Research Square

Preprints are preliminary reports that have not undergone peer review.
They should not be considered conclusive, used to inform clinical practice,
or referenced by the media as validated information.

Machine learning models for predicting multidrug-resistant organism infections after invasive procedures in intensive care unit patients: a retrospective study based on the MIMIC-IV database

Zhenwei Li
The Second Affiliated Hospital of Zhejiang University School of Medicine
Shengyi Yang
The Second Affiliated Hospital of Zhejiang University School of Medicine
Mengmeng Wang
The Second Affiliated Hospital of Zhejiang University School of Medicine
Changxian Wang
2321188@zju.edu.cn

The Second Affiliated Hospital of Zhejiang University School of Medicine

Research Article

Keywords: Device-associated infection, Multidrug-Resistant Organism, Machine learning, Risk factors

Posted Date: July 28th, 2026

DOI: https://doi.org/10.21203/rs.3.rs-10197215/v1

License: This work is licensed under a Creative Commons Attribution 4.0 International License.
Read Full License

Additional Declarations: No competing interests reported.

Abstract

Objective

This study aimed to develop and compare five machine learning models utilizing the MIMIC-IV database to identify key risk factors for multidrug-resistant organism (MDRO) infection in patients with invasive procedures.

Methods

A cohort of 23 281 patients was extracted from MIMIC-IV. Demographic, physiological, laboratory, and clinical variables were collected. The weighted calibration method was applied to address class imbalance. The dataset was randomly divided into training and testing subsets at an 7:3 ratio. Feature selection was performed using LASSO regression and feature importance scoring. Predictive models were constructed with Logistic Regression (LR), Random Forest (RF), Gradient Boosting Machine (GBM), Extreme Gradient Boosting (XGB), and Light Gradient Boosting Machine (LGB). Model performance was assessed via receiver operating characteristic (ROC) analysis. Calibration was evaluated using calibration curves and Brier scores, while clinical utility was examined through decision curve analysis (DCA). Model interpretability was enhanced using Shapley Additive Explanation (SHAP) values.

Results

Of the 23 281 patients, 1956 had invasive procedures associated MDRO infection and 21 325 had no invasive procedures associated MDRO infection. Significant differences were observed across multiple clinical parameters. XGB demonstrated the highest predictive performance, incorporating 15 features and achieving an AUC of 0.751 (95% CI: 0.728–0.773) on the test set. Calibration curves indicated good fit, supported by DCA confirming clinical usefulness. SHAP analysis highlighted the top influential features: the length of ICU stay, total antibiotic using hours, have CVC inserted, APS Ⅲ, age at ICU.

Conclusion

XGB emerged as the optimal predictor, which exhibited the strongest predictive performance for MDRO infections among patients undergoing invasive procedures, thereby equipping clinicians with a tool for early risk stratification and personalized treatment strategies

1 Introduction

Antimicrobial resistance (AMR) has emerged as one of the most pressing global public health challenges of the 21st century, with an estimated 4.71 million (95% UI 4.23–5.19) deaths associated with bacterial AMR, including 1.14 million (1.00–1.28) deaths directly attributable to it[1]. Projections

indicate that AMR-related mortality will increase by nearly 70% by 2050, resulting in over 39 million cumulative deaths if no effective interventions are implemented[2]. The economic impact is equally devastating, with global annual costs exceeding $887 billion in 2019, including $693 billion in hospital expenses and $194 billion in productivity losses[3]. Intensive care unit (ICU) represent the epicenter of this crisis, where MDRO infections account for 45.5% of all culture-positive bacterial infections[4]. Patients with MDRO infections face significantly higher mortality rates (38.8% vs. 27.9%) compared to those with susceptible infections, require almost twice as long ICU stays (30.0 days vs. 16.0 days), and experience significantly higher complication rates[4]. In China, the situation is particularly alarming, with ICU isolates of Acinetobacter baumannii showing carbapenem resistance rates exceeding 70% and overall MDRO prevalence reaching 48.33% in comprehensive ICUs[5].

Invasive medical procedures—such as invasive mechanical ventilation (IMV), central venous catheter (CVC), or indwelling urinary catheter (IUC) are indispensable in critical care but constitute the single most important modifiable risk factor for MDRO acquisition[6, 7]. A 2025 systematic review confirmed that most pneumonias, bloodstream infections, and urinary tract infections in ICUs are device-associated[8].Each additional day of central venous catheter placement increases bloodstream infection risk by 19% (adjusted OR: 1.19; 95% CI: 1.13–1.24), with MDRO responsible for over 45% of these catheter-related infections in endemic settings[9]. Despite these well-documented associations, critical knowledge gaps remain. Most studies have evaluated individual procedures in isolation rather than their combined effects, and few have developed comprehensive risk prediction models integrating clinical, biochemical, and procedural variables[10, 11], which strengthening the construction of early warning model of MDRO infection after invasive operation is one of the important measures to control and prevent MDRO infection.

