RESEARCH ARTICLE

Construction of an early-warning nursing model for critically ill patients based on biomarkers

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Critically ill patients refer to individuals with unstable vital signs and potential life-threatening conditions resulting from severe trauma, infection, or other critical illnesses, requiring urgent medical intervention and intensive monitoring. Currently, clinical management primarily relies on conventional monitoring, organ function assessment, and traditional scoring systems to guide diagnosis, treatment, and nursing care. However, these traditional approaches are susceptible to subjective factors and often suffer from delayed warning of clinical deterioration and intervention, leading to poor patient outcomes. This study aimed to identify key biomarkers for clinical deterioration in critically ill patients, develop and validate a practical early warning nursing model to address the delayed assessment and intervention issues in traditional methods, and provide healthcare professionals with a precise warning tool to improve patient prognosis. The study analyzed 2,104 critical patients in Union Hospital from January 2021 to December 2023. The patients were divided into training (1,472) and validation (632) groups. Within 24 hours of admission, 15 significant indicators were extracted. Multivariable logistic regression uncovered independent risk factors. R software was used to construct the proposed model and nomogram. Model performance was assessed *via* receiver operating characteristic (ROC) curves and Hosmer-Lemeshow tests with stability checked by 10-fold cross-validation and bootstrap sampling, while a nursing scoring scale was also developed. The results showed that blood oxygen saturation (SpO_2), white blood cell count (WBC), procalcitonin (PCT), lactic acid (LA), and alanine aminotransferase (ALT) were independent risk factors ($P < 0.01$). The model based on these biomarkers had excellent performance with training group's area under the curve (AUC) of 0.854 (95% CI: 0.835 - 0.872), sensitivity of 0.820, specificity of 0.737 and validation group's AUC of 0.857 (95% CI: 0.827-0.887), sensitivity of 0.708, specificity of 0.864, respectively. Both groups showed good calibration. The model outperformed sequential organ failure assessment (SOFA) scores with AUC of 0.759 and single biomarkers. The scoring scale had a content validity index (CVI) larger than 0.8, enabling risk stratification for monitoring frequency. This proposed model offered high predictive accuracy and clinical applicability, aiding early identification of high-risk patients and guiding personalized nursing plans, providing a reliable basis for precise nursing care in critical patients.

Keywords: critically ill; patients; biomarkers; logistic regression; nomogram; predictive nursing model.

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Introduction

With the advancement of critical care medicine and the refinement of standardized nursing systems, the early mortality rate of critically ill patients has been significantly controlled. However, in clinical practice, some patients remain in the intensive care unit (ICU) for

extended periods due to their inability to be weaned from life support measures such as mechanical ventilation after surviving the acute critical phase. This clinical condition is defined as chronic critical illness (CCI), which is characterized by core pathological features including persistent inflammatory response, immune suppression, and protein hypercatabolism. It not only leads to recurrent nosocomial infections, prolonged hospitalization, and reduced long-term quality of life but also results in substantial consumption of medical resources. Sepsis, as a life-threatening organ dysfunction syndrome caused by a dysregulated host response to infection, serves as a key risk factor for triggering CCI. Epidemiological data indicated that, among ICU patients in five U.S. states, the incidence of CCI reached 7.6% with over 60% of cases secondary to acute sepsis and other critical illnesses [1]. Therefore, the early identification of high-risk populations progressing from critical illness to CCI has become a crucial link in improving patient outcomes and optimizing the allocation of medical resources.

