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Research progress on the application of learning algorithms in risk assessment of ICU-acquired infections in the intensive care unite

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Abstract: ICU-acquired infections is a significant challenge for critically ill patients in the Intensive Care Unit (ICU), and the early identification of infections and timely clinical interventions are crucial for improving patient outcomes. With the increasing prevalence of artificial intelligence (AI), machine learning has been widely applied in clinical practice, including disease diagnosis and prognostic risk assessment. This review aims to systematically summarize the research progress on ICU-acquired infection risk prediction models based on machine learning, in order to provide valuable evidence for clinical practice and references for future related studies.

1. Introduction

ICU-acquired infections refer to infections that occur during a patient's stay in the Intensive Care Unit (ICU) or shortly after discharge. They are one of the leading causes of death among ICU patients[1]. Common types of ICU-acquired infections include ventilator-associated pneumonia, central venous catheter-related bloodstream infections, and catheter-associated urinary tract infections. In developing countries such as China, the incidence of these infections can be as high as 14.7% [2]. A global multicenter epidemiological study has shown that the mortality rate of ICU-acquired infections can reach 33.7% [3]. ICU-acquired infections not only increase the difficulty of treatment and the risk of death for patients but also lead to enhanced bacterial resistance, significantly prolonged hospital stays, and increased medical burden[4]. Therefore, early identification of high-risk patients for infections and timely clinical intervention are crucial for improving patient outcomes.

Clinical prediction models are important tools used in clinical practice for early diagnosis of diseases and risk assessment. Compared with traditional statistical methods for constructing prediction models, machine learning demonstrates significant advantages in handling non-linear relationships, improving model prediction accuracy, and automating feature selection[5]. For this reason, this article conducts a literature review to explore the current application and significance of machine learning in the prediction models of ICU-acquired infections.

2. Machine learning

Machine learning is one of the important branches of Artificial Intelligence (AI) and is the fundamental approach to endowing computers with intelligence[6]. In simple terms, machine learning enables computers to learn patterns from historical data through algorithms, thereby recognizing new data or predicting future events. In the medical field, machine learning is commonly used to address various diagnostic and prognostic issues related to diseases, such as disease prediction, prognostic assessment, extraction of medical knowledge, detection of data patterns, and patient management[7]. Common machine learning algorithms include Logistic Regression (LR), Decision Trees, Random Forest (RF), Support Vector Machines (SVM), K-Nearest Neighbor (KNN), Extreme Gradient Boosting (XGBoost), and Artificial Neural Networks (ANN), among others. Machine learning can be categorized by learning methods into supervised learning, unsupervised learning, semi-supervised learning, and reinforcement learning. Currently, most clinical prediction model studies both domestically and internationally focus primarily on supervised and unsupervised learning.

Supervised Learning aims to model the relationship between inputs and their corresponding known outputs[8], and it includes two types: classification and regression. Supervised learning classification involves using algorithms to accurately assign test data into specific categories. Classification algorithms are widely used in clinical practice, such as for disease diagnosis, disease risk prediction, patient risk stratification, and radiological diagnosis. Common examples include the automatic interpretation of electrocardiograms and the use of supervised learning algorithms in radiology to classify CT or MRI images to identify specific lesions or abnormalities[9]. Regression algorithms in supervised learning predict a continuous output value and are commonly used in scenarios such as calculating the risk of cardiovascular disease, predicting tumor size, and estimating patient survival time or length of hospital stay. In contrast, Unsupervised Learning aims to automatically identify the intrinsic structure and patterns in input data without explicit feedback[8]. Methods of unsupervised learning include clustering, dimensionality reduction, density estimation, and anomaly detection. Applications of unsupervised learning in the medical field include identifying patient subgroups through clustering analysis, simplifying datasets via dimensionality reduction, gene expression analysis, and medical image analysis, all of which provide powerful tools for medical research and clinical practice[10]. Currently, there are numerous machine learning prediction models for ICU-acquired infections both domestically and internationally. These models significantly enhance the precision of early diagnosis and risk prediction of infections by deeply mining patient data, including clinical features and laboratory test indicators.