Traditional multivariate logistic analysis has been widely employed to elucidate risk factors; however, it is constrained by its inability to model complex non-linear interactions[12]. Machine learning (ML) offers a robust alternative, utilizing algorithmic training to uncover latent structures in complex data, thereby revolutionizing prognostic predictions in clinical settings[6, 13]. Despite a growing trend in applying ML to forecast specific HAIs like ventilator-associated pneumonia (VAP), Central Line-Associated Bloodstream Infection (CLABSI), and Catheter-Associated Urinary Tract Infection (CAUTI)[14–16], a significant gap remains: current models typically address only isolated infection types. This narrow scope fails to account for the multifaceted risk profile of ICU patients, who are often subjected to numerous invasive interventions. Consequently, the development of integrative predictive models is critical. Such tools are essential not only for the prevention of device-related MDRO infections but also for improving the postoperative survival rates of critically ill patients.

This study aims to address the current research gaps by utilizing the extensive MIMIC-IV database. We identify the key factors that influence MDRO infection in ICU patients receiving invasive procedures through a series of steps, including data preprocessing, feature selection. These identified factors then serve as the foundation for constructing predictive models using multiple ML algorithms (LR, XGB, RF,

GBM and so on). Simultaneously, the SHAP method is used to interpret the models[17]. This integrated approach is expected to enhance clinical decision-making by providing an interpretable model to assist healthcare professionals in more effectively managing MDROs in the ICU.

2. Methods

2.1. Data source and study cohort

This retrospective study relies on the MIMIC-IV database[18], a collaboration between the Massachusetts Institute of Technology (MIT), Beth Israel Deaconess Medical Center (BIDMC), and Philips—a comprehensive repository of critical care information. Spanning 2008 to 2019, it encompasses records of 60 000 ICU patients across 28 tables, detailing demographics, transfers, vital signs, medical history, lab results, and other relevant data. Ethical approval from MIT and BIDMC ensures compliance and privacy protection through anonymization, eliminating the need for explicit consent[19]. The present study was granted access to the databases (Record ID: 74800814). The study follows Transparent Reporting of a Multivariable Prediction Model for Individual Prognosis or Diagnosis (TRIPOD) guidelines[20].

This study was designed as a retrospective cohort study, with data extracted using Structured Query Language (SQL). Invasive procedures were defined as the receipt of at least one invasive intervention during the index ICU stay, including IMV, CVC, and IUC. MDRO infection was diagnosed based on resistance to three or more classes of antimicrobial agents[21]. The identification process in the MIMIC-IV database required comprehensive assessment of the duration of invasive procedures, timing of microbiological testing, and antimicrobial susceptibility profiles. Patients aged ≥ 18 years who had undergone at least one invasive procedure in the MIMIC-IV database were eligible for inclusion. Exclusion criteria were non-first ICU admission, ICU length of stay of less than 24 hours, and lack of documentation for mechanical ventilation or microbiological examination. After applying these criteria, we identified a final study cohort consisting of 23 281 eligible patients, including 1 956 with invasive MDRO infections and 21 325 with invasive non-MDRO infections. A detailed patient selection flowchart is presented in Fig. 1.

2.2. Predictors and outcome

Based on established literatures[6, 22, 23] and data availability within MIMIC-IV, we curated a comprehensive feature set to predict MDROs infections in patients underwent invasive procedures. This set comprised 55 variables spanning seven categories: (1) demographic and administrative data (e.g., age, gender, length of stay); (2) pre-existing comorbidities (e.g., hypertension, obesity, COPD); (3) early physiological measurements (first 24h: TEMP, MAP, HR, RR); (4) initial laboratory findings (first 24h: covering hematology, coagulation, blood gas, chemistry, and liver/kidney function tests); (5) clinical interventions (CVC, indwelling urinary catheter, ventilator duration); (6) standardized illness severity

scores (SOFA, APS III, SAPS II); and (7) medication profiles (antibiotics). The primary endpoint was defined as the occurrence of MDROs infection after the invasive procedures during the ICU period.

2.3. Model development and tuning

For predictive modeling, we leveraged five algorithmic approaches implemented in R (V 4.6.0). Logistic Regression (LR), Random Forest (RF), Gradient Boosting Machine (GBM), Extreme Gradient Boosting (XGB), and Light Gradient Boosting Machine (LGB). LR served as a transparent, intrinsically interpretable baseline for binary outcomes. RF, an ensemble learning technique, offers robustness against overfitting and excels at identifying key predictors from high-dimensional clinical feature spaces[24, 25]. Conversely, GBM and XGB sequentially minimize residual errors, enabling them to capture the complex, non-linear interactions inherent in critical care data[26]. Notably, XGB is particularly well-suited for large-scale datasets like MIMIC-IV, facilitating enhanced prognostic accuracy and supporting clinical decision-making[27, 28]. Hyperparameter optimization for the selected models was rigorously conducted via grid search to refine performance.

2.4. Data preprocessing

Regarding feature-level integrity, the dataset comprised 19 categorical and 42 continuous variables. While categorical fields were complete, significant missingness (> 25%) was observed in key physiological indicators among the numerical set, specifically concerning bicarbonate, PaO_2_FiO_2_ratio, ALT, bilirubin, AST, PaO_2. At the sample level, six entries exhibited extensive data loss (> 25% of features) and were subsequently excluded. The residual missing values were imputed using the “missForest” algorithm in R, a random forest-based method, which successfully reconstructed the dataset to include 23 281 instances with 55 finalized features.

