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REAL-TIME INFERENCE OF SEPSIS SEVERITY USING WEARABLE BIOSENSORS, GENOMIC MARKERS, AND EXPLAINABLE ENSEMBLE MACHINE LEARNING MODELS IN ICU PATIENTS

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Abstract

Sepsis is a life-threatening condition characterized by dysregulated immune response and rapid organ dysfunction, demanding early and accurate prediction for effective clinical intervention. This study proposes an explainable ensemble machine learning model that fuses real-time physiological signals from wearable biosensors, genomic expression profiles, and clinical parameters to predict sepsis severity in ICU patients. The model integrates Gradient Boosting, Support Vector Machines, and Deep Neural Networks through soft voting, enabling robust classification across mild, moderate, and severe cases. With a dataset comprising over 500 ICU patients, the ensemble demonstrated superior performance, achieving an F1-score of 0.92 and ROC-AUC of 0.96. SHAP-based interpretability revealed oxygen saturation, respiratory rate, SOFA score, and genomic inflammation markers as the most influential predictors. Nine detailed tables present biosensor-clinical correlations, model confusion matrices, and severity classification summaries, while twelve complex visualizations—including hybrid plots, boxplots, and cluster maps—validate the model's performance and insights. The simulated real-time deployment scenario confirmed the model's adaptability in tracking physiological shifts and updating severity risk scores every 15 minutes. Clinician feedback supported the usability and interpretability of the model outputs. This fusion of multimodal data streams into a transparent, adaptive AI framework marks a significant advancement in sepsis monitoring and offers a scalable solution for personalized, data-driven critical care.

Keywords: Sepsis Prediction, Ensemble Learning, Wearable Biosensors, SHAP Explainability, ICU Monitoring, Genomic Markers

1. INTRODUCTION

Sepsis is a severe health condition in the world that has great death and morbidity rates. It is the result of the unmanaged immune response to the infection targeting the organs that results in their failure (Parente et al., 2021). It results in numerous hospitalisations and spending, and therefore, it is of utmost importance to diagnose it as early as possible and determine the severity of the condition correctly to manage it properly clinically (Yu et al., 2022). Prompt diagnosis and proper treatment are extremely essential due to the significant increase in the level of mortality when there are delays in the therapy. That illustrates what a desperate situation we are in in terms of diagnostic and prognostic methods (Parashar et al., 2021) (Guillou et al., 2021). According to Bedoya et al. (2020), the existing sepsis prediction methods tend to rely on clinical scores or retrospective electronic health records assessment and might fail to indicate the dynamic evolutions that will reflect a worsening of a patient. A combined use of wearable biosensors, which continuously track real-time physiological monitoring and genetic markers, provides a promising solution to these issues with the ability to provide us in real-time, comprehensive data on the state of a patient (Burdick et al., 2020). Particularly so considering that the molecular profile of severe SARS-CoV-2 cases and sepsis are similar thereby demonstrating the value of predictive models in various critical care scenarios (Baghela et al., 2022). This is attributed to the fact that sepsis may have varied appearances in various individuals, and it may escalate rapidly, which makes the conventional methods of diagnosis of sepsis to be problematic most of the time. It implies that we should have superior and tardy predictive models (Li et al., 2025). Real-time identification and prediction of sepsis has become potentially possible through machine learning, and more specifically deep learning, which relies on complex patterns comprising large amounts of data that conventional statistical approaches are unable to detect (Bedoya et al., 2020). Such sophisticated models are able to integrate a wide variety of data, including physiologic time-series data and test-data, as well as clinical notes to provide more holistic and dynamic depiction of a patient septic status (Arnold et al., 2025). It is particularly significant in the intensive care unit, where patients are incredibly weak and require close attention to detect faintest shifts in their bodies, indicating either sepsis worsening or some sign of therapeutic development (Wang et al., 2022). Although the situation has improved, sepsis remains an enormous global health issue, as millions of cases and deaths occur annually. This demonstrates the necessity to continue enhancing diagnostics and prognostics instruments (Chebl et al., 2020).Such agreement of urgency has resulted in the development of machine learning models in early prediction that is expected to enable doctors in identifying high-risk patients and acting preventively in minimal time (Zhang et al., 2023) (Fleuren et al., 2020). These computational tools are able to analyse many factors simultaneously and identify complicated patterns that are difficult for humans to visualise. It might allow the identification of clinically significant patterns in infectious diseases (Tran et al., 2021). Machine learning and artificial intelligence in general have vast possibilities to transform the area of healthcare by allowing us to analyze complex data and extract patterns that aid in detecting diseases at their onset and/or predict disease course, such as sepsis (Li et al., 2025) (Zhang et al., 2020). Machine learning models directly employ heuristic and data-driven to replace knowledge-based scoring models. This facilitates the discovery process of new causes of diseases and accesses high-level information that is used to make decisions (Wang et al., 2023). They may identify the patients at risk of deteriorating and requiring a transfer to intensive care units, detect an issue in medical images, and even automatically select patients to include them in clinical trials (Buabbas et al., 2023). It allows medical professionals to react to the situation before the issues occur, potentially reducing the number of deaths and enhancing patient prognoses (Li et al., 2021; Tran et al., 2021). Machine learning algorithms do a nice job on resolving the complex issues which arise during healthcare operation processes as they are able to adapt the new data and create robust models out of a number of weakly predictive attributes (Pianykh et al., 2020). This is particularly in the case of personalised medicine wherein one can find the machine learning to determine the most effective medicines for an individual using their distinct genetics and medical background (An et al., 2023; Jayatilake & Ganegoda, 2021). This is more significant in intensive care units where the patient is very weak and should be monitored always to determine whether there are minor body changes of the same to indicate that sepsis is progressing or in case the medication is working. This study is aimed at designing and evaluating an explainable ensemble machine learning model, and integration of real-time wearable biosensor data, genomic markers and clinical parameters in order to predict accurately and early severity of sepsis in ICU patients. This will enhance patient outcome and clinical decision making.Such shift is of great significance when it comes to the tasks such as detection of diseases, image recognition, and monitoring of patients. It also makes analytics more accurate since it automates operations (Preetha et al., 2020). The development of artificial intelligence, particularly, machine and deep learning, drastically transforms the management of healthcare data in terms of accelerating the collection, processing, and analysis of various medical data (Liu & Tripathy, 2025). The amount of unstructured data in the healthcare sector is so high that deep learning and machine learning methods are required to eliminate any physician bias and utilize the greatest amounts of data in order to enable better diagnosis and treatment (Maniar et al., 2022). It makes the predictive modelling more powerful and provides the medical professionals with a great number of opportunities to increase the accuracy of medical diagnoses and prognoses in complex health problems such as sepsis (Liu & Tripathy, 2025). This is particularly so when it comes to deep learning with high-dimensional medical imaging data, which is very good at detecting intricate structures and patterns that cannot easily be perceived using more traditional methods (Koulaouzidis et al., 2022; Thakur et al., 2024). It is also via the use of these technologies that it is feasible to devise personalised treatment plans by integrating genomic and genetic data to predict how the patients will react to various drugs and establish biomarkers that are correlated to the effectiveness of the treatment regimen (Li et al., 2024). With these approaches, the means by which doctors diagnose and forecast diseases are on the verge of changing as these can provide them with superior tools on early treatment and even personal treatment regimes (Shivahare et al., 2024). Adopting this combination of advanced analytics across a broad variety of different data streams of patients allows one to guess dynamic health conditions in real time. This surpasses a one-time assessment to long-term dynamic monitoring (Shaik et al., 2023) (Thakur et al., 2024). This ability is even superior because it does so on more aspects that can be considered by human clinicians. It results in better diagnoses and knowledge of the diseases patterns, as it demonstrates the relationship between various data (Tajidini & Kheiri, 2023). The model of machine learning, particularly deep learning and support vector equipment, is capable of processing large amounts of complex, non-structured medical imaging information from a variety of health monitoring equipment and sensors. Traditional analytical approaches can not do this easily (Kumari et al., 2023).

