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Study on the Prognostic Prediction Model and Clinical Application Value of Machine Learning-based Approach for Septic Children in PICU

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Abstract: Objective: To explore the application value of a machine learning-based prediction model in assessing the prognosis of septic children in the pediatric intensive care unit (PICU) and provide data support for clinical decision-making. Methods: A total of 180 septic children admitted to the PICU of a tertiary hospital from January 2020 to December 2024 were selected. They were divided into a control group (90 cases, using traditional scoring methods to predict prognosis) and an observation group (90 cases, using a multivariable model based on machine learning algorithms to predict prognosis) according to the random number table method. General information, laboratory indicators, and clinical interventions were collected. Various models such as Random Forest (RF), Support Vector Machine (SVM), and Logistic Regression (LR) were established. The model performance was evaluated using ROC curve, AUC value, accuracy, sensitivity, and specificity. Results: The machine learning models performed better than traditional scoring methods in predicting the 28-day mortality rate of septic children. Among them, the RF model achieved an AUC value of 0.921, a sensitivity of 85.6%, and a specificity of 88.1%, which were significantly higher than the PIM3 score (AUC 0.762). The prediction accuracy and timeliness of clinical intervention in the observation group were significantly improved, leading to a shortened hospital stay and reduced mortality rate ($p < 0.05$). Conclusion: The prediction model based on machine learning can more accurately assess the prognostic risk of septic children in PICU, showing good clinical application prospects and providing references for individualized treatment and optimal resource allocation.

Keywords: Machine learning; Sepsis; PICU; Prognostic prediction; Clinical application

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1. Introduction

Sepsis is one of the common critical illnesses in pediatric intensive care units (PICU), and its core pathological mechanism involves systemic inflammatory responses and multiple organ dysfunction triggered by infection. In recent years, with the continuous improvement of anti-infection and organ support treatment, the fatality rate of septic children has decreased but still remains at a high level of 15–30%, posing a serious threat to children's lives and health. Clinically, accurate assessment of prognosis risk in children is crucial for developing individualized treatment plans, optimizing resource allocation, and improving the success rate of treatment. Currently used scoring systems such as PRISMIII and PIM3 can be used for risk stratification to some extent, but they rely on limited clinical indicators and cannot fully reflect the complex pathological process of sepsis, resulting in limited prediction accuracy and dynamic adaptability. With the rapid development of medical big data and artificial intelligence technology, machine learning is increasingly being applied in disease risk prediction. It can achieve precise assessment of disease prognosis by integrating multi-dimensional clinical features and identifying complex nonlinear relationships [1]. This study intends to construct a prognosis prediction model for septic children in PICU based on machine learning, compare it with traditional scoring systems, and explore its application value in clinical practice, hoping to provide a more scientific basis for early intervention and individualized treatment.

2. Materials and methods

2.1. General information

The subjects included in this study were septic children admitted to the PICU of a tertiary hospital from January 2020 to December 2024, totaling 180 cases.

2.1.1. Inclusion criteria

(1) All children met the diagnostic criteria of the "International Guidelines for the Management of Sepsis and Septic Shock" (Sepsis-3 pediatric version).
(2) The age range was from 1 month to 14 years old.
(3) Clinical medical records, laboratory tests, and imaging data were complete.

2.1.2. Exclusion criteria

(1) Patients with severe underlying diseases before admission, such as active malignant tumors, severe neurological or genetic metabolic diseases.
(2) Hospitalize less than 24 hours, unable to obtain complete follow-up and outcome data.
(3) Guardians refuse to sign the informed consent form.

Among the 180 children finally included, there were 102 males and 78 females, aged from 1 month to 14 years, with a median age of 6 years and an average age of (5.8 ± 3.2) years. According to the severity of the disease, there were 120 cases of sepsis and 60 cases of septic shock; 92 cases with lung infection, 54 cases with bloodstream infection, and the remaining 34 cases were urinary and abdominal infections. All children received routine anti-infection, fluid resuscitation, and organ support treatment. There was no statistically significant difference between the two groups (control group: 90 cases, observation group: 90 cases) in terms of gender, age, basic infection site, and disease severity distribution ($p > 0.05$), so they were comparable.