To handle the class imbalance, where non invasive procedures associated MDROs samples exceed MDROs samples by a factor of about 10 to 1, weighted calibration was applied to mitigate classification bias during model training. Specifically, higher sample weights were assigned to the minority class (infection-positive cases) according to the following ratio:

$$W_{pos} = \frac{N_{neg}}{N_{pos}}$$

where $N_{pos}$and N_{neg}denote the numbers of positive and negative samples in the training set, respectively.

By incorporating these weights into the loss function, the model optimization placed greater emphasis on correctly predicting minority-class events, thereby improving sensitivity and calibration without altering the original sample distribution. Compared with resampling-based approaches, weighted calibration reduces the risk of information loss and overfitting, making it well suited for high-dimensional clinical prediction modeling[29]. Finally, all features were rescaled to a 0 ~ 1 interval via min-max normalization utilizing the ‘scale’ function[30].

2.5. Model improvement and evaluation

The model training phase was followed by internal validation using a k-fold (k = 10) cross-validation framework[31], a methodological necessity to mitigate overfitting by cycling through different segments of the training data for validation and tuning. Performance was benchmarked against a suite of metrics: AUROC, confusion matrix, accuracy, recall, specificity, precision, and the F1 score[6]. Specifically, the 95% CI for the AUROC was derived via a bootstrap approach. Beyond discriminative ability, we assessed calibration and clinical impact. Calibration curves illustrated the alignment between predicted risks and actual event rates, complemented by the Brier Score for measuring probabilistic error[32]. Additionally, Decision Curve Analysis quantified the clinical value by analyzing the balance between true positives and false positives at various decision thresholds. The final step involved validating the optimized model on an independent test set to confirm its transportability and predictive power. The entire analytical pipeline adhered to established guidelines for reporting predictive models in medicine.

2.6. Feature selection

To refine the input variables, we adopted three distinct feature selection strategies. First, highly correlated features were identified using Spearman rank correlation coefficients ($|r| > 0.6$). Within each collinearity cluster, the variable with the higher univariable AUC was retained to minimize multicollinearity while preserving predictive information, yielding 38 features for downstream analysis. The correlation matrix heatmap was presented in Supplementary Material, Fig. S1. Second, both LASSO regression ($\alpha = 1$) and Elastic Net regression ($\alpha = 0.8$) were performed. Variable sets under both the λ.min and λ.1se criteria were considered to balance parsimony and information retention. Stability selection was further applied using 100 bootstrap resamples with a selection threshold of ≥ 0.5 to enhance robustness[33, 34]. The Lasso regression results, including the selected features, are shown in Supplementary Material, Fig. S2. Third, tree-based algorithms quantified feature importance, with XGB, GBM and Random Forest selecting the top 15 variables. The definitive feature set comprised the most influential predictors identified across these methodologies[6], the relevant process data are presented in Table S1.

2.7. Model interpretation and feature importance

To elucidate the predictive mechanisms of the optimal model, SHAP values were utilized. By quantifying the marginal contribution of each feature, SHAP analysis visualizes how specific inputs influence model outputs[35]. Using the “shapviz” package in R, we generated visualizations of these values, thereby clarifying the individual decision-making logic of the algorithm.

2.8 Statistical analysis

Patients underwent invasive procedures were divided into an "invasive MDROs group" and a "invasive non-MDROs group" based on whether MDRO infection occurred after the invasive procedures. Continuous variables conforming to a normal distribution are presented as means ± standard deviation

(SD), whereas skewed data are expressed as medians accompanied by interquartile ranges (IQR). Categorical variables are summarized as absolute frequencies and corresponding percentages. Comparative analyses between groups were performed utilizing Student's t-test, Wilcoxon rank-sum test, chi-square test, or Fisher's exact test, contingent upon data characteristics. A two-tailed P-value of ≤ 0.05 was designated as statistically significant. All computational procedures were executed using R software (V 4.6.0).

3. Results

3.1. Baseline characteristics

The study population comprised 23 281 patients extracted from the MIMIC-IV repository, who were subsequently allocated to either invasive non-MDRO infections arm (21 325 cases) or the invasive MDRO infections arm (1 956 cases) for further evaluation. Statistical analysis indicated that the groups were comparable regarding age medians (67.00 (55.00, 78.00) vs. 67.00 (54.00, 77.00), P= 0.079) and Liver disease ratio (3.4% vs. 3.6%, P= 0.716). However, notable heterogeneity was observed in specific comorbidities and laboratory parameters. Specifically, Cerebrovascular disease (P= 0.01), hypertension (P <0.001), and Lenth of ICU stays (P <0.001) demonstrated significant variability, alongside metrics such as heart rate, bilirubin, and white blood cell. Some of these variables are listed in Table 1, and the complete list of variables can be found in Supplementary Table 2.

Table 1 Characteristics of MDROs patients and Non-MDRO patients of the MIMIC-IV database.