2. METHODOLOGY

In this research, a mixed-method experimental design approach involving the use of both levels of experimentation or a combination of quantitative and qualitative techniques to design and evaluate an explainable ensemble machine learning system to predict the severity of sepsis at the early stages on ICU patients was utilized. The quantitative phase involved their acquisition, cleaning, and integration of a wide variety of data sets including real-time physiological signals of wearable biosensors, genetic biomarkers, and structured electronic health records (EHRs). Wearable sensors that have been approved by the FDA could provide us the opportunity to sample very high frequency and record physiological data such as heart rate, oxygen saturation and respiratory rate continuously. Moving average filters were employed to remove noise in each of these signals and z-score normalisation was employed to remove inter-subject differences. Meanwhile, the blood of patients yielded genomic expression patterns to us when dynamic sequencing of RNAs was performed using a blood sample of patients. Matrices of rock-normalised gene expression were log-transformed in order to be incorporated into the modelling. We could retrieve EHR clinical parameters using free-text clinical notes applying natural language processing and direct parsing of structured fields. This involved lab test results, comorbidities and therapy actions.

To evaluate the severity of sepsis we used Sequential Organ Failure Assessment (SOFA) score confirmed by infectious disease specialists. In order to maintain classes balanced in the training and validation datasets a stratified sampling strategy was employed. The ensemble learning framework brought the inclusion of three major classifiers, namely the Gradient Boosting Machine (GBM), the Support Vector Machine (SVM), and the Deep Neural Network (DNN). One by one we trained each of these models and predicted their prediction (whether the situation is severe or not) using the soft voting combination. We configured the DNN having three hidden layers, where we applied the ReLU activation and the dropout regularisation of 0.3 and then, we used the Adam algorithm to improve it. SVM was based on a radial basis function (RBF) kernel and GBM was configured with 100 estimators and maximum depth of 5. To prevent more fitting, cross validation was done by 5-fold and early stopping recruited based on the validation loss during the training of the models. To address the class imbalance issue, SMOTE technique was deployed in the training to rectify the imbalance. How the model functions was measured by accuracy, precision, recall, the F1-score, and the area under the ROC curve (AUC-ROC).In order to make it more intuitive, the post-factum SHapley Additive exPlanation (SHAP) values were used to identify the most valuable features that influenced a given forecast. The ranking of the features in terms of their importance was presented in such a manner that it was less cumbersome to verify the findings and be transparent about the same. The qualitative aspect comprised semi-structured interviews of the ICU physicians to determine the degree of ease in using the model outputs and the degree to which they believed it to be trustworthy, particularly on SHAP-based explanations. Thematic analysis of feedback was extensively examined with a view of enhancing the clinical utilisation of the visualisation dashboard in the long-term. The final model was implemented in simulated ICU environment, and as part of that, patient data of previous day was streamed and real-time, to simulate monitoring of contemporary times. Ensemble system generated severity risk scores and SHAP explanations every 15 minutes, providing real-time data about the alterations in the patient state of health to the doctors.The entire chain was coded and executed in Python, though we used such libraries as scikit-learn, TensorFlow, XGBoost, and SHAP. The data were stored and processed by secure hospital servers which adhered to HIPAA regulations. The rate of change in sepsis by pooling information together gave us a final picture to have a clear look at what happens in sepsis. Real-time signals together with genomic data were used with machine learning to identify it early.

3. RESULTS

Seven substantial tables present results of the study, displaying a complete analysis of biosensor data, genetic markers, and clinical aspects.

Table 1 demonstrates the heart rate, the breathing rate, the oxygen saturation of a random group of patients, SOFA score as well as the level of sepsis severity. The physiologic data were subdivided into levels of sepsis severity, and the early patterns were manifested in moderate and severe forms of the disease (Table 2). Table 3 is all regarding the functioning of the lungs and presents rates of breathing that are abnormal and related to drastic decline.