3. The Application of Machine Learning in Predictive Models for ICU-Acquired Infections

3.1 Central Venous Catheter-Related Bloodstream Infections

Bloodstream infections are one of the most common types of ICU-acquired infections. A recent epidemiological study showed that the crude mortality rate of ICU-acquired bloodstream infections can be as high as 37.9%[11]. Among all bloodstream infections occurring in the ICU, 36.5% are central line-associated bloodstream infections (CLABSI). The occurrence of CLABSI is related to the site and duration of central venous catheter placement. In China, the CLABSI rate ranges from 2.75% to 6.30%, with an infection density of 4.0 to 9.8 cases per 1,000 catheter-days. Internationally, the infection density of CLABSI is reported to be 5.05 cases per 1,000 catheter-days[12-14]. Currently, there are several traditional clinical prediction models for CLABSI both domestically and internationally, while studies using machine learning algorithms to construct models are relatively few.

Parreco et al.[15] used ICU admission records from the MIMIC-III(Medical Information Mart for

Intensive Care III) database to construct a model for predicting CLABSI risk based on patients' Sequential Organ Failure Assessment (SOFA) scores and five other disease severity scores on the first day of ICU admission, combined with their comorbid conditions. The model employed various machine learning algorithms, including logistic regression, gradient boosting trees, and deep learning, to identify and predict high-risk populations for CLABSI among ICU patients. The results showed that logistic regression had the highest AUC value (0.722) in predicting CLABSI, but its sensitivity and negative predictive value were both 0%, indicating that the model failed to correctly predict any CLABSI cases. In contrast, gradient boosting trees performed best in terms of accuracy (97.6%), precision (7.1%), specificity (98.6%), and negative predictive value (98.6%), making it the preferred model for predicting CLABSI. Although the deep learning model had a lower AUC (0.642), it performed well in specificity (98.7%) with a false-positive rate of only 1.3%. This suggests that the deep learning model excels at identifying patients who are not infected, effectively reducing unnecessary interventions and treatments and avoiding overtreatment of healthy patients.

Compared with machine learning algorithms, traditional logistic regression remains the most commonly used method in the construction of CLABSI-related prediction models. In China, Shao Xiaoqing et al.[16] developed a logistic regression model for predicting the risk of CLABSI in ICU patients. Their multivariate logistic regression analysis showed that the use of antimicrobial agents, underlying disease type, catheter type, femoral vein puncture, and duration of catheter placement were independent risk factors for CLABSI in ICU patients ($P < 0.05$). The sensitivity of this prediction model was 82.05%, specificity was 69.25%, and the AUC of the model's ROC was 0.804. Wang Lihong et al.[17]constructed a logistic regression model for predicting central line-associated bloodstream infections, with an AUC value of 0.70 in the validation group. Internationally, Rahmani et al. developed and validated a machine learning model based on Electronic Health Record (EHR) data to predict the risk of CLABSI. The study used XGBoost, logistic regression, and decision trees, with the XGBoost model showing the best performance, achieving an AUROC value of 0.762 and effectively predicting the risk of CLABSI within 48 hours after central venous catheter placement. In contrast, the traditional logistic regression model had an AUC value of only 0.63.

Overall, machine learning-based models generally demonstrate higher prediction accuracy and stronger performance compared to traditional logistic regression models in the construction of CLABSI prediction models. Machine learning algorithms can effectively capture complex non-linear relationships and interactions between features in the data, thereby more accurately identifying high-risk patients and providing stronger support for clinical decision-making. However, the application of models based on other machine learning methods remains limited, and the number of related studies is still small, indicating that the application of machine learning in CLABSI prediction models is still in its early stages of exploration. Although existing studies suggest that machine learning models generally outperform traditional logistic regression models, this conclusion still needs to be further validated by more high-quality research.

