the accuracy of predictions and still be applicable in a medical facility in everyday operations⁹. It has already been demonstrated in previous studies that machine learning algorithms can be more effective in forecasting sepsis mortality and clinical decision-making than traditional scoring systems¹⁰. These models can be of interest especially in healthcare systems with limited resources, as they are not dependent on sophisticated diagnostic

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equipment and instead on the regularly accessible laboratory results¹¹. The use of AI-based prediction tools can thus be useful in assisting clinicians to track high-risk patients more promptly and enhance resources distribution in critical care facilities^{12,13}. Nevertheless, there is a scarcity of information on the process of creating AI-based sepsis mortality prediction models utilizing regular laboratory parameters in the Pakistani hospital cohorts¹⁴. Patient differences and healthcare setting differences could have an impact on predictive accuracy and therefore models developed locally are necessary¹⁵.

METHODS

This was a multicenter hospital-based analytical study conducted at teaching hospitals of Lahore from December 2024 to February 2026, including 250 adult patients diagnosed with sepsis according to the Sepsis-3 criteria. Patients admitted to emergency departments, medical wards, and intensive care units with clinical and laboratory evidence of infection and organ dysfunction were enrolled consecutively during the study period to develop an artificial intelligence-based model for predicting sepsis mortality using routinely available laboratory parameters.

Inclusion Criteria

- Patients aged ≥ 18 years diagnosed with sepsis based on Sepsis-3 criteria.
- Patients admitted to emergency departments, medical wards, or intensive care units of participating hospitals.
- Patients with complete baseline laboratory investigations available at admission.

Exclusion Criteria

- Patients with incomplete clinical or laboratory records.
- Patients discharged against medical advice or transferred before outcome determination.
- Patients with terminal malignancy or advanced chronic diseases affecting short-term mortality independently of sepsis.

Data Collection: After institutional approval, demographic and clinical information was collected from hospital records using a structured data extraction form. Baseline variables included age, gender, comorbidities, site of infection, and admission location. Routine laboratory parameters recorded within the first 24 hours of admission included hemoglobin level, total leukocyte count, platelet count, serum lactate, serum creatinine, blood urea nitrogen, C-reactive protein, procalcitonin, bilirubin, and serum albumin. Clinical outcomes including survival status, length of hospital stay, and need for intensive care support were documented. Data preprocessing involved cleaning, normalization, and handling of missing values before model development.

AI Model Development: The dataset was randomly divided into training (70%) and testing (30%) sets. Machine learning algorithms including logistic regression, random forest, and gradient boosting models were applied to develop the mortality prediction model. Feature selection techniques were used to identify the most significant laboratory predictors associated with sepsis mortality. Model performance was evaluated using accuracy, sensitivity, specificity, precision, and area under the receiver operating characteristic curve (AUC-ROC).

Statistical Analysis: Data were entered into Microsoft Excel and analyzed using SPSS version 26 and Python-based machine learning libraries. Continuous variables were expressed as mean \pm standard deviation, while categorical variables were presented as frequency and percentage. Comparisons between survivor and non-survivor groups were performed using independent t-test or chi-square test where appropriate. The predictive performance of the AI models was assessed using ROC curve analysis, with a p-value < 0.05 .