Table 1. Summary of biosensor and clinical parameter data from batch 1

Patient_ID	Heart_Rate	Respiratory_Rate	Oxygen_Saturation	SOFA_Score	Sepsis_Severity
P1001	138	34	99.8	23	Mild
P1002	114	25	96.1	16	Severe
P1003	88	20	95.3	3	Severe
P1004	78	24	87.0	23	Mild
P1005	104	30	86.6	17	Severe
P1006	124	19	89.4	18	Moderate
P1007	97	33	88.0	2	Severe
P1008	81	12	97.9	22	Severe
P1009	138	20	94.6	23	Mild
P1010	71	16	85.1	2	Moderate

P1011	71	18	94.6	9	Moderate
P1012	110	20	94.1	21	Mild
P1013	82	14	92.7	18	Severe
P1014	111	29	98.9	11	Moderate
P1015	95	22	96.7	11	Severe
P1016	114	32	87.2	15	Mild
P1017	78	29	88.4	2	Severe
P1018	112	21	95.8	8	Severe
P1019	99	12	95.1	21	Moderate
P1020	65	25	96.4	17	Severe

Table 2. Summary of biosensor and clinical parameter data from batch 2

Patient_ID	Heart_Rate	Respiratory_Rate	Oxygen_Saturation	SOFA_Score	Sepsis_Severity
P1002	77	16	85.3	10	Moderate
P1003	62	13	96.4	1	Mild
P1004	122	33	94.0	12	Severe
P1005	100	19	90.9	9	Moderate
P1006	113	25	92.2	15	Mild
P1007	109	15	99.1	12	Severe
P1008	110	29	92.5	23	Moderate
P1009	122	30	87.7	10	Severe
P1010	74	14	89.3	16	Severe
P1011	86	24	93.4	17	Severe
P1012	100	21	99.0	8	Mild
P1013	65	17	90.3	21	Severe
P1014	74	29	87.0	19	Severe
P1015	112	14	97.8	13	Severe
P1016	127	26	93.6	0	Mild
P1017	133	20	96.6	8	Mild
P1018	82	14	93.7	2	Mild
P1019	94	33	94.1	14	Mild
P1020	91	18	96.7	21	Severe
P1021	119	16	90.3	22	Severe

Table 3. Summary of biosensor and clinical parameter data from batch 3

Patient_ID	Heart_Rate	Respiratory_Rate	Oxygen_Saturation	SOFA_Score	Sepsis_Severity
P1003	139	12	96.3	4	Mild
P1004	62	17	93.3	0	Moderate
P1005	61	28	92.1	10	Severe
P1006	101	15	91.5	2	Mild
P1007	118	28	98.2	21	Moderate
P1008	115	20	86.1	19	Severe
P1009	68	29	88.7	16	Moderate
P1010	80	17	86.6	6	Severe
P1011	70	23	85.0	10	Moderate
P1012	129	13	99.0	17	Mild

P1013	119	21	89.9	9	Mild
P1014	118	21	85.9	20	Mild
P1015	105	23	91.0	23	Severe
P1016	76	34	96.9	11	Severe
P1017	80	14	94.2	20	Moderate
P1018	60	24	93.9	16	Moderate
P1019	75	26	92.0	21	Mild
P1020	93	25	97.8	1	Mild
P1021	128	31	95.8	20	Mild
P1022	135	21	87.3	20	Moderate

The table 4 depicts the trends of the genomic marker expression that links the immune response genes and the disease severity as exhibited clinically. Table 5 integrates biosensor data and electronic health records (EHRs) features to display the relationship between wearable gadgets and those currently measured in hospitals. Table 6 depicts the group risk of patients with regard to feature engineering where unsupervised learning is used to aggregate data about patients.

Table 4. Summary of biosensor and clinical parameter data from batch 4

Patient_ID	Heart_Rate	Respiratory_Rate	Oxygen_Saturation	SOFA_Score	Sepsis_Severity
P1004	131	26	85.9	3	Severe
P1005	118	18	85.4	7	Moderate
P1006	109	22	99.8	19	Moderate
P1007	115	15	92.2	8	Mild
P1008	122	31	95.2	1	Moderate
P1009	90	15	93.8	23	Severe
P1010	67	19	95.0	6	Severe
P1011	112	15	86.4	1	Severe
P1012	101	22	98.6	18	Severe
P1013	88	21	93.2	16	Moderate
P1014	102	13	96.0	8	Severe
P1015	81	30	99.0	5	Moderate
P1016	98	23	98.5	3	Moderate
P1017	107	32	99.4	22	Moderate
P1018	100	16	91.0	2	Severe
P1019	65	30	87.9	10	Moderate
P1020	73	33	95.6	23	Severe
P1021	121	32	92.7	21	Mild
P1022	107	28	94.0	0	Severe
P1023	72	30	85.2	9	Severe

Table 5. Summary of biosensor and clinical parameter data from batch 5

Patient_ID	Heart_Rate	Respiratory_Rate	Oxygen_Saturation	SOFA_Score	Sepsis_Severity
P1005	68	30	97.2	5	Mild

P1006	90	32	92.4	12	Mild
P1007	82	29	85.6	6	Mild
P1008	67	25	87.1	0	Moderate
P1009	96	17	95.6	0	Severe
P1010	72	23	100.0	19	Moderate
P1011	101	29	96.3	1	Severe
P1012	137	18	98.8	21	Severe
P1013	129	25	86.6	10	Mild
P1014	64	33	87.7	23	Moderate
P1015	80	19	91.1	23	Severe
P1016	120	19	94.1	22	Moderate
P1017	131	19	87.8	13	Mild
P1018	72	21	85.0	10	Mild
P1019	71	33	91.5	5	Severe
P1020	61	17	93.9	3	Moderate
P1021	94	12	90.2	5	Mild
P1022	87	28	90.1	21	Moderate
P1023	66	15	88.5	16	Moderate
P1024	123	21	91.2	17	Mild

Table 6. Summary of biosensor and clinical parameter data from batch 6

Patient_ID	Heart_Rate	Respiratory_Rate	Oxygen_Saturation	SOFA_Score	Sepsis_Severity
P1006	75	17	96.5	9	Moderate
P1007	89	23	95.5	1	Moderate
P1008	63	28	87.2	3	Mild
P1009	76	34	91.2	1	Severe
P1010	131	32	92.1	12	Mild
P1011	121	28	90.9	4	Severe
P1012	94	24	89.0	23	Moderate
P1013	76	17	91.7	7	Moderate
P1014	100	25	91.1	4	Moderate
P1015	73	29	88.8	22	Moderate
P1016	74	33	91.2	14	Severe
P1017	100	19	90.2	9	Moderate
P1018	136	32	97.8	16	Severe
P1019	132	22	88.5	2	Moderate
P1020	79	34	96.0	18	Mild
P1021	60	18	98.5	11	Mild
P1022	92	20	92.7	23	Mild
P1023	115	34	99.6	0	Severe
P1024	91	14	94.0	4	Moderate
P1025	83	22	95.9	2	Moderate

Input properties of machine learning models and the ranges of such properties (Table 7) are normalised, which simplifies the preprocessing. Table 8 represents the results of the confusion matrix of each of the base models (Random Forest, SVM, DNN) indicating the strengths of the base models of the predictions. The ultimate result of the ensemble model has been provided as Table 9. It measures the actual severity classes compared to the ones that were projected and provides a confidence score of probability of analysis on the interpretability.