2.2. Method

Control group: 90 children were selected, and the traditional PIM3 (Pediatric Index of Mortality 3) scoring system was used to assess the prognosis risk. The scoring system mainly calculates the probability of death risk by recording variables such as blood pressure, heart rate, respiratory status, pupil reaction, mechanical ventilation status, and primary diagnosis at the time of PICU admission. Clinicians stratify risks based on scoring results and treat and follow up under routine diagnosis and treatment pathways. 90 children were selected, and a prognostic prediction model was established and validated using machine learning. The research process is as follows:

2.2.1. Variable collection and preprocessing

Collect clinical features within 24 hours of PICU admission, including general information (gender, age), vital signs (body temperature, heart rate, respiratory rate, mean arterial pressure), laboratory indicators (white blood cell count, blood lactate, C-reactive protein, procalcitonin, liver and kidney function, electrolytes), organ function status (respiratory support, circulatory support, whether combined with multiple organ dysfunction), etc., totaling more than 40 indicators. Missing values are processed using multiple imputation methods, and continuous variables are standardized.

2.2.2. Feature selection

Key variables that significantly impact prognosis are selected through univariate analysis and LASSO regression, reducing dimensionality redundancy and preserving the most predictive features.

2.2.3. Model construction

Three algorithms, Logistic Regression (LR), Support Vector Machine (SVM), and Random Forest (RF), are used to establish prognostic prediction models. LR is used to build a linear baseline model; SVM can handle complex non-linear boundary problems; RF improves prediction accuracy through the integration of multiple decision trees.

2.2.4. Model training and validation

The dataset is randomly divided into a training set and a validation set at a 7:3 ratio. Five-fold cross-validation is used for internal validation to prevent overfitting, and average performance metrics are calculated.

2.2.5. Performance evaluation

The model's performance is comprehensively evaluated using the Area Under the ROC Curve (AUC), accuracy, sensitivity, specificity, and F1 score, and compared with the PIM3 score.

2.2.6. Clinical application

The best model is embedded into an electronic health record system for simulation predictions, and its impact on clinical intervention timing, treatment decisions, and prognostic improvement is evaluated.

2.3. Observation indicators

2.3.1. Prediction model performance metrics

The model's discriminatory ability is evaluated using the Receiver Operating Characteristic (ROC) curve and Area Under the Curve (AUC). Sensitivity, specificity, accuracy, Positive Predictive Value (PPV), and Negative Predictive Value (NPV) are calculated to comprehensively reflect the diagnostic and predictive efficacy of each model under different thresholds. The DeLong test is used to compare differences in AUC between different models.

2.3.2. Clinical outcome indicators

28-day mortality rate: Death within 28 days of admission to the PICU is considered the primary outcome event.

(1) Length of hospital stay: The total number of days from admission to discharge from the PICU is recorded to evaluate the potential role of the model in reducing the length of hospital stay.
(2) Duration of mechanical ventilation: Record the duration of invasive or non-invasive mechanical ventilation, which reflects the impairment of respiratory function and the intensity of treatment intervention.

2.3.3. The auxiliary decision-making value of the model in clinical practice

Timing of intervention initiation: Record the average time for medical staff to initiate enhanced interventions such as vasopressors, blood purification, anti-infection upgrades after being prompted by the model, and compare it with the conventional clinical judgment of the control group.

Medical satisfaction was conducted by using a questionnaire survey with a maximum score of 100 to evaluate the recognition of medical staff on the model's assistance in clinical decision-making, improving work efficiency, and prognosis improvement. The options are divided into "very satisfied, satisfied, average, and dissatisfied."

2.4. Data processing

Statistical analysis was performed using SPSS 26.0 and Python 3.10. Measurement data were expressed as mean ± standard deviation, and comparisons between groups were made using the t-test. Counting data were analyzed using χ^2 test. The prediction performance of the models was compared by assessing differences in the area under the curve (AUC) using the DeLong test, with $p < 0.05$ considered statistically significant.