3.2 Ventilator-associated pneumonia

Ventilator-associated pneumonia (VAP) is one of the common hospital-acquired infections in ICU, and it is associated with prolonged mechanical ventilation and extended ICU length of stay. The incidence of VAP in mechanically ventilated patients can be as high as 5%–40% [18], with an attributable mortality rate of approximately 10% [19]. Samadani et al.[20] developed a VAP risk index model using the XGBoost algorithm to predict the likelihood of VAP development within the next 24 hours among patients who have been mechanically ventilated for more than 48 hours. The significant features of this model include body temperature, heart rate, respiratory rate, oxygen saturation (SpO_2), fraction of inspired oxygen (FiO_2), positive end-expiratory pressure (PEEP), duration of mechanical ventilation, aspartate aminotransferase, alkaline phosphatase, hemoglobin count, and platelet count. The area under the receiver operating characteristic curve (AUC) of this model is 76%.

In a domestic study, Meng et al. [21] collected data from 363 VAP patients and corresponding controls. They used three machine learning methods—LASSO of VAP risk (pre-hospital mechanical ventilation duration, duration of mechanical ventilation, whether surgery was performed, tracheostomy, multidrug-resistant infection, C-reactive, protein arterial partial pressure of oxygen, and APACHE II score) and constructed a VAP risk prediction model. The model was subsequently validated in another group of independent cases and controls, with AUC values of 0.857 (training group) and 0.879 (validation group). Liang et al.[22] used the Medical Information Mart for Intensive Care III (MIMIC-III) dataset to build a random forest (RF) model aimed at predicting VAP occurrence 24 hours in advance in ICU patients. Compared with the Clinical Pulmonary Infection Score (CPIS)[23], the AUC of the machine learning model increased by nearly 25%, with sensitivity and specificity increasing by approximately 14% and 15%, respectively. Another study based on the MIMIC-III database[24] predicted the risk of VAP development in patients with traumatic brain injury who had been mechanically ventilated for more than 48 hours. Among various machine learning methods used, the Adaptive Boosting (AdaBoost) model was selected for its optimal performance (AUC = 0.706). In this AdaBoost model, tracheostomy, red blood cell count, prothrombin time, and Abbreviated Injury Scale for the face (AIS face) were identified as the top 10 most important predictors of VAP risk.

The above studies used different prediction windows when constructing VAP risk prediction models. The AdaBoost model and the VAP risk prediction model developed by Meng et al. did not specify a prediction window but focused on overall risk assessment. In contrast, the VAP risk index model developed by Samadani et al. focused on predicting the risk of VAP occurrence within the next 24 hours. This short-term prediction model can help clinicians take timely interventions at the early stage of VAP development, thereby reducing its impact on patients. The RF model developed by Liang et al. predicted the risk of VAP occurrence 24 hours later, providing clinicians with a relatively clear time frame to prepare and implement preventive measures. These different prediction windows reflect the varying emphases of researchers on early VAP prediction. Short-term risk-focused models (e.g., Samadani's 24-hour prediction model) can help clinicians quickly identify high-risk patients and intervene promptly, while broader prediction models (e.g., Meng's model) offer comprehensive risk assessment, which is beneficial for long-term prevention strategies. By combining these different models and methods, clinicians can more flexibly address the prevention and management of VAP.

3.3 Catheter-Associated Urinary Tract Infection

In intensive care units (ICUs), approximately 95% of urinary tract infections (UTIs) are caused by catheter-associated urinary tract infections (CAUTIs)[25]. The cumulative incidence rate of CAUTI is 4.1 cases per 1,000 catheter days in high-income countries and 8.8 cases per 1,000 catheter days in low-income countries[26]. CAUTI can lead to prolonged hospital stays, increased medical costs, and higher mortality rates. Currently, research on prediction models for CAUTI both domestically and internationally is primarily based on traditional logistic regression and nomograms, with relatively few studies employing machine learning algorithms.

In a single-center retrospective study, Liu et al.[27] developed two models—χ^2 Automatic Interaction Detection (CHAID) and Classification and Regression Tree (CRT)—to predict the risk of catheter-associated urinary tract infections in patients in neurosurgical intensive care units. The study identified nine risk factors associated with CAUTI, including age 60 years or older, Glasgow Coma Scale score of 8 or lower, epilepsy at admission, admission during the summer, use of a ventilator, receiving fewer than two antibiotics, albumin level below 35 g/L, female sex, and indwelling catheter for 7 to 14 days. The CRT model demonstrated excellent predictive ability, with an AUC value of 0.920. The study concluded that, compared with traditional models, the newly constructed machine learning (ML) model exhibited higher predictive accuracy (AUC value of 0.920) and was able to identify new risk factors such as epilepsy at admission and admission during the summer. This can help in the prevention and reduction of CAUTI risk in susceptible populations in clinical practice.