Biomarkers as objectively quantifiable indicators of physiological or pathological states can reflect pathophysiological changes in the body hours to days before typical clinical symptoms appear, providing an important technical means for early warning of critical illness. Yin *et al*. developed a risk prediction model for CCI secondary to sepsis in elderly patients based on the medical information mart for intensive care IV (MIMIC-IV) database, incorporating clinical indicators such as age, respiratory rate within 24 hours of ICU admission, body temperature, hematocrit, red blood cell distribution width (RDW), blood urea nitrogen (BUN), lactate, and activated partial thromboplastin time (aPTT). The model achieved area under the receiver operating characteristic curve (AUC) values of 0.733 and 0.817 in the training and external validation cohorts, respectively, confirming the feasibility of multi-indicator joint prediction [2]. Huang *et al*. integrated inflammatory markers including serum procalcitonin (PCT), C-reactive protein (CRP), and interleukin-6 (IL-6) to construct a dynamic early warning model for septic shock using a hybrid algorithm combining logistic regression and machine learning. Validated with 1,876 patients from 12 tertiary hospitals, the model achieved prediction accuracy of 82.3% and an AUC value of 0.88 [3]. Wang *et al*. developed an early warning model for respiratory failure in patients with severe pneumonia using core indicators including PCT, CRP, ratio of partial pressure of arterial oxygen to fraction of inspired oxygen (PaO_2/FiO_2), and interleukin-10 (IL-10) through the random forest algorithm. Validated in a multicenter retrospective cohort of 1,200 patients from five tertiary hospitals nationwide, the model achieved an AUC value as high as 0.892 with sensitivity and specificity of 86% and 83%, respectively [4]. These studies have laid a solid foundation for the application of biomarkers in the field of critical illness early warning. Despite the promising development, this field still faces critical issues and challenges that require urgent resolution. Most models lack rigorous external validation and multicenter data support. Some studies rely solely on single-center cohorts or public databases for analysis, and the stability and generalization capability of these models have not been fully validated, making direct application to clinical institutions at different levels difficult. Further, existing early warning models predominantly focus on single endpoint events such as septic shock and respiratory failure, while research on early warning for the progression from critical illness to CCI remains relatively scarce, failing to meet the clinical need for early identification of high-risk CCI populations. In addition, some models incorporate overly complex indicators involving specialized testing items or invasive monitoring parameters that are difficult to implement in routine nursing practice at primary hospitals, limiting clinical applicability. Additionally, traditional nursing assessment methods primarily rely on vital sign monitoring and clinical manifestation observation with related indicators often showing abnormalities only after significant clinical deterioration, frequently leading to delayed intervention timing, which

further highlights the necessity of constructing efficient and practical early warning models.

This study identified key biomarkers for clinical deterioration and progression to CCI in critically ill patients and developed and validated an early warning nursing model that combined high predictive performance with clinical practicality. The proposed model addressed the issue of delayed intervention in traditional nursing assessments, provided healthcare professionals with precise risk stratification tools, and ultimately achieved the core objective of improving patient outcomes. This research employed a retrospective cohort study to systematically collect clinical data including demographic characteristics, vital signs, and laboratory test results within 24 hours of admission to univariate analyze and screen potential indicators associated with clinical deterioration followed by multivariate logistic regression modeling to identify independent risk factors and determine core biomarkers and clinical indicators for constructing the early warning model. R software was utilized to develop the early warning model and visual nomogram. Model predictive performance was evaluated using metrics such as AUC, sensitivity, and specificity with model calibration validated through Hosmer-Lemeshow testing. Model stability was further verified using 10-fold cross-validation and Bootstrap sampling. Based on the selected core indicators, a supporting nursing assessment scale was developed, and its content validity and reliability were tested to ensure applicability in clinical nursing practice. The implementation of this research held significant theoretical value and clinical importance. It clarified the early warning value of core biomarkers in the progression from critical illness to CCI, enriched the theoretical system of combined biomarker prediction, and provided methodological references for subsequent related research. Further, the developed early warning model and supporting assessment scale were operationally simple and highly practical, enabling nursing staff to quickly identify high-risk patients and guide the formulation of individualized monitoring plans, facilitating the transition from "passive intervention" to "active warning", which not only helped reduce the incidence of CCI, shorten ICU length of stay, and improve long-term quality of life but also provided scientific basis for optimizing medical resource allocation, alleviating societal healthcare burdens, and promoting precision development in the field of critical care nursing.