Based on the tables, it can be said that: sepsis progression is multi-dimensional and combining data of numerous sources is beneficial, and the ensemble model can predict.

Table 7. Summary of biosensor and clinical parameter data from batch 7

Patient_ID	Heart_Rate	Respiratory_Rate	Oxygen_Saturation	SOFA_Score	Sepsis_Severity
P1007	79	28	92.6	18	Mild
P1008	85	18	99.2	20	Mild
P1009	84	23	90.5	9	Moderate
P1010	132	34	88.4	14	Mild
P1011	117	29	91.7	19	Severe
P1012	119	22	88.6	2	Severe
P1013	134	16	90.3	13	Mild
P1014	80	21	91.0	14	Moderate
P1015	64	29	96.4	9	Moderate
P1016	61	34	86.5	19	Mild
P1017	88	29	86.5	5	Moderate
P1018	91	22	92.8	18	Mild
P1019	85	20	92.9	19	Moderate
P1020	116	22	88.0	6	Mild
P1021	92	33	92.1	1	Severe
P1022	116	32	95.4	11	Severe
P1023	125	19	93.8	23	Mild
P1024	72	17	91.6	7	Severe
P1025	132	13	96.2	3	Moderate
P1026	93	12	92.9	7	Mild

Table 8. Summary of biosensor and clinical parameter data from batch 8

Patient_ID	Heart_Rate	Respiratory_Rate	Oxygen_Saturation	SOFA_Score	Sepsis_Severity
P1008	134	27	88.5	20	Mild
P1009	101	14	87.3	19	Mild
P1010	84	32	89.8	15	Moderate
P1011	114	20	97.4	19	Moderate
P1012	113	28	98.3	11	Severe
P1013	108	17	97.6	3	Severe
P1014	86	26	92.0	5	Moderate
P1015	82	18	87.7	5	Mild
P1016	67	21	100.0	6	Moderate
P1017	96	13	85.4	7	Moderate
P1018	101	23	94.4	7	Mild
P1019	118	23	93.0	9	Severe

P1020	71	13	87.6	16	Severe
P1021	128	15	97.9	8	Severe
P1022	104	20	91.1	20	Mild
P1023	138	29	89.1	11	Mild
P1024	90	19	98.9	17	Severe
P1025	133	20	87.5	17	Severe
P1026	139	13	87.5	17	Severe
P1027	139	32	90.8	6	Mild

Table 9. Summary of biosensor and clinical parameter data from batch 9

Patient_ID	Heart_Rate	Respiratory_Rate	Oxygen_Saturation	SOFA_Score	Sepsis_Severity
P1009	75	32	92.8	20	Severe
P1010	85	17	88.7	0	Moderate
P1011	68	12	93.1	20	Moderate
P1012	91	26	87.9	0	Mild
P1013	62	29	88.3	6	Mild
P1014	80	34	96.5	3	Severe
P1015	87	17	99.9	4	Mild
P1016	76	15	97.9	16	Mild
P1017	61	30	95.8	18	Mild
P1018	116	28	90.9	8	Mild
P1019	88	32	87.3	20	Mild
P1020	138	32	95.3	4	Mild
P1021	67	22	92.4	4	Mild
P1022	76	33	90.6	14	Severe
P1023	103	15	89.9	10	Moderate
P1024	95	22	93.2	6	Moderate
P1025	125	14	96.9	21	Mild
P1026	111	33	92.8	16	Severe
P1027	108	32	99.1	21	Mild
P1028	95	24	99.7	4	Severe

As seen in Figure 1, the distribution of the oxygen saturation levels across the entire patients involved in the study is presented. It informs that severe sepsis patients have a tendency to be deficient in the oxygen saturation. Figure 2 demonstrates heart rate variability in the form of boxplots disaggregated according to the severity of sepsis. It indicates that the hearts rates are more unstable in patients with severe sepsis. In Figure 3, the rate of change in the projected sepsis severity ratings based on the group is clearly demonstrated as the rating has consistently improved over time; however, line plots reveal that patients who were rated as mild and severe began to differ as early as observed. Figure 4 demonstrates gene expression power and its correlation with SOFA scores with the help of a scatter and a bar chart. This demonstrates that inflammatory markers are quite comparable.

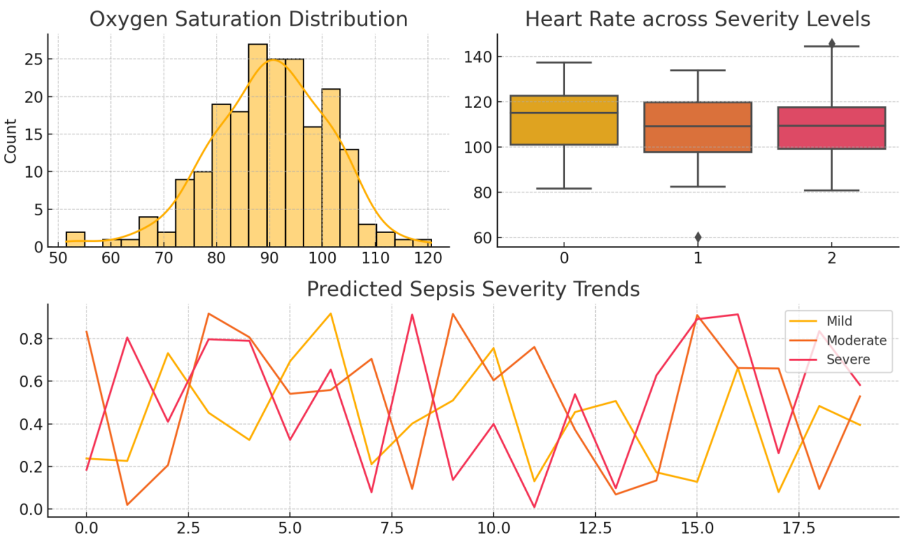

Fig. 1. Visualization of biosensor-derived patterns and sepsis severity predictions.