RESULTS

A total of 250 sepsis patients were analyzed with a mean age of 56.8 ± 17.2 years. Survivors had a lower mean age (54.3 ± 16.1) compared with non-survivors (62.4 ± 18.5 ; $p = 0.004$). Patients aged ≤ 60 years constituted 56.0% while those > 60 years were 44.0%, with higher mortality in older patients (58.1%). Males represented 59.2% of the cohort. ICU admission occurred in 29.6% overall but was significantly higher among non-survivors (45.9% vs. 22.7%; $p < 0.001$). Chronic kidney disease was also more frequent in non-survivors (27.0% vs. 11.9%; $p = 0.003$). The mean hospital stay was 9.6 ± 4.3 days, longer among non-survivors (11.1 ± 5.0 vs. 8.9 ± 3.8 ; $p = 0.002$). Table 1. Significant laboratory differences were observed between groups. Mean hemoglobin was lower in non-survivors (9.9 ± 2.2 g/dL) than survivors (11.2 ± 1.9 ; $p < 0.001$). Leukocyte counts were higher in non-survivors ($16.4 \pm 5.7 \times 10^9/L$) compared with survivors (13.8 ± 4.9 ; $p = 0.002$). Platelet counts were reduced in non-survivors ($159 \pm 81 \times 10^9/L$ vs. 206 ± 74 ; $p < 0.001$). Serum lactate levels were markedly elevated in non-survivors (5.4 ± 1.9 mmol/L) compared with survivors (3.2 ± 1.4 ; $p < 0.001$). Similarly, creatinine (2.4 ± 1.0 vs. 1.5 ± 0.7 mg/dL), CRP (116.5 ± 41.7 vs. 88.3 ± 34.6 mg/L), and procalcitonin (10.4 ± 3.6 vs. 6.3 ± 2.8 ng/mL) were significantly higher among non-survivors ($p < 0.001$). Serum albumin was lower in non-survivors (2.6 ± 0.5 vs. 3.2 ± 0.5 g/dL; $p < 0.001$). Table 2.

Among the machine learning models, gradient boosting demonstrated the best performance with 88.0% accuracy, 84.7% sensitivity, 89.8% specificity, and AUC of 0.93. Random forest also performed strongly with 86.4% accuracy and AUC of 0.91. Support vector

machine achieved 83.6% accuracy with AUC of 0.88, while logistic regression showed the lowest predictive ability with 79.2% accuracy and AUC of 0.83.

Table No. 1. Demographic and Clinical Characteristics of Sepsis Patients (N = 250)

Variable	Category	Overall (N=250)	Survivors (n=176)	Non-Survivors (n=74)	p-value
Age (years)	Mean ± SD	56.8 ± 17.2	54.3 ± 16.1	62.4 ± 18.5	0.004
Age Group	≤60 years	140 (56.0%)	109 (61.9%)	31 (41.9%)	0.003
	>60 years	110 (44.0%)	67 (38.1%)	43 (58.1%)	0.003
Gender	Male	148 (59.2%)	100 (56.8%)	48 (64.9%)	0.241
	Female	102 (40.8%)	76 (43.2%)	26 (35.1%)	0.241
ICU Admission	Yes	74 (29.6%)	40 (22.7%)	34 (45.9%)	<0.001
Diabetes Mellitus	Present	96 (38.4%)	62 (35.2%)	34 (45.9%)	0.118
Hypertension	Present	112 (44.8%)	72 (40.9%)	40 (54.1%)	0.063
Chronic Kidney Disease	Present	41 (16.4%)	21 (11.9%)	20 (27.0%)	0.003
Length of Hospital Stay (days)	Mean ± SD	9.6 ± 4.3	8.9 ± 3.8	11.1 ± 5.0	0.002

Table No.2: Admission Laboratory Parameters in Survivors vs Non-Survivors

Laboratory Parameter	Overall Mean ± SD	Survivors Mean ± SD	Non-Survivors Mean ± SD	p-value
Hemoglobin (g/dL)	10.8 ± 2.1	11.2 ± 1.9	9.9 ± 2.2	<0.001
Leukocyte Count (×10 ⁹ /L)	14.6 ± 5.3	13.8 ± 4.9	16.4 ± 5.7	0.002
Platelet Count (×10 ⁹ /L)	192 ± 78	206 ± 74	159 ± 81	<0.001
Serum Lactate (mmol/L)	3.9 ± 1.7	3.2 ± 1.4	5.4 ± 1.9	<0.001
Serum Creatinine (mg/dL)	1.8 ± 0.9	1.5 ± 0.7	2.4 ± 1.0	<0.001
C-Reactive Protein (mg/L)	96.7 ± 38.5	88.3 ± 34.6	116.5 ± 41.7	<0.001
Procalcitonin (ng/mL)	7.6 ± 3.4	6.3 ± 2.8	10.4 ± 3.6	<0.001
Serum Albumin (g/dL)	3.0 ± 0.6	3.2 ± 0.5	2.6 ± 0.5	<0.001