Materials and methods

Research subjects and diagnostic criteria

The study enrolled 2,104 critically ill patients in the EICU and ICU at Union Hospital, Huazhong University of Science and Technology (Wuhan, Hubei, China) from January 2022 to December 2024. Among them, there were 1,286 males (61.1%) and 818 female (38.9%) with the average age of 56.8 ± 15.2 years old, the median age of 58 years old, and the interquartile range from 45 to 68 years old. The main causes of admission to the ICU were 684 cases (32.5%) of sepsis, 547 cases (26.0%) of respiratory failure, 326 cases (15.5%) of severe trauma, 298 cases (14.2%) of cardiac insufficiency, and 249 cases (11.8%) of other acute and critical conditions such as acute cerebrovascular disease, acute pancreatitis, *etc*. The inclusion criteria were that (1) patients aged between 18 and 75 years; (2) ICU admission duration was between 24 and 72 hours; (3) APACHE II scores upon admission were from 15 to 30, focusing on patients with moderate to severe critical illnesses [5, 6]. The exclusion criteria included disease, treatment, and individual characteristics as (1) patients undergoing extracorporeal membrane oxygenation (ECMO) or continuous renal replacement therapy (CRRT) for over 48 hours; (2) patients with end-stage renal disease (ESRD) or decompensated liver cirrhosis; (3) patients with mechanical ventilation duration less than 12 hours or missing vital sign monitoring data exceeding 15%; (4) patients positive for human immunodeficiency virus (HIV) or with acquired immunodeficiency syndrome (AIDS) [7]. The diagnosis of critically ill patients was based on the

Sepsis-3.1 criteria released by the Surviving Sepsis Campaign (SSC) in 2021 [8]. Under the premise of infection evidence, a patient was diagnosed as critically ill if they met at least two of the following criteria including (1) a Sequential Organ Failure Assessment (SOFA) score increasing 2 points and above from baseline; (2) lactic acid (LA) levels higher than 2 mmol/L; (3) peripheral blood white cell count less than 4×10^9/L or larger than 12×10^9/L [9]. All procedures of this research were approved by the Ethics Review Board (IRB) of Huazhong University of Science and Technology (Wuhan, Hubei, China).

Data acquisition

The patients' data were retrieved from the hospital's electronic medical record (EMR) system and the Critical Care Information System (CIS) and randomly split into two subsets with 1,472 patients in the training set and 632 patients in the external validation set, adhering to a 7:3 proportion [10]. The training subset was utilized to develop a biomarker-informed early warning nursing model, while the validation subset was designated to appraise the model's predictive efficacy and cross-applicability, thus affirming its robustness and clinical utility. The patient-related indicators extracted from the dataset were demographic characteristic variables including age, gender, body mass index (BMI), history of diabetes, history of hypertension and vital signs including body temperature, heart rate, respiratory rate, mean arterial pressure, blood oxygen saturation. The laboratory examination indicators included white blood cell count and differentiation, the absolute values of lymphocytes and neutrophils, platelet count, C-reactive protein, D-dimer, fibrinogen, and blood gas analysis parameters of pH value, bicarbonate concentration, and oxygenation index (PaO_2/FiO_2). Liver and kidney function indicators included alanine aminotransferase (ALT), aspartate aminotransferase (AST), serum lactate dehydrogenase (LDH), serum creatinine, blood urea nitrogen (BUN), and inflammation-related biomarkers of procalcitonin (PCT) and interleukin-6 (IL-6). Regarding treatment measures, whether patients received vasoactive drugs including norepinephrine and epinephrine, fluid resuscitation, and continuous renal replacement therapy (CRRT) were recorded. In addition, disease severity scores of Sequential Organ Failure Assessment (SOFA) and the quick Sequential Organ Failure Assessment (qSOFA) were included. These biomarkers overcame the limitations of traditional clinical signs that usually lagged actual physiological changes by capturing early molecular signals of stress response, uncontrolled inflammation, and organ damage to provide a quantifiable basis for early clinical warning [11]. All the indices were extracted from the patient's records within the first 24 hours of admission to the ICU. For vital sign indicators, statistical methods were used to calculate the mean values, aiming to reflect the patient's overall physiological state during this period, while the laboratory test results and imaging scores were assessed based on the worst values within 24 hours, given the critical role of extreme values in determining disease severity.