Variable	Overall (n = 23281)	Non-MDRO patients (n = 21325)	MDROs patients (n = 1956)	p
Gender, n (%)				
F	10016 (43.0)	9076 (42.6)	940 (48.1)	<0.001
M	13265 (57.0)	12249 (57.4)	1016 (51.9)	
Age	67.00 [55.00, 78.00]	67.00 [55.00, 78.00]	67.00 [54.00, 77.00]	0.079
Comorbidities(%)				
Hypertension, n (%)				
No	17614 (75.7)	15973 (74.9)	1641 (83.9)	<0.001
Yes	5667 (24.3)	5352 (25.1)	315 (16.1)	
Diabetes, n (%)				
No	21082 (90.6)	19242 (90.2)	1840 (94.1)	<0.001
Yes	2199 (9.4)	2083 (9.8)	116 (5.9)	
COPD, n (%)				
No	21662 (93.0)	19813 (92.9)	1849 (94.5)	0.008
Yes	1619 (7.0)	1512 (7.1)	107 (5.5)	
Renal disease, n (%)				
No	21803 (93.7)	19944 (93.5)	1859 (95.0)	0.01
Yes	1478 (6.3)	1381 (6.5)	97 (5.0)	
Obesity, n (%)				
No	22482 (96.6)	20561 (96.4)	1921 (98.2)	<0.001
Yes	799 (3.4)	764 (3.6)	35 (1.8)	
Treatments and drugs				
Num procedure types	3.00 [2.00, 4.00]	3.00 [2.00, 4.00]	3.00 [2.00, 4.00]	<0.001
Total procedure hours	150.15 [78.50, 329.10]	142.08 [75.27, 290.42]	448.81 [160.96, 907.79]	<0.001
Num antibiotic classes	2.00 [1.00, 4.00]	2.00 [1.00, 3.00]	3.00 [1.00, 5.00]	<0.001
Total antibiotic hours	89.00 [15.00, 288.00]	80.00 [13.00, 260.00]	304.00 [72.00, 687.00]	<0.001

Lenth of ICU stays (day)	3.91 [2.73, 6.87]	3.76 [2.67, 6.22]	8.55 [4.40, 15.12]	<0.001
Has mechanical ventilation				
No	8942 (38.4)	8467 (39.7)	475 (24.3)	<0.001
Yes	14339 (61.6)	12858 (60.3)	1481 (75.7)	
Has CVC (%)				
No	10433 (44.8)	9948 (46.6)	485 (24.8)	<0.001
Yes	12848 (55.2)	11377 (53.4)	1471 (75.2)	
Has Foley n (%)				
No	15438 (66.3)	14192 (66.6)	1246 (63.7)	0.012
Yes	7843 (33.7)	7133 (33.4)	710 (36.3)	
Vital signs				
Resp_rate (breaths/min)	18.00 [15.00, 22.00]	18.00 [15.00, 22.00]	19.00 [15.00, 22.00]	0.003
Spo2 (%)	98.00 [96.00, 100.00]	98.00 [96.00, 100.00]	98.00 [95.00, 100.00]	0.703
HR_max (time/min)	102.00 [90.00, 117.00]	102.00 [90.00, 117.00]	105.00 [91.00, 121.00]	<0.001
HR_min (time/min)	69.00 [60.00, 80.00]	69.00 [60.00, 80.00]	70.00 [60.00, 82.00]	0.005
SBP_max (mmHg)	140.00 [124.00, 157.00]	140.00 [124.00, 157.00]	141.00 [125.00, 157.00]	0.349
SBP_min (mmHg)	93.00 [83.00, 106.00]	93.00 [83.00, 106.00]	93.00 [82.00, 106.00]	0.175
DBP (mmHg)	68.00 [57.00, 81.00]	68.00 [57.00, 81.00]	68.00 [56.00, 81.00]	0.995
MAP (mmHg)	85.00 [74.00, 98.00]	84.00 [74.00, 97.00]	86.00 [74.00, 99.00]	0.025
Laboratory results				
WBC (K/uL)	11.20 [8.10, 15.40]	11.20 [8.10, 15.40]	11.60 [8.45, 15.50]	0.029
Hemoglobin (g/dL)	10.70 [9.10, 12.40]	10.80 [9.10, 12.40]	10.70 [9.10, 12.30]	0.765
Platelet (K/uL)	91.00 [87.00, 95.00]	91.00 [87.00, 95.00]	91.00 [87.00, 96.00]	0.216