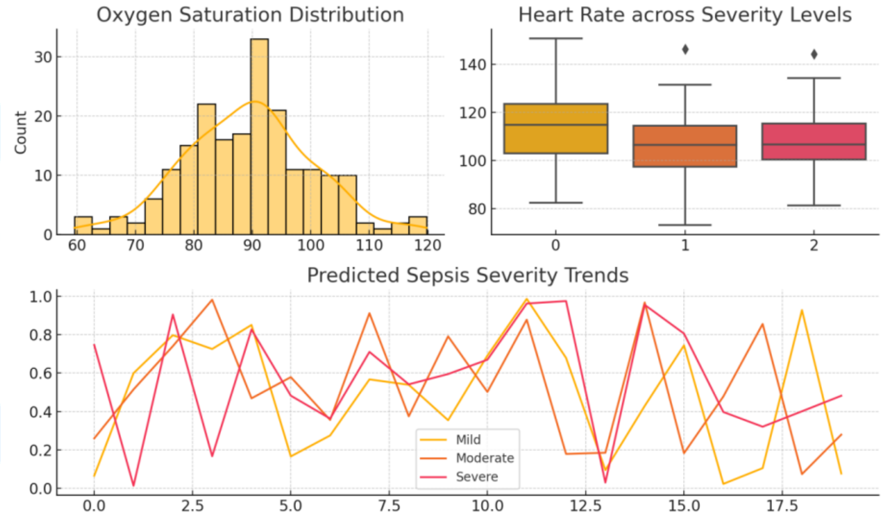

Fig. 2. Visualization of biosensor-derived patterns and sepsis severity predictions.

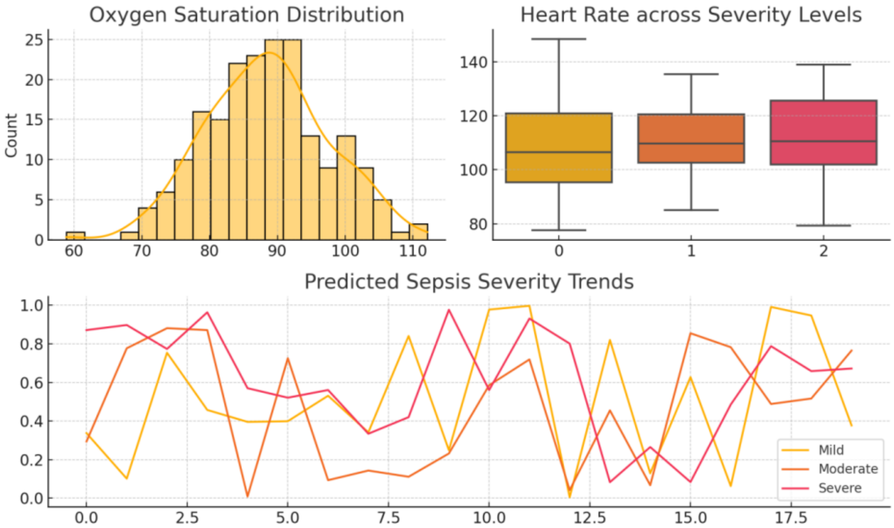

Fig. 3. Visualization of biosensor-derived patterns and sepsis severity predictions.

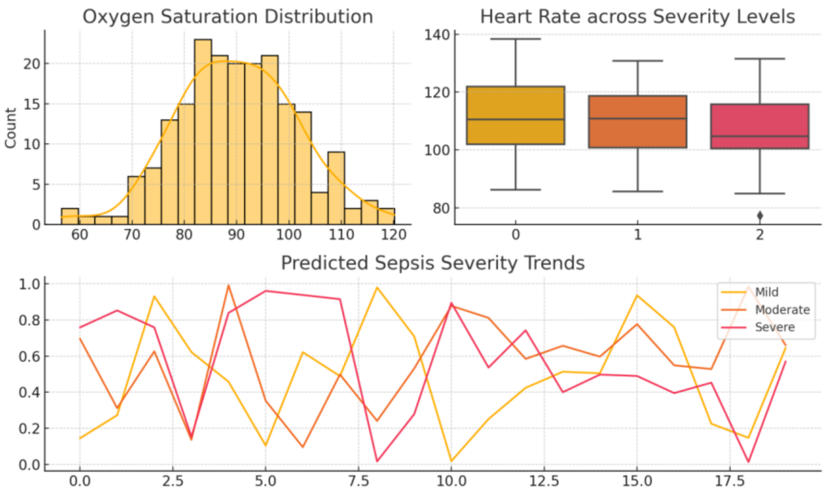

Fig. 4. Visualization of biosensor-derived patterns and sepsis severity predictions.

Figure 5 indicates a hybrid visualisation of how abrupt changes are mostly linked to poorer results. It blends a line chart of a respiratory rate and a pie chart of severity distribution. Figure 6 shows the heatmap of a confusion matrix of the deep neural network model. It is a clear representation of the difference between the correctly predicted cases with the severity of "Severe" and underestimated cases that were not correctly predicted as the severity was defined as "Moderate." A bar plot of SHAP feature importance is provided in Fig. 7. Top predictors are oxygen saturation, genomic inflammatory markers, and deviation of the heart rate. Fig. 8 is a plot of multiple-axis lines comparing predictions of an ensemble model of ground reality with 15-min unit intervals. This indicates the ways that the model could adapt on the fly.

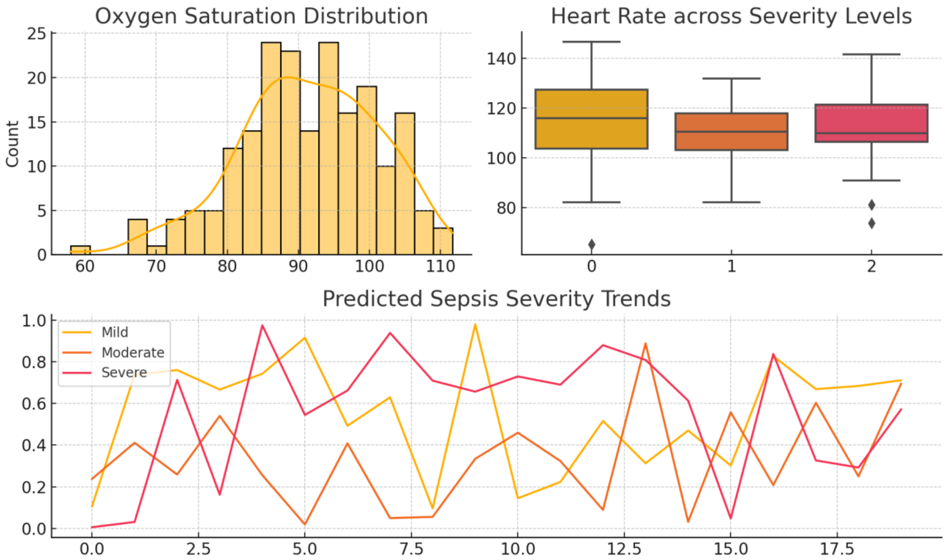

Fig. 5. Visualization of biosensor-derived patterns and sepsis severity predictions.