Data processing

The dataset might have manual entry errors by medical staff and monitoring interference from equipment [12, 13]. A stratified data-cleaning approach, combining clinical knowledge and statistical methods, was adopted. Absolute abnormal thresholds for core indicators were established based on normal clinical physiological ranges with data exceeding these thresholds being directly excluded. For data exhibiting statistically abnormal fluctuations within the absolute range, the 3σ rule was applied [14]. Data beyond the $\mu \pm 3\sigma$ range and unsupported by clinical events were substituted with the mean value of the indicator from the preceding and following 1-hour periods. To address missing data post-cleaning and inherent data gaps, interpolation techniques were employed [15]. The data preprocessing process first involved reading the data based on patient ID and extracting feature values hour by hour. Then, it checked whether the feature values for the first hour were missing. If it was not null value, the process proceeded directly to linear interpolation, otherwise, a further check was

made to see if the entire feature sequence consisted of null values. The "similar mean imputation" method was applied, while the "mean imputation" method was applied if the sequence was not all null values. After completing the imputation, linear interpolation was performed on the data, and then it was checked whether there were still null values at the end of the sequence. If there were null values, the "forward filling" method was used to fill in these null values. If there were not, the data preprocessing process was finalized. To meet early warning needs, the disease progression trends were extracted from continuous monitoring data. A feature time window of the first 24 hours post-ICU admission was set and divided into 3-hour analytical units [16]. Core features were extracted in three dimensions including median of the indicator within the window as numerical level, difference between the median of the current window and the previous window divided by the 3-hour interval as the rate of change, and interquartile range of the indicator within the window, reflecting stability as fluctuation amplitude [17]. The data was then time-aligned with the target event of critical deterioration.

Biomarker screening based on logistic regression

The observational indicators of the two patient groups were analyzed. Variance Inflation Factor (VIF) was used to test multicollinearity among independent variables [18]. For variables with multicollinearity, Principal Component Analysis (PCA) was applied for dimensionality reduction. The strength and independence of the association between each factor and the risk of disease deterioration were clarified. The initially selected indicators were used as core input variables and combined with clinically significant features that were not included in the preliminary screening model to construct a multiple logistic regression model. Based on logistic regression, the complex data were preliminarily classified to obtain risk stratification of disease deterioration in patients. The analysis results were then used as input variables and combined with clinical characteristics of patients. The analysis was further refined through regression models to uncover potential feature relationships in the data. Biomarkers closely related to critical and severe illnesses were then Identified [19]. To evaluate a model's discrimination capability, a Receiver Operating Characteristic (ROC) curve was plotted, which showed the trade-off between sensitivity (true positive rate) and 1-specificity (false positive rate). A curve closer to the upper-left corner signified better discrimination. The Area Under the Curve (AUC) quantified this performance with values from 0.5 to 1.0. An AUC below 0.7 suggested poor discrimination, while 0.7 - 0.8 indicated fair, 0.8 - 0.9 denoted good, and larger than 0.9 reflected excellent discrimination. To assess the model's clinical utility, the sensitivity, specificity, positive predictive value (PPV), and negative predictive value (NPV) were calculated at the ROC curve's optimal threshold. Chi-square tests were conducted to compare expected results with observed event rates. The Hosmer-Lemeshow test was employed to assess calibration by dividing patients into decile groups based on predicted risk. Calibration reflected the consistency between a model's predicted risks and actual patient outcomes, crucial for model reliability [20]. The calibration curve visually displayed the results. The closer the curve was to the ideal 45° line, the better the calibration effected. The Brier score on a 0 - 1 scale complemented this evaluation with lower scores indicating better calibration [21]. This process helped identify potential risk factors and biomarkers associated with patient deterioration.

Results and discussion

Comparison of baseline indicators between the two groups of patients

The specific biomarkers tested covered four major categories, which were inflammation-related indicators including procalcitonin (PCT), C-reactive protein (CRP), interleukin-6 (IL-6), interleukin-10 (IL-10); hematological indicators

including red blood cell distribution width (RDW); biochemical and coagulation function indicators including blood urea nitrogen (BUN) and activated partial thromboplastin time (aPTT); the core indicator of blood gas analysis including the ratio of arterial partial pressure of oxygen to inhaled oxygen concentration (PaO_2/FiO_2). The univariate analysis comparing the two patient groups identified 15 statistically significant indicators including age, body temperature, heart rate, respiratory rate, blood oxygen saturation (SpO_2), white blood cell (WBC) count, platelet (PLT) count, C-reactive protein (CRP), alanine aminotransferase (ALT), serum lactate dehydrogenase, procalcitonin (PCT), lactate (LA), vasopressor use, broad-spectrum antibiotic use, and quick Sequential Organ Failure Assessment (qSOFA) score. There was no statistically significant difference between the training group and the validation group.