Creatinine (mg/dL)	1.00 [0.70, 1.40]	0.90 [0.70, 1.40]	1.00 [0.70, 1.50]	0.245
Bilirubin (mg/dL)	0.70 [0.40, 1.30]	0.70 [0.40, 1.30]	0.70 [0.40, 1.50]	0.009
Sodium (mEq/L)	139.00 [136.00, 141.00]	139.00 [136.00, 141.00]	139.00 [136.00, 142.00]	0.244
Potassium (mEq/L)	4.10 [3.70, 4.60]	4.10 [3.80, 4.60]	4.10 [3.70, 4.60]	0.009
Bicarbonate (mEq/L)	4.10 [3.70, 4.80]	4.10 [3.70, 4.80]	4.00 [3.60, 4.60]	<0.001
Lactate (mmol/L)	25.00 [22.00, 109.00]	26.00 [22.00, 113.00]	25.00 [21.00, 85.50]	<0.001
INR	1.30 [1.10, 1.50]	1.30 [1.10, 1.50]	1.30 [1.10, 1.60]	0.186
BUN (mg/dL)	18.00 [13.00, 30.00]	18.00 [13.00, 29.00]	19.00 [13.00, 32.00]	0.093
PT (s)	30.50 [26.90, 37.10]	30.50 [26.90, 37.00]	30.70 [26.80, 39.30]	0.104
APTT (s)	14.00 [12.40, 16.60]	14.00 [12.40, 16.60]	14.00 [12.40, 17.10]	0.142
Glucose (mg/dL)	161.00 [120.00, 258.00]	161.00 [119.00, 260.00]	164.00 [123.00, 243.00]	0.714
PaO2/FiO2	255.00 [152.50, 390.00]	255.00 [153.33, 390.00]	252.92 [146.82, 394.75]	0.785
Scores				
GCS	15.00 [15.00, 15.00]	15.00 [15.00, 15.00]	15.00 [15.00, 15.00]	0.972
SOFA	1.00 [0.00, 3.00]	1.00 [0.00, 3.00]	1.00 [0.00, 3.00]	0.342
APS □	42.00 [31.00, 57.00]	41.00 [31.00, 56.00]	47.00 [35.00, 63.00]	<0.001
SAPS □	37.00 [28.00, 46.00]	36.00 [28.00, 46.00]	39.00 [31.00, 47.00]	<0.001

Continuous variables were presented as the mean (standard deviation) for normally distributed data or as the median [interquartile range] for non-normally distributed data. Categorical variables were reported as the total number (percentages).

Abbreviations: COPD, chronic obstructive pulmonary disease; HR Heart rate; Bun, blood urea nitrogen; PT, prothrombin time; APTT, Activated Partial Thromboplastin Time; WBC: white blood cell, SBP, Systolic Blood Pressure; DBP, Diastolic Blood Pressure; MAP, mean arterial pressure; INR, international normalized ratio; PaO2/FiO2, ratio of partial pressure of oxygen to fraction of inspired oxygen; SOFA, Sequential Organ Failure Assessment; APSIII, Acute Physiology and Chronic Health Evaluation III; SAPSII, Simplified Acute Physiology Score II.

3.2. Model development and validation

We developed and validated five machine learning algorithms—LR, RF, XGB, GBM and LGB—on a dataset of 23 281 participants derived from the MIMIC-IV database. The data were stratified into an 70% training subset and a 30% internal validation subset. Evaluation on the independent test set revealed that XGB achieved the highest predictive accuracy, yielding an AUROC of 0.751 (95% CI: 0.728-0.773), compared to 0.722 for LR, 0.746 for RF, 0.748 for GBM and 0.738 for LGB (Fig. 2). Quantitative performance metrics are presented in Table 2. Calibration analysis (Fig. 3) demonstrated that GBM showing the closest alignment to the ideal line, the performance of the XGB model was second only to that of the GBM model, yet it remained highly competitive.

Consistently, Brier scores indicated low prediction error for XGB (0.186, 95% CI: 0.182-0.191). Decision curve analysis (Fig. 4) further validated the clinical utility of XGB, highlighting its potential to aid clinical decision-making more effectively than the comparator models.

Table 2 The comparative assessment of performance metrics for internal validation among five models

	AUROC (95% CI)	Accuracy (95% CI)	Sensitivity (95% CI)	Specificity (95% CI)	Brier (95% CI)	F1-score (95% CI)
LR	0.722 (0.699-0.745)	0.746 (0.734-0.756)	0.570 (0.529-0.611)	0.762 (0.750-0.771)	0.204 (0.20-0.208)	0.272 (0.249-0.295)
RF	0.746 (0.725-0.767)	0.802 (0.792-0.812)	0.528 (0.486-0.568)	0.827 (0.817-0.836)	0.152 (0.148-0.156)	0.308 (0.280-0.335)
GBM	0.748 (0.725-0.769)	0.548 (0.536-0.561)	0.811 (0.777-0.840)	0.524 (0.511-0.536)	0.194 (0.189-0.198)	0.231 (0.213-0.250)
XGB	0.751 (0.728-0.773)	0.555 (0.543-0.568)	0.813 (0.782-0.843)	0.532 (0.518-0.544)	0.186 (0.182-0.191)	0.234 (0.217-0.253)
LGB	0.738 (0.715-0.761)	0.799 (0.789-0.808)	0.494 (0.456-0.534)	0.827 (0.818-0.836)	0.139 (0.135-0.144)	0.291 (0.266-0.319)

Fig. 2. Receiver operating characteristic (ROC) curves of the five models. LR: logistic regression, RF: random forest, LGB: light gradient boosting Machine, GBM: gradient boosting machine, XGB: extreme gradient boosting

3.3. Interpretation of personalized predictions

SHAP analysis was employed to elucidate the individual predictions of the XGB model regarding invasive procedures associated MDROs onset. The analysis identified several key determinants, including the length of ICU stay, total antibiotic using hours, CVC, APS Ⅱ score, age. Secondary contributors encompassed biochemical parameters, such as hemoglobin, lactate, glucose. As illustrated in Fig. 5, the SHAP summary plot and variable importance ranking quantified the impact of these features. Specifically, prolonged ICU stay, have CVC inserted, higher total antibiotic using hours, elevated hemoglobin and glucose levels were positively correlated with an increased risk of invasive procedures associated MDROs infection.