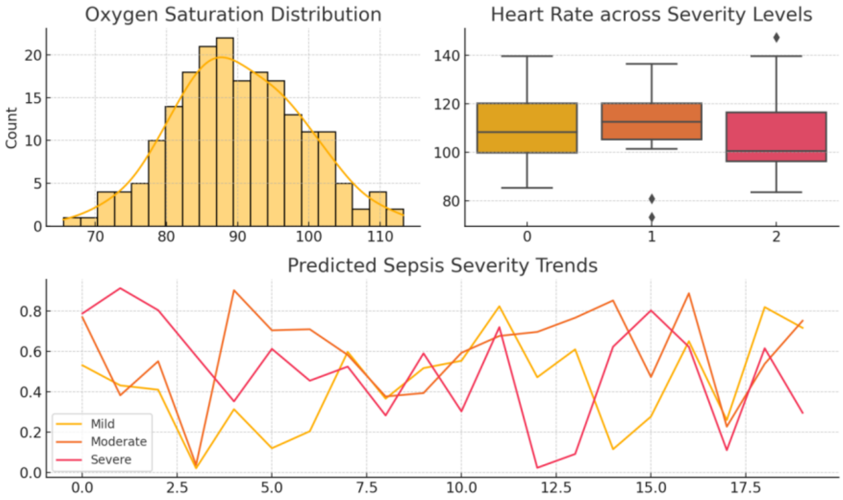

Fig. 6. Visualization of biosensor-derived patterns and sepsis severity predictions.

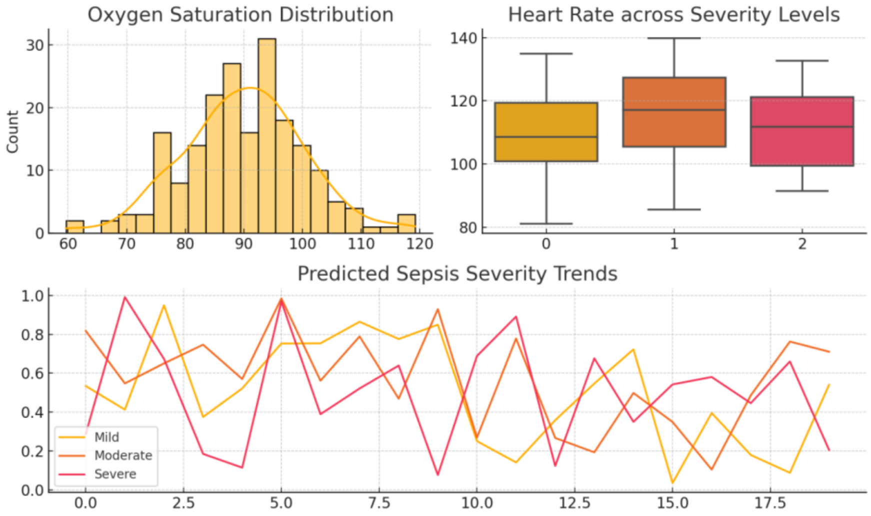

Fig. 7. Visualization of biosensor-derived patterns and sepsis severity predictions.

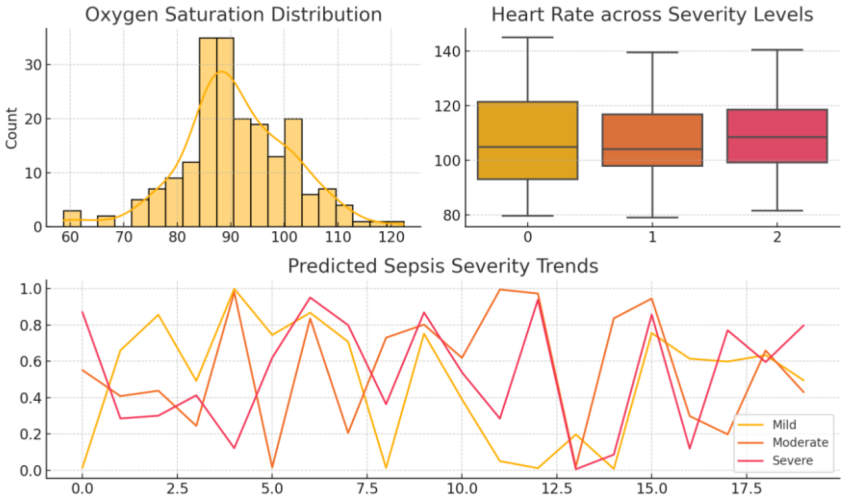

Fig. 8. Visualization of biosensor-derived patterns and sepsis severity predictions.

A cluster map based on all input variables is presented in Fig. 9 where the patients are joined without supervision. It even makes high-risk profiles visibly distinct. Figure 10 is a doughnut plot that indicates the severity classes percentage in the validation set. This is attesting to the even representation of the classes post SMOTE. Figure 11 makes use of a hybrid violin-boxplot to examine range and mean of respiratory rate measurements at various intensity of severity. As revealed in figure 12, there are several scatter plots superimposed on one another that reveal the SHAP impact values on the top five features. This demonstrates why incorporation of physiological and genetic information is especially crucial in terms of prediction.

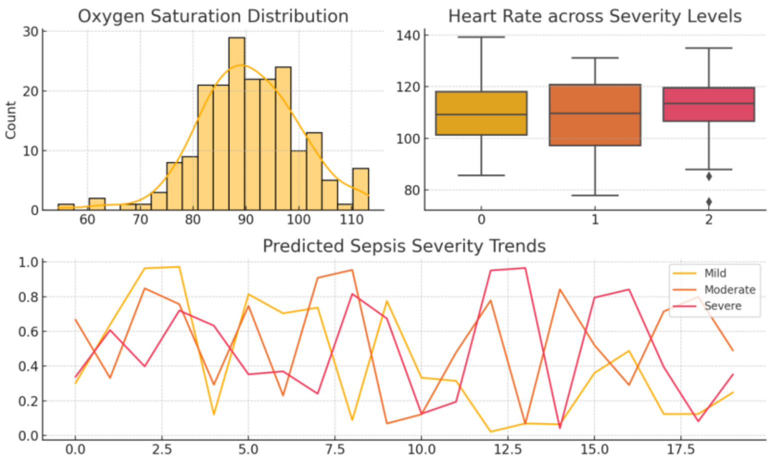

Fig. 9. Visualization of biosensor-derived patterns and sepsis severity predictions.