Risk factors for critically III patients

The results of multivariable logistic regression analysis of 15 indicators showed that, as the different regularization parameters (λ) decreased, the coefficients of some variables gradually became non-zero and stabilized (Figure 1).

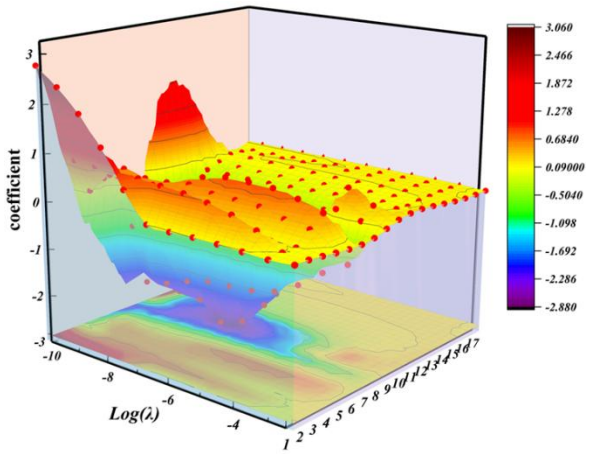


Figure 1. Biomarker screening for critical illness early warning models based on LASSO regression. Each colored curve represented an independent variable.

The cross-validation error that corresponded to different λ values and demonstrated the point of minimal error and the point of minimal error plus one standard error was shown in Figure 2.

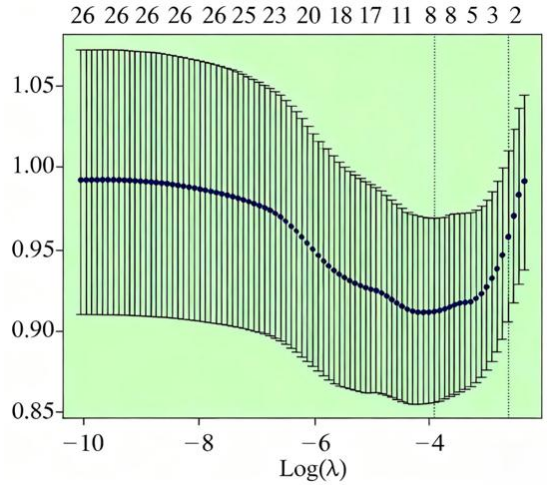


Figure 2. Critical and acute conditions based on LASSO regression cross-validation for screening and optimization of biomarkers for early warning models.

The final regularization parameter was then selected for this study. The analysis results indicated that the proposed model fitted best when incorporating five indicators of SpO_2, WBC count, PCT, LA, and ALT. Changes in these indicators were associated with the risk of severe critical illness in ICU patients [20] (Table 1).

Development and predictive performance of the nomogram

According to the results of univariate and multivariate logistic regression analyses, SpO_2, WBC, PCT, LA, and ALT were identified as significant risk factors for critical illness in patients. The Hosmer-Lemeshow test result indicated that the model was well-calibrated and had good fitness ($P > 0.1$). The final early warning regression model was then presented as follows.

$$log\ \left(\frac{P}{1-P}\right) = -3.79 + 0.112X_1 + 0.122X_2 + 0.001X_3 + 0.062X_4 + 0.222X_5 \quad (1)$$

Table 1. Results of logistic regression analysis of related risk factors.

Indicator	Training group (n = 1,472)	Test group (n = 632)	*P* value
SpO_2 (%)	95.8 (92.3, 98.1)	95.6 (92.1, 97.9)	0.091
WBC (× 10^9/L)	12.5 (8.3, 18.7)	12.3 (8.1, 18.5)	0.056
PCT (ng/mL)	0.85 (0.32, 2.56)	0.83 (0.31, 2.52)	0.029
LA (mmol/L)	2.3 (1.4, 4.1)	2.2 (1.3, 4.0)	0.084
ALT (U/L)	58 (32, 112)	56 (31, 110)	0.047

where X_1 to X_5 were the 5 index factors of SpO_2, WBC, PCT, LA, and ALT, respectively. A nomogram was then constructed based on the five biomarkers. The patient's risk of critical illness was determined by adding all the scores to identify the probability of the risk (Figure 3).