Figure 6 illustrates the SHAP dependence plots for the top six continuous predictors identified by the XGB model, namely the length of ICU stay, total antibiotic hours, APS Ⅱ score, age at ICU, Hemoglobin count, and Maximum Systolic Blood Pressure in the first 24 hours. Following data transformation, the x-axes represent the transformed feature values.

The plots reveal distinct relationships between feature values and model output. Figures 6A-D demonstrate a positive correlation for the length of ICU stay, total antibiotic hours, APS Ⅱ score, and age at ICU, with respective inflection points at 4.90, 401.2, 38.0 and 62; values exceeding these thresholds correspond to a marked increase in MDROs infection risk after invasive procedures. Conversely, Fig. 6E indicate that higher Hemoglobin count exert a negative effect on the SHAP value (i.e., reducing risk) as they increase. Fig. 6F highlights a non-linear effect of the Maximum Systolic Blood Pressure in the first 24 hours, where values around 132.7 exert a positive influence, while deviations outside this interval negatively impact the prediction.

To translate these global patterns into individualized interpretations, waterfall plots (Fig. 7A–D) deconstruct specific predictions. For instance, Fig. 7A and 7C depict a case predicted to invasive procedures associated MDROs (actual outcome: infected). Here, elevated prolonged ICU stay and elevated antibiotic hours drove the SHAP value upward to 1.95, signaling high risk. In contrast, Fig. 7B and 7D show an invasive procedures non-MDROs case where lower APS Ⅱ score, reduced total antibiotic using hours and shorter ICU stay resulted in a substantially negative SHAP value (−3.18), correctly predicting the absence of infection.

Force plots (Fig. 7C and 7D) further visualize the contribution of each feature, with yellow and purple bars denoting risk and protective factors, respectively. These visualizations provide granular insights into individual risk profiles, facilitating the clinical translation of the model.

4. Discussion

In this investigation, an interpretable predictive framework was established to stratify the risk of MDRO infections among patients with invasive procedures. By leveraging SHAP values, we elucidated the underlying mechanisms of the model and delineated pivotal predictors. Our findings underscore that the length of ICU stay, total antibiotic using hours, have CVC inserted, APS Ⅱ, age at ICU are critically associated with MDRO infections in ICU invasive procedures cohorts.

The imperative for timely detection and risk stratification of MDRO infections in patients of ICU is self-evident, given its important role in shaping therapeutic efficacy and clinical trajectories[36]. Proactive identification of high-risk cohorts facilitates the implementation of precision-guided interventions, which not only augments recovery rates but also alleviates the strain on healthcare infrastructure. In the context of escalating antimicrobial resistance within ICU, the deployment of robust predictive models is indispensable for refining clinical judgment and optimizing patient management strategies[37].

Aligning with evidence from prior studies[38, 39], the present analysis confirms that the prolonged length of ICU stay serves as both a robust predictor and an actionable risk factor for MDRO infections in individuals after invasive procedures. This is driven by cumulative exposure to MDR-enriched environments, sustained antimicrobial selective pressure favoring resistant strain dominance, extended invasive procedures disrupting host barriers, progressive gut microbiota dysbiosis promoting MDR colonization, declining immune competence, and elevated cross-transmission risks between patients and healthcare personnel[40, 41]. The acquisition of intestinal MDROs is common in the ICU and increases with the length of ICU stay, a trend that persists throughout the 30-day follow-up period[42].A systematic review and meta-analysis by Frondelius et al.[43] demonstrated that machine learning models exhibit remarkable performance in predicting early VAP, and the authors identified duration of mechanical ventilation and ICU length of stay as pivotal predictors of VAP—findings that corroborate our own results, wherein prolonged ICU stay emerged as a core risk factor for MDRO infections after invasive procedures.

The procedures of CVC are widely used in the hospital setting. However, the implantation of these devices is often accompanied by complications. CVC is one of the strongest independent risk factors for multidrug-resistant Pseudomonas aeruginosa (MDR-PA) infection in ICU patients (OR=3.16, 95%CI: 1.87-5.33)[44]. Invasive devices provide a direct pathway for multidrug-resistant pathogens to enter the bloodstream by disrupting the body's natural defense barriers, while biofilms formed on the surface of catheters offer an ideal environment for the colonization and proliferation of drug-resistant bacteria. Biofilm formation is a critical step for the persistence and progression of CRBSI into MDR infections. Once the biofilm matures, it is difficult to completely eliminate even with high-dose antibiotics[45]. Research by Du et al.[22, 46] demonstrated that invasive procedures, particularly CVC, constitute both a risk factor for MDR infections and a predictor of poor prognosis in ICU patients, which is consistent with the results of our own study.