3. Results

3.1. Comparison of model prediction performance

In this study, three prediction models, including logistic regression (LR), support vector machine (SVM), and random forest (RF), were established and compared with the traditional PIM3 score. The results showed that the RF model performed best in predicting the 28-day mortality rate of septic children in the PICU, with an area under the ROC curve (AUC) of 0.921, which was better than SVM (0.884) and LR (0.842), and significantly higher than the traditional PIM3 score (0.762, $p < 0.05$). In terms of sensitivity and specificity, the RF model achieved 85.6% and 88.1%, respectively, which were significantly better than the PIM3 score (71.2% and 73.5%). The results suggest that machine learning models, especially the RF model, can provide higher accuracy and stability in prognosis prediction. (See **Table 1** and **Figure 1**)

Table 1. Comparison of the performance of different prediction models

Model	AUC	Sensitivity (%)	Specificity (%)	Accuracy (%)
PIM3 Score	0.762	71.2	73.5	72.3
LR Model	0.842	77.5	80.1	78.9
SVM Model	0.884	82.3	85.0	83.7
RF Model	0.921	85.6	88.1	86.9

Note: AUC = Area Under the Receiver Operating Characteristic Curve; LR = Logistic Regression; SVM = Support Vector Machine; RF = Random Forest. The DeLong test was used to compare the AUCs of the models, and there was a statistically significant difference between the RF model and the PIM3 score ($p < 0.05$).

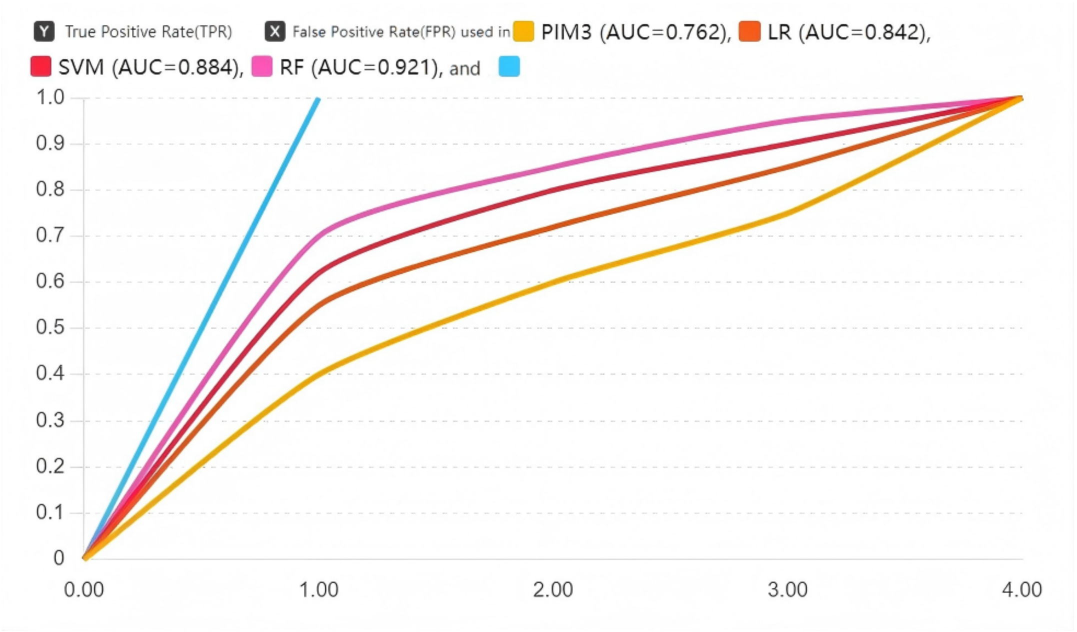

Figure 1. Comparison of ROC curves for different prediction models.

3.2. Clinical outcomes

In terms of clinical outcomes, the prognosis of the observation group was significantly better than that of the control group. The 28-day mortality rate in the observation group was 12.2%, which was significantly lower than the 21.1% in the control group ($p < 0.05$). The average length of hospital stay was (12.8 ± 4.2) days, which was significantly shorter than the (15.6 ± 4.7) days in the control group ($p < 0.05$). Additionally, the average time to initiate clinical intervention measures in the observation group was approximately 6 hours earlier than that in the control group, suggesting that the early warning function based on the machine learning model can effectively improve the timeliness of treatment. Meanwhile, the overall satisfaction of medical staff with the model-assisted decision-making reached 93.5%, which was significantly higher than the satisfaction level under the traditional scoring mode in the control group. The results indicate that the model has significant clinical value in reducing mortality, shortening hospital stay, and improving the efficiency of clinical intervention. (See **Table 2**)

Table 2. Comparison of clinical outcomes between the two groups of children

Indicator	Control group (n = 90)	Observation group (n = 90)	*p*-value
28-day Mortality Rate (%)	21.1	12.2	< 0.05
Hospital Stay (days, mean ± standard deviation (SD))	15.6 ± 4.7	12.8 ± 4.2	< 0.05
Intervention Initiation Time	Routine	Approximately 6 hours earlier	< 0.05
Healthcare Staff Satisfaction (%)	82.1	93.5	< 0.05

Note: Data are expressed as mean ± standard deviation or percentage; comparisons between the two groups were performed using the t-test or χ^2 test; all indicators in the observation group were better than those in the control group, and the differences were statistically significant ($p < 0.05$).