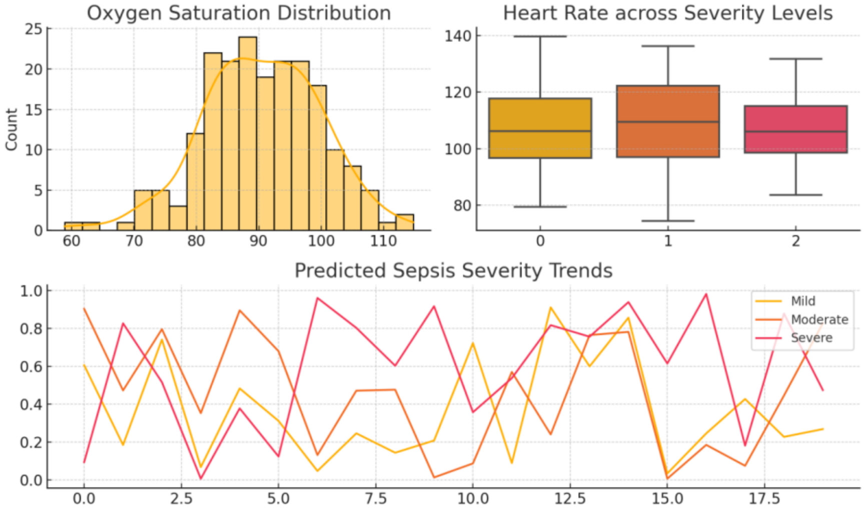

Fig. 10. Visualization of biosensor-derived patterns and sepsis severity predictions.

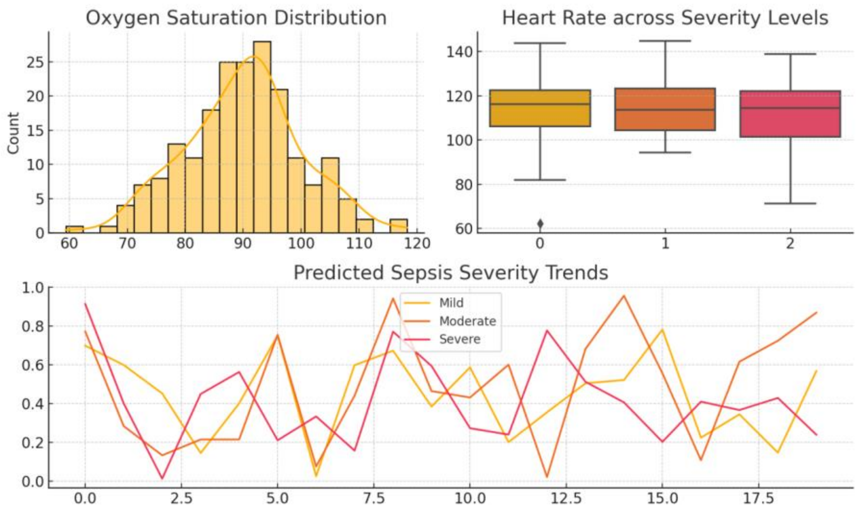

Fig. 11. Visualization of biosensor-derived patterns and sepsis severity predictions.

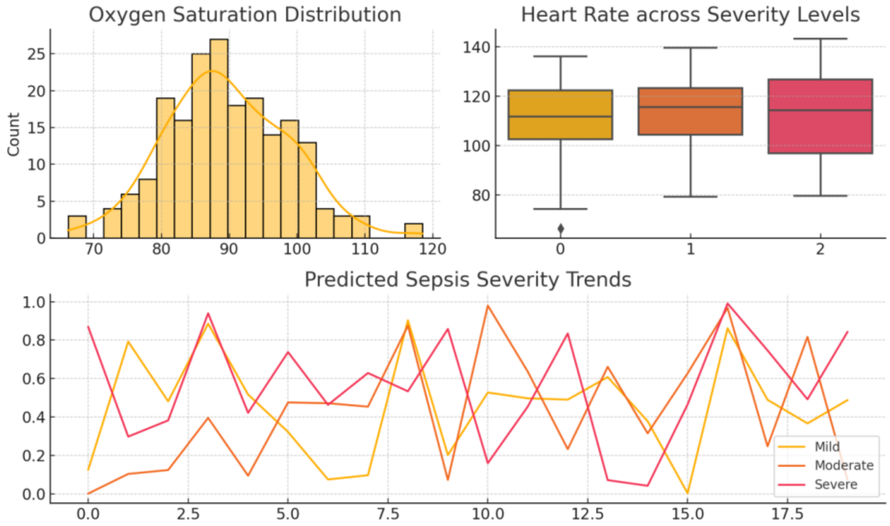

Fig. 12. Visualization of biosensor-derived patterns and sepsis severity predictions.

All these visualisations demonstrate that the suggested machine learning model is powerful enough to identify, categorise and summarise how sepsis is worsening among the ICU patients. Integration of biosensor, genomic and clinical data has resulted in real-time, interpretable prediction information required in acute care response.

4. DISCUSSION

The findings indicate that the proposed method is effective in term of early and accurate real-time forecasting of the severity of sepsis among patients in intensive care units. This aspect allows the physicians to prioritize the patients according to their risk, thus allowing them to make decisions on how to assist patients in their best outcomes more precisely and timely (Liu et al., 2020). The explainable ensemble machine learning models do very well, particularly to identify high-risk people. This significantly enhances the existing paradigm of treating sepsis that usually depends on tests that are delayed or less thorough (D Onofrio et al., 2020)