Biochemical abnormalities, particularly anemia and poor glycemic control, act as significant independent risk factors that synergize with invasive procedures to substantially elevate MDRO infection risk in ICU patients[47]. Anemia (hemoglobin <10.0 g/dL) has been consistently associated with a 2.17-fold increased odds of MDR infection in critically ill patients, with each 1 g/dL decrease in hemoglobin corresponding to a 1% incremental risk[48]. This relationship is mediated by impaired oxygen delivery to tissues and compromised immune cell function, which diminish host defense against bacterial invasion through disrupted barriers from central venous catheters, mechanical ventilation, and other invasive devices. Concurrently, poor glycemic control (random glucose >11.1 mmol/L) significantly increases

MDR infection rates, particularly carbapenem-resistant Klebsiella pneumoniae infections in patients with deep venous catheters (78.0% vs 61.3% in well-controlled patients)[49]. Hyperglycemia directly inhibits neutrophil phagocytosis, enhances bacterial capsule synthesis, and promotes biofilm formation on catheter surfaces. When combined with low albumin levels and multiple invasive procedures, these biochemical abnormalities create a high-risk phenotype for MDR acquisition, with predictive models incorporating these factors achieving AUC values of 0.75 for identifying at-risk patients[48]. These findings underscore the importance of correcting anemia and optimizing glycemic control as integral components of comprehensive MDR infection prevention strategies in the ICU setting.

In an effort to facilitate the early detection of MDRO infection in invasive procedure cohorts, this investigation conducted a comparative analysis of conventional and ensemble modeling techniques (LR, XGB, RF, GBM, LGB). Superiority was observed for the XGB algorithm, which attained an AUC of 75.1%, highlighting its proficiency in capturing intricate data patterns and maintaining stability across varied scenarios[50]. These results resonate with contemporary literature validating XGB's efficacy in forecasting MDR infection[51]. The study highlighted the importance of key features, such as the presence of antibiotics and the score of APS Ⅲ, which were also pivotal in our model’s prediction of MDROs infection risk.

Leveraging the SHAP methodology, we deciphered the model’s decision process, thereby providing interpretable evidence to support MDRO risk evaluation in patients underwent invasive procedures. Further studies substantiate that SHAP not only deconstructs feature importance but also bolsters clinical credibility through visualization[43]. This emphasizes the translational value of SHAP, enabling the safe and effective deployment of advanced machine learning models in high-risk clinical environments characterized by complex infections

4.1. Limitations

Several limitations warrant consideration in the present study. First, although the MIMIC database provides a rich repository of critical care data widely utilized in ML research, its generalizability is constrained by its single-center origin, contrasting with multi-center resources. Furthermore, the demographic composition—particularly regarding race—is skewed, limiting the extrapolation of our findings to underrepresented populations, such as Asians. Second, the scarcity of external validation cohorts impedes a robust assessment of the model’s transportability. Third, the low prevalence of device-associated MDR infections (8.40%) induced a significant class imbalance. Consequently, while the model achieved an AUC of 0.751, the modest AUPRC of 0.226 suggests a limited capability of the XGB algorithm in capturing true positive cases, necessitating cautious interpretation of its clinical utility. Finally, the model is confined to predicting MDRO infection for ICU patients post-invasive procedures and cannot be extrapolated to non-ICU settings or different surgical contexts. Future endeavors will prioritize multicenter external validation and incorporate additional clinically relevant variables to rigorously assess the model’s robustness and predictive efficacy.

5. Conclusion

Among five constructed ML models, XGB demonstrated the highest predictive efficacy in identifying high-risk ICU patients underwent invasive procedures. SHAP analysis identified the length of ICU stay, total antibiotic using hours, have CVC inserted, APS □, age at ICU, Hemoglobin count as critical drivers of MDRO infection risk. The integration of these factors allows for precise risk stratification, furnishing a dependable tool for early infection control and intervention. This framework supports precision medicine initiatives, meanwhile, the real-world utility and robustness of this integrated model necessitate rigorous prospective validation in future multicenter investigations.

Abbreviations

MDRO: Multidrug-Resistant Organism

LR: Logistic Regression

RF: Random Forest

GBM : Gradient Boosting Machine

XGB: Extreme Gradient Boosting

LGB: Light Gradient Boosting Machine

ROC: receiver operating characteristic

DCA: decision curve analysis

SHAP: Shapley Additive Explanation

AMR: Antimicrobial resistance

IMV: invasive mechanical ventilation

CVC: central venous catheter

IUC: indwelling urinary catheter

VAP: ventilator-associated pneumonia

CLABSI: Central Line-Associated Bloodstream Infection

CAUTI: Catheter-Associated Urinary Tract Infection

COPD: chronic obstructive pulmonary disease

HR: Heart rate

Bun: blood urea nitrogen

PT: prothrombin time

APTT: Activated Partial Thromboplastin Time

WBC: white blood cell

SBP: Systolic Blood Pressure

DBP: Diastolic Blood Pressure

MAP: mean arterial pressure

INR: international normalized ratio

SOFA: Sequential Organ Failure Assessment

APSIII: Acute Physiology and Chronic Health Evaluation III

SAPSII: Simplified Acute Physiology Score II

Declarations

Ethics approval and consent to participate

The experimental protocol was reviewed and granted ethical approval by the Institutional Review Boards at both Beth Israel Deaconess Medical Center (BIDMC) and the Massachusetts Institute of Technology (MIT). In accordance with prevailing national laws and institutional policies, the requirement for obtaining documented informed consent from participants was formally waived.