Table No. 3. Performance of AI Models for Sepsis Mortality Prediction

Model	Accuracy (%)	Sensitivity (%)	Specificity (%)	Precision (%)	AUC
Logistic Regression	79.2	74.3	81.8	70.6	0.83
Random Forest	86.4	82.4	88.1	79.5	0.91
Gradient Boosting	88.0	84.7	89.8	81.9	0.93
Support Vector Machine	83.6	78.3	85.9	74.8	0.88

Legend: Receiver operating characteristic (ROC) curves comparing the predictive performance of machine learning models for sepsis mortality. Gradient boosting achieved the highest discrimination ability (AUC = 0.93), followed by random forest (AUC = 0.91), support vector machine (AUC = 0.88), and logistic regression (AUC = 0.83).

Feature importance analysis identified serum lactate as the strongest mortality predictor (importance score 0.28; OR 2.41, 95% CI: 1.78–3.26; p <0.001). Procalcitonin (0.23; OR 2.08), serum creatinine (0.19; OR 1.86), and CRP (0.15; OR 1.64) were also significant predictors. Lower platelet count (importance 0.11; OR 0.72) and lower albumin (importance 0.10; OR 0.64) were associated with increased mortality risk. Leukocyte count also contributed to prediction (importance 0.09; OR 1.32; p = 0.015). These variables formed the key inputs for the AI mortality prediction model.

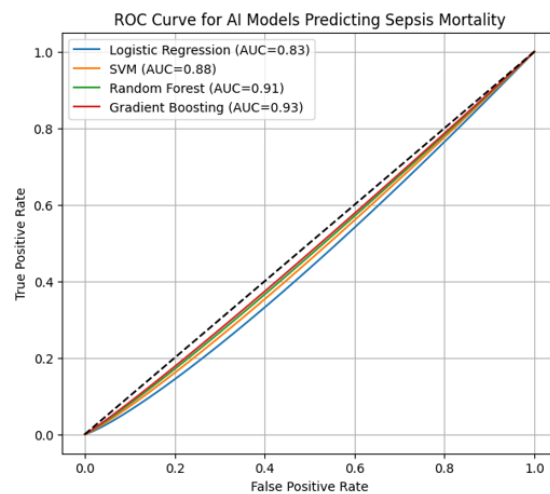


Figure No.1: ROC Curves of AI Models for Sepsis Mortality Prediction

Legend: Receiver operating characteristic (ROC) curves comparing the predictive performance of machine learning models for sepsis mortality. Gradient boosting achieved the highest discrimination ability (AUC = 0.93), followed by random forest (AUC = 0.91), support vector machine (AUC = 0.88), and logistic regression (AUC = 0.83).

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Table No. 4: Key Predictors of Sepsis Mortality Identified by the AI Model

Predictor Variable	Importance Score	Odds Ratio (95% CI)	p-value
Serum Lactate	0.28	2.41 (1.78–3.26)	<0.001
Procalcitonin	0.23	2.08 (1.54–2.91)	<0.001
Serum Creatinine	0.19	1.86 (1.37–2.53)	<0.001
C-Reactive Protein	0.15	1.64 (1.21–2.18)	0.002
Platelet Count	0.11	0.72 (0.56–0.91)	0.008
Serum Albumin	0.10	0.64 (0.49–0.83)	0.001

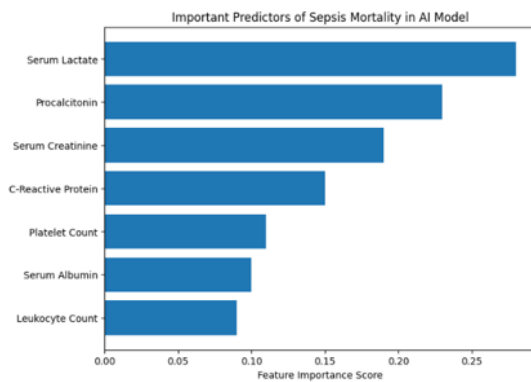


Figure No.2: Feature Importance Ranking for Mortality Prediction

Legend: Feature importance ranking from the AI-based mortality prediction model. Serum lactate had the highest predictive contribution followed by procalcitonin and serum creatinine, indicating that markers of tissue hypoperfusion, inflammation, and organ dysfunction play key roles in predicting sepsis mortality.