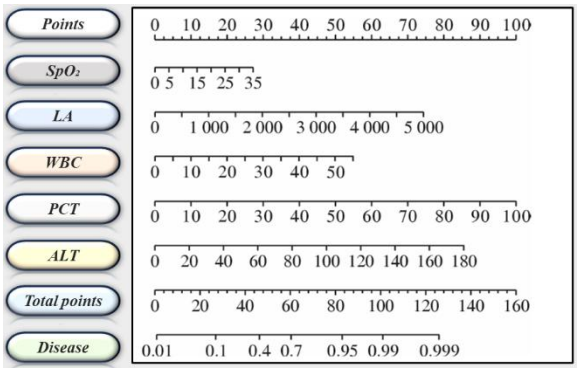
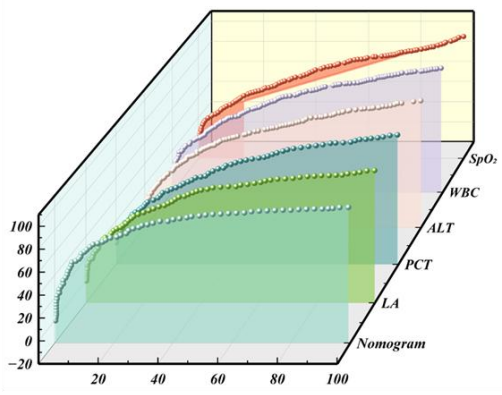
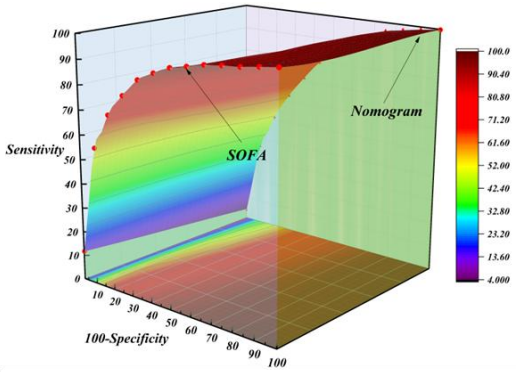


Figure 3. The nomogram of early warning model for acute and critical condition prediction.

In the training dataset, 10-fold cross-validation was utilized to evaluate the training data against performance benchmarks of accuracy, sensitivity, and specificity. The nomogram exhibited strong discrimination, achieving an AUC of 0.854 (95% CI: 0.835 – 0.872) for critical illness prediction with corresponding sensitivity and specificity of 82.0% and 73.7%, respectively, in proposed model, while the SOFA score in traditional method presented a lower AUC of 0.759 (95% CI: 0.735 – 0.783) and sensitivity/specificity values of 0.699 and 0.682, respectively. Various biomarkers including SpO_2 with AUC of 0.655, WBC with AUC of 0.712, PCT with AUC of 0.717, LA with AUC of 0.783, and ALT with AUC of 0.716 demonstrated different predictive capabilities. AUC analysis confirmed the nomogram's superior predictive accuracy over SOFA scores and single inflammatory markers. The ROC curves for the nomogram and individual biomarkers and the nomogram alongside the SOFA score were shown in Figure 4.



a, ROC curves for the nomogram and individual biomarkers



b, ROC curves for the nomogram and SOFA score

Figure 4. ROC curves for the nomogram and individual biomarkers (a), nomogram and SOFA score (b).

The nomogram showed strong predictive performance in the validation set with an AUC of 0.857 (95% CI [0.827, 0.887]), sensitivity of 70.8% (95% CI [0.651, 0.760]), and specificity of 86.4% (95% CI [0.823, 0.899]). The results confirmed that the model was stable as there was no significant difference in AUC between the training and validation sets (P = 0.879) (Figure 5).