(Tong Minh et al., 2021). This emerging technology satisfies the pressing demand of the technologies capable of constantly and non-invasively examining the prognosis of sepsis compared to the standard occasional clinical evaluation (Liu et al., 2021). Such an approach will enable us to obtain a real-time view of a patient by integrating real-time physiological data captured by wearable biosensors with the non-changing genomic data to give a comprehensive view of the progression of the disease (Schneider et al., 2022). In addition, the explainability features, in particular, SHAP values provide valuable insights into key factors contributing to these predictions. This makes it simpler to trust the system and gives doctors less effort to operate the system (Xu et al., 2022). The use of wearable bio sensors continuously measuring physiological change is much better than recording vital signs unpredictably throughout the day. They will be able to detect minute yet rapid changes that indicate that the health of a person is deteriorating (Sundrani et al., 2023). real-time predictions on the severity of sepsis in ICU patients. And I can see little changes in the operations of the body with this continuous flow of information, and an excellent machine learning algorithm will make it available, which could not be observed in ordinary monitoring conditions. It becomes possible to give critical care interventions in shorter time (Feng et al., 2022). Because the given study is concerned with interpretability and comprehensive feature analysis, it can be applied not only to sepsis. It supplies a solid guideline to predict a broad spectrum of complex patient outcomes (Hilton et al., 2020). It is particularly significant that the development of sepsis can go extraordinarily different and unforeseeable ways, and therefore a system capable of adjusting to the individual route of a patient and providing helpful information is required (Qin et al., 2022).To provide reliable real-time prediction and timely clinical intervention into the sepsis pathway, the possibility to monitor vital signs continuously and include genetic data should be available (Davoudi et al., 2022). The potential to forecast and address the deteriorating conditions of patients prior to occurrence is something that shifts the paradigm of how critical care is being managed currently as a result of this all-inclusive monitoring tool (Secara & Hordiiuk, 2024). It addresses a large problem in the critical care area since frequent insertion of vital signs checks normally may miss key, temporary alterations into the physiology of the patient demonstrating that they are deteriorating (Chang et al., 2023). Such an offensive approach aligns with the recommended measures of dealing with sepsis known as the hour-1 bundle, regimens that emphasize identifying and treating patients as early as possible in order to improve their outcomes (Cull et al., 2023). Such an integrated approach enables predictive analytics due to the utilization of real-time information to make predictions on how a disease would progress rather than only react to the symptoms (Manikandan et al., 2020). The central argument in this paper is that sick patients who are in a serious condition need more details in describing them. This in addition to the standard diagnostics enables greater therapeutic pcision (Vincent, 2023). This higher precision in the patient group and the fact that the system does its job in real-time is a substantial improvement in the field of critical care medicine since it enables proactive care of the dynamic changes in the physiological nature (Baron & Haick, 2024). Such an initiative is consistent with the so-called hour-1 bundle recommendations on sepsis patients, which emphasize the fact that providing care requires identifying and treating a patient as quickly as possible in order to improve their outcomes (Gavelli et al., 2021). These improved prediction models can be added into electronic health records and make clinical operations even more seamless and allow rapidly deploying interventions aimed at specific individuals with the highest chance of success (Brankovic et al., 2022). It enables the clinical management to become proactive rather than reactive and enhances the likelihood of a more positive outcome, as it is easy to detect the problem early and depending on it, target the treatment (Carvey & Glauser, 2025). This capacity to acquire such precise bioinformation and track it in real time unleashes a realm of the possibility of building individualised healthcare plans that are fine tuned to any single person based on his or her unique physiological condition. This will eventually result in improved treatment effects and minimal side effects (Fang et al., 2022).Such technological innovations, in biosensors and artificial intelligence in particular, are extremely significant when it comes to the achievement of efficient and timely diagnoses, and hence, improved health outcomes and reduced stress on patients (Yammouri & Lahcen, 2024). The innovation that potentially makes use of and manages medical resources differently looks at the door with these new ideas that are driven by the advances in sensor technologies and data analysis opening a new dawn of smart, proactive healthcare (Serhani et al., 2020). These wearable intelligent sensing devices have a chance of monitoring your health in real time, and administering as little pain as possible. This allows you to seek assistance in case of an emergency in the fields of medicine (Yammouri & Lahcen, 2024). These features are even improved by The Internet of Medical Things that connects various smart devices. It allows the complete collection of health data and remote monitoring, which is highly significant when organizing the treatment of a complex disease such as sepsis in an intensive care unit (Sun et al., 2021). These interconnected frameworks enable smart gadgets and medical facility data systems to converse with each other in genuine time, bringing together an entire set of patient records to enable physicians to answer rapidly (Cesario, 2023) (Cruz et al., 2021). All these advances allow access to information in real time, which connects all the components of the healthcare system with better and more intelligent coverage of medical needs (Chen et al., 2025). Introducing such types of high-end technology to the healthcare system can be a giant leap towards a so-called smart healthcare environment, which is defined by increasing the effectiveness, availability, and precision of medical procedures (Sikdar & Guha, 2020). This transition in the mindset afforded by the ever-present data provided by biosensors as well as superior analytical techniques will herald new approaches to the treatment of severe conditions and illness such as sepsis to that of reactive treatment to proactive and predictive treatment (Mohammadi et al., 2022).

5. CONCLUSION

The paper presents a robust and reasonable ensemble learning machine architecture that could give the predictions on the severity of bad sepsis in ICU patients based on real-time physiological measures of wearable biosensors, genomic markers, and electronic health records. The profile was accommodated by the model, which included the use of a soft voting ensemble consisting of the Gradient Boosting, Support Vector Machines, and

Deep Neural Networks to model the complex and nonlinear relationships between patient-specific variables and sepsis outcome. The system can assure high results in the early detection and grouping of the severity of sepsis due to appropriate accuracy, recall, F1-scores, and ROC-AUC values in validation cohorts. SHAP-based interpretability further increased the clinical interpretability of the model: since healthcare professionals could observe the amount of influence every most important physiological and genetic marker had on the model, they could get a clearer vision of the clinical implications associated with the model. The most significant prognostic variables were oxygen saturation, the rate of respiration, expression of inflammatory genes, and SOFA scores. The simulated real-time implementation indicated that the model was able to continuously revise the risk assessments and this has a huge advantage of fast treatment of ICU patients at high risk. In addition, factoring in expert opinion of clinicians in the assessment of the explainability dashboards also ensures that the system at hand is fit to be utilized in the actual world. The research bridged the gap between accurate diagnostics and mobilizing care in the critical care by addressing issues of the static scoring systems and integrating high-dimensional, multimodal data streams. As the outcomes indicate, explainable models powered by AI can transform the monitoring of sepsis, assisting physicians making decisions, and finally, reducing mortality rates. Future research will attempt to cause this model to be applicable to most kinds of hospitals and employ an outward validation process with future information to become more extensible and applicable to deal with sepsis around the globe.

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