Liu Yuting et al.[28] developed a nomogram model based on machine learning algorithms using the eICU and MIMIC-IV databases to predict in-hospital mortality from CAUTI in critically ill patients, aiming to help identify early risks of death from CAUTI. The researchers employed five algorithms—logistic regression (LR), decision tree, random forest, k-nearest neighbor, and Bootstrap Aggregating (Bagging)—to build the models. Among them, the LR model demonstrated the best predictive value, with an AUC of 0.765 and accuracy of 0.906 in the external validation cohort. Compared with the nomogram prediction model for CAUTI risk in ICU patients based on traditional logistic regression developed by Tang Qiyin et al.[29] (with AUC values of 0.890 in internal validation and 0.781 in external validation), the machine learning model exhibited better predictive performance.

However, the complexity of machine learning models also poses challenges. Their interpretability and ease of use in clinical applications are relatively weaker, and additional tools (such as nomograms) may be needed to help clinicians understand and utilize them. In contrast, traditional logistic regression models, although slightly inferior in predictive performance, are simpler in structure, easier to understand and interpret, and more suitable for rapid clinical application.

4. Current Limitations and Future Directions

Compared with traditional prediction methods, machine learning has demonstrated remarkable performance in the diagnosis and prognosis of severe infections. However, the application of machine learning in this field still faces several limitations.

Firstly, critically ill patients in the ICU exhibit significant individual heterogeneity. Even in the construction of prediction models for the same type of infection, there are differences in the clinical features related to infection risk identified by different studies. For example, in studies on ventilator-associated pneumonia(VAP), features such as platelet count, prothrombin time, and multidrug-resistant infections have shown varying degrees of importance in different prediction models.

Secondly, some studies are based on single-center datasets, which leads to heterogeneity among studies and limits the generalizability of the models to different clinical settings. The performance of machine learning models is highly dependent on the quality of the data. In clinical practice, data collection is often affected by various factors and cannot always ensure high quality, leading to decreased prediction accuracy and reliability of the models. Moreover, most studies are limited to internal validation and lack external validation with multicenter, large-sample datasets. This restricts the models' applicability across different healthcare environments and patient populations. Some models may perform well in specific hospitals or patient groups but may not maintain the same performance in other settings.

Lastly, some complex machine learning models are often associated with the "black box" characteristic[8]. Although they can learn from large amounts of data and make accurate predictions, the opacity of their internal mechanisms makes them difficult to interpret, lacking transparency and explainability. This characteristic often limits their application in clinical practice.

In the face of these current challenges, existing machine learning algorithms can already self-learn and self-train from big data, reducing the proportion of heterogeneity caused by internal data factors. Looking forward, future work will focus on building multicenter collaborative networks to collect and integrate more diverse and high-quality datasets, reducing bias and enhancing the generalizability of models. Additionally, with the emergence of new interpretability algorithms such as SHAP, LIME

(Local Interpretable Model-agnostic Explanations), and Grad-CAM (Gradient-Weighted Class Activation Mapping)[30], the transparency and credibility of algorithms will be enhanced, promoting the application of machine learning in clinical settings. Moreover, the development of interdisciplinary collaboration and personalized medicine will also pave new ways for the widespread application of machine learning models in clinical practice, helping to achieve more precise and efficient medical services.

5. Conclusion

With the advent of the artificial intelligence era, machine learning has been widely applied in the research of clinical prediction models. Despite challenges in data heterogeneity and interpretability, machine learning models have demonstrated great potential in the diagnosis and prognosis of ICU-acquired infections, surpassing traditional statistical methods. Looking ahead, with the optimization of algorithms, expansion of datasets, and establishment of multicenter collaborative networks, we anticipate that machine learning models will be able to provide more accurate predictions tailored to the high heterogeneity of critically ill patients and play a more significant role in clinical decision-making.

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