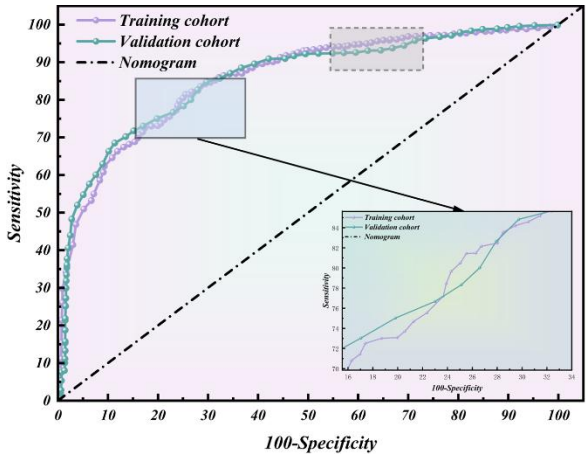
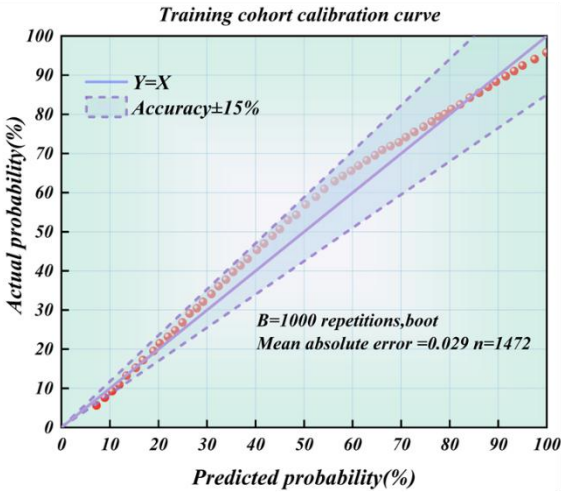


Figure 5. The ROC curves of the training set and the validation set.

The calibration curves demonstrated that the model's predicted probabilities of critical illness in ICU patients closely matched the actual probabilities, indicating good consistency for both the training set and the test set (Figure 6).

A.



B.

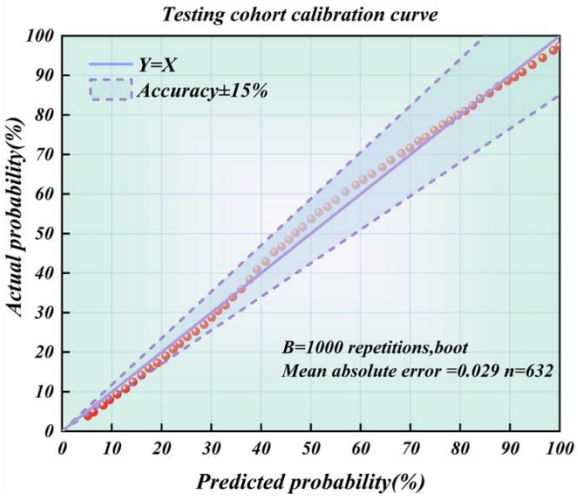


Figure 6. Calibration curves of nomogram for predicting critical illness in ICU patients. **A.** Training set. **B.** Test set.

The results of Hosmer-Lemeshow test of P > 0.1, calibration curve closing to the ideal diagonal line), Brier score of 0.08, 10-fold cross-validation with AUC variation < 0.01, and Bootstrap validation with 1,000 resamples and AUC decline < 0.005 confirmed the model's high differentiation, calibration, and stability. Moreover, the nomogram exhibited significant clinical utility, outperforming the traditional SOFA score and any single biochemical indicator (P < 0.01) (NRI = 0.218, IDI = 0.076). The decision curve demonstrated continuous positive net benefit in the threshold probability range of 5 – 60%.