4. Discussion

4.1. Advantages of machine learning in prognosis prediction

The traditional PIM3 score relies on limited indicators and heavily emphasizes static variables at the time of admission, making it difficult to fully reflect the dynamic pathological process of sepsis. This study demonstrates that machine learning models such as RF, SVM, and LR outperform the PIM3 score in terms of prediction accuracy, sensitivity, and specificity. In particular, the RF model significantly improves predictive ability with an AUC of 0.921. Its advantages mainly lie in the ability to integrate multi-dimensional clinical data, including vital signs, laboratory indicators, and organ function, as well as handle complex nonlinear relationships between variables. Additionally, it provides a feature importance ranking function, which facilitates clinical understanding and interpretation. Therefore, machine learning methods are more suitable for clinical needs in early identification and risk stratification of sepsis [2].

4.2. Reasons for the superior performance of the RF model

Among various machine learning methods, Random Forest (RF) stands out for its exceptional performance. Its advantages are primarily reflected in the following aspects: Firstly, it reduces the bias and variance of a single model by integrating multiple decision trees, thereby enhancing the stability of the model. Secondly, it is less sensitive to outliers and missing values, making it more suitable for the clinical data environment. Thirdly, it can automatically evaluate the importance of variables, indicating which physiological indicators or laboratory parameters are closely related to prognosis, and thus providing direction for further research [3]. The results of this study show that lactate level, mean arterial pressure, and C-reactive protein are important features of the model, which is highly consistent with clinical experience and enhances the interpretability of the model.

4.3. Improvement in clinical outcomes

Research has found that after applying the machine learning model, the 28-day mortality rate of children in the observation group decreased to 12.2%, significantly lower than the 21.1% in the control group. The average hospital stay was reduced by about 3 days, suggesting that early intervention assisted by the model can improve disease progression and resource utilization efficiency. Meanwhile, the average time for clinical intervention initiation was advanced by about 6 hours, indicating that the model's early warning function has significant advantages in improving the timeliness of treatment. The satisfaction rate of medical staff with the model application is as high as 93.5%, reflecting the acceptability and practicality of this tool in clinical work. Thus, risk prediction based on machine learning not only improves prediction accuracy but also brings practical benefits at the clinical level.

4.4. Significance of the model in clinical practice

The introduction of machine learning models is helpful in promoting the development of precision medicine. It can serve as a decision-making tool for clinicians, assisting in early identification of high-risk children to allocate medical resources reasonably and optimize treatment strategies. Through continuous training and iteration, the model can adapt to different centers and population characteristics, thereby enhancing its generalization ability [4]. The visualization and explanatory analysis of model results can help medical staff understand risk factors and improve doctor-patient communication efficiency. In the complex and information-intensive environment of the PICU, the application of artificial intelligence technology can alleviate medical pressure and improve treatment efficiency.

4.5. Research limitations and prospects

Although the research results are encouraging, this study still has certain limitations. Firstly, the sample size of 180 cases is relatively limited, and further validation is needed in larger samples and multicenter data. Secondly, the data comes from a single hospital, which may introduce regional bias, and the universality of the model needs to be strengthened. Thirdly, this study mainly uses static data to construct the model without incorporating continuously monitored data. In the future, dynamic monitoring and time series modeling can be combined to improve the real-time performance and accuracy of prediction. Finally, although the RF model has good interpretability, some deep learning models may exhibit stronger performance in large sample data. Future research should explore the combination of deep neural networks and traditional machine learning methods [5].

5. Conclusion

Based on the above, machine learning-based prediction models demonstrate significant potential for more accurately assessing prognosis in pediatric sepsis patients within the PICU. These models hold considerable promise for clinical application by supporting individualized treatment strategies and optimizing resource allocation.

Disclosure statement

The author declares no conflict of interest.

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