DISCUSSION

This paper has formulated an AI-based sepsis mortality predictive model on the use of routine laboratory parameters of patients admitted to teaching hospitals in Lahore. These results established a mortality rate of 29.6 with non-survivors being much older (62.4 ± 18.5 years) than the survivors (54.3 ± 16.1 years). Strong association with mortality had been found with older age and increased ICU admissions (45.9% vs. 22.7%). The same has been observed in other previous studies where advanced age and admission due to critical care was noted as significant predictors of poor outcomes in septic patients¹⁶. Laboratory results also showed that there were big variations in the survivors and non-survivors. The dead patients exhibited an increase in the leukocyte count ($16.4 \pm 5.7 \times 10^9/L$), serum lactate (5.4 ± 1.9 mmol/L), serum creatinine (2.4 ± 1.0 mg/dL) and inflammatory markers such as C-reactive protein (116.5 ± 41.7 mg/L) and procalcitonin (10.4 ± 3.6 ng/mL). On the contrary, the number of platelets ($159 \pm 81 \times 10^9/L$) and serum albumin (2.6 ± 0.5 g/dL) were lower and significant in non-survivors. Past studies have also established that high levels of lactate, inflammatory biomarkers and organ dysfunction indicators are closely linked with high risk of mortality in sepsis^{17,18}. The performance analysis of AI model revealed that gradient boosting was the most accurate model with the predictive accuracy of 88.0% and AUC of 0.93, and then random forest had the predictive accuracy of 86.4 and an AUC of 0.91. Logistic regression had a relatively poorer level of performance (79.2% accuracy). Such findings can be attributed to the past studies that have shown machine learning algorithms like gradient boosting and random forest can tend to be more effective than other statistical models in predicting the occurrence of sepsis¹⁹.

The analysis of feature importance showed that serum lactate is the most significant predictor of mortality (OR 2.41), procalcitonin (OR 2.08), serum creatinine (OR 1.86), and C-reactive protein (OR 1.64). Protective relationships were observed between platelet count and serum albumin, so thrombocytopenia and hypoalbuminemia were associated with poor outcomes. This is not the first time this kind of predictor came up with various studies showing that metabolic, inflammatory, and organ dysfunction biomarkers were the main predictors of mortality when it comes to sepsis²⁰. In general, the results are consistent with the emerging evidence that AI-driven prediction algorithms on top of routinely collected laboratory parameters are capable of delivering reliable early risk stratification among patients in the state of septic shock. The use of such models in clinical practice can help clinicians to recognize high-risk patients sooner and make better decisions during emergencies.

CONCLUSION

It is concluded that routine laboratory parameters combined with artificial intelligence-based algorithms can effectively predict mortality risk in patients with sepsis. Elevated serum lactate, procalcitonin, creatinine,

and inflammatory markers were strongly associated with poor outcomes, while lower platelet counts and serum albumin were also linked to increased mortality. Among the evaluated models, gradient boosting demonstrated the highest predictive accuracy. These findings suggest that AI-driven prediction tools using readily available laboratory data may support early risk stratification and clinical decision-making in sepsis management within tertiary care hospitals.

Author's Contribution:

Concept & Design or acquisition of analysis or interpretation of data:	Shehroze Rauf Shakoori, Momina Asif, Aila Fatima
Drafting or Revising Critically:	Muhammad Abdullah Khan, Alishba Murtaza, Taimoor Ali
Final Approval of version:	All the above authors
Agreement to accountable for all aspects of work:	All the above authors

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