Early warning nursing strategies for critical illness

Based on the verified multivariate logistic regression model, a visual risk assessment tool, the Early Warning Nursing Score for critically ill patients, was developed for quick clinical application [21, 22]. The risk contributions of key biomarkers were scored by using a 1-to-3-point scale with a total score of the scale ranging from 0 to 12 (Table 2). Nurses could use point-of-care testing (POCT) to get biomarker values and calculate the score and categorize patients into three risk levels based on their scores with corresponding care and treatment plans. The

high-risk group was defined as a score ≥ 5 and a risk of disease progression > 30%. Intensive monitoring and emergency preparedness should be implemented with monitoring SpO_2, vital signs, LA, PCT every 30 minutes, WBC count and ALT every 2 hours, prioritizing respiratory support and organ function maintenance, and having emergency resources such as ventilators and continuous renal replacement therapy (CRRT) equipment readily available. The moderate-risk group was defined as a score between 3 and 4 and a risk of deterioration of 10 - 30%. The monitoring should be strengthened to prevent disease progression with monitoring SpO_2, vital signs, LA, PCT hourly, and other indicators every 4 hours, focusing on infection control and metabolic regulation. If indicators fluctuated by more than 20%, intervention measures should be immediately strengthened. The low-risk group was defined as a score < 3 and a risk of deterioration < 10%. The routine monitoring and prevention management should be carried out with monitoring SpO_2 and vital signs every 2 hours and biomarkers every 8 hours. The basic nursing and complication prevention should be emphasized. For immuno-compromised patients, PCT should be retested every 6 hours.

Table 2. Biomarker scoring criteria.

Biomarker	Assignment standard
SpO_2	≥ 95% = 0; 90 - 94% = 1; < 90% = 3
WBC	≥ 95% = 0; 90 - 94% = 1; < 90% = 3
PCT	≥ 95% = 0; 90 - 94% = 1; < 90% = 3
LA	≥ 95% = 0; 90 - 94% = 1; < 90% = 3
ALT	≥ 95% = 0; 90 - 94% = 1; < 90% = 3

The results of this research found that SpO_2, WBC, PCT, LA, and ALT were independent risk factors for early mortality in critical illness. The AUC of the proposed risk prediction model based on the combination of these factors surpassed the predictive value of using individual indicators. Clinically, early intervention and enhanced monitoring of these indicators might improve patient prognosis. SpO_2 as a key indicator of oxygenation is a significant independent risk factor for early mortality in critical illness. When SpO_2 is persistently below 92%, the risk of early death increases 2.3 to 3.1 times. WBC is a common inflammatory marker and indicates infection when elevated or reduced. PCT is primarily secreted by thyroid C cells and rises following bacterial infection. Multiple studies have confirmed that PCT levels are associated with sepsis occurrence and prognosis. A Meta-analysis of 19 studies indicated that the AUC for PCT in early predicting sepsis in critical patients was 0.84. LA reflects tissue hypoperfusion and enhanced anaerobic metabolism. In critical patients with shock, severe infection, or organ dysfunction, inadequate microcirculation perfusion causes tissue hypoxia, leading to increase LA production. LA accumulation exacerbates intracellular acidosis, impairing myocardial contractility and immune function, thus creating a vicious cycle. ALT level indicates the degree of liver function damage and predicts the risk of multi-organ failure. As the central organ for metabolism, detoxification, and synthesis, liver dysfunction in critically ill patients manifested as elevated ALT caused by infection, ischemia, or drug toxicity can reduce albumin synthesis, cause coagulation disorders, and lead to toxin accumulation. These issues may trigger renal impairment, immunosuppression, and other multi-organ cascading reactions. The resulted nursing intervention strategies according to the Early Warning Nursing Score enabled bedside risk stratification within short time and quickly implementation of corresponding monitoring frequencies and intervention priorities, achieving closed-loop management of "assessment-stratification-intervention" and significantly improving nursing efficiency and precision. The "5 biomarker" nomogram developed and validated in this study demonstrated high predictive performance and clinical feasibility, providing a reliable and simple evidence-based tool for health providers to identify high-risk patients early, implement individualized monitoring and interventions, and advance the precise nursing of critical patients. This study has several limitations. The study used

only data from the ICU database of a tertiary hospital with the most infection cases, which was insufficient to cover uninfected patients. Future research should collaborate with multiple medical centers to include diverse ICU data and enhance the generalizability of the findings through internal and external validation. Further, the number of indicators was limited. Other clinical characteristics of critical illness patients were not incorporated, which might affect the predictive performance of the proposed model. Multidimensional indicators need to be added in future work to optimize the model's accuracy. As a retrospective analysis, selection bias might be present. Subsequent prospective studies are needed to further refine and improve the model.

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