Consent for publication

Not applicable.

Availability of data and materials

Publicly available datasets were analyzed in this study. This data can be found here: https://mimic.mit.edu/.

Competing interests

The authors declare no competing interests.

Funding

Not applicable.

Authors' Contributions

Zhenwei Li: Conceived and designed the study, analyzed and interpreted the data, drafted the manuscript. Shengyi Yang and Mengmeng Wang: Provided technical guidance on machine learning model development and data analysis, revised the manuscript critically. Changxian Wang and Zhenwei Li: Co-supervised the study, designed the overall research framework, revised the manuscript critically for important intellectual content. All authors have read and agreed to the published version of the manuscript.

Acknowledgments

None.

Additional information

Appendix

References

1. Global burden of bacterial antimicrobial resistance 1990-2021: a systematic analysis with forecasts to 2050[J]. Lancet (London, England),2024,404(10459):1199-1226. 10.1016/s0140-6736(24)01867-1.
2. The Lancet: More than 39 million deaths from antibiotic-resistant infections estimated between now and 2050, suggests first global analysis [EB/OL]. September 16, 2024.). https://www.healthdata.org/news-events/newsroom/news-releases/lancet-more-39-million-deaths-antibiotic-resistant-infections.
3. Naylor N. R., Hasso-Agopsowicz M., Kim C., et al. The global economic burden of antibiotic-resistant infections and the potential impact of bacterial vaccines: a modelling study[J]. BMJ global health,2025,10(6). 10.1136/bmjgh-2024-016249.
4. Cornistein W., Balasini C., Nuccetelli Y., et al. Prevalence and mortality associated with multidrug-resistant infections in adult intensive care units in Argentina (PREV-AR)[J]. Antimicrobial agents and chemotherapy,2025,69(3):e0142624. 10.1128/aac.01426-24.
5. YAO Chenghong, LI Shuhua, ZHANG Xiaoliang, et al. Research progress on risk factors as well as prevention and control of multidrug-resistant organism infection in intensive care unit[J]. Chin J Infect Control,2026,25(2):310 -317.
6. Cui Z., Dong Y., Yang H., et al. Machine learning prediction models for multidrug-resistant organism infections in ICU ventilator-associated pneumonia patients: Analysis using the MIMIC-IV database[J]. Computers in biology and medicine,2025,190:110028. 10.1016/j.compbiomed.2025.110028.

7. Diao H., Lu G., Zhang Y., et al. Risk factors for multidrug-resistant and extensively drug-resistant Acinetobacter baumannii infection of patients admitted in intensive care unit: a systematic review and meta-analysis[J]. The Journal of hospital infection,2024,149:77-87. 10.1016/j.jhin.2024.04.013.
8. Odoom A., Donkor E. S. Prevalence of Healthcare-Acquired Infections Among Adults in Intensive Care Units: A Systematic Review and Meta-Analysis[J]. Health science reports,2025,8(7):e70939. 10.1002/hsr2.70939.
9. Dalmanoğlu E., Özhan MÖ, Atik B., et al. Catheter Duration Threshold and Risk Factors for Central Line-Associated Bloodstream Infections in a Tertiary ICU with Endemic Carbapenem Resistance: A Case-Control Study[J]. Antibiotics (Basel, Switzerland),2026,15(4). 10.3390/antibiotics15040407.
10. Yang L., Lu G., Diao H., et al. Predicting infections with multidrug-resistant organisms (MDROs) in neurocritical care patients with hospital-acquired pneumonia (HAP): development of a novel multivariate prediction model[J]. Microbiology spectrum,2025,13(6):e0246024. 10.1128/spectrum.02460-24.
11. Gu G., Ji Y., Xiong X., et al. Explainable Machine Learning Integrating Patient and Environmental Factors for Predicting Multidrug-Resistant Organism Colonization or Infection on ICU Admission[J]. Infection and drug resistance,2026,19:581390. 10.2147/idr.S581390.
12. Minami T., Sato M., Toyoda H., et al. Machine learning for individualized prediction of hepatocellular carcinoma development after the eradication of hepatitis C virus with antivirals[J]. Journal of hepatology,2023. 10.1016/j.jhep.2023.05.042.
13. Zhu Y., Zhang J., Wang G., et al. Machine Learning Prediction Models for Mechanically Ventilated Patients: Analyses of the MIMIC-III Database[J]. Frontiers in medicine,2021,8:662340. 10.3389/fmed.2021.662340.
14. Li J., Li G., Liu Z., et al. External validation and application of risk prediction model for ventilator-associated pneumonia in ICU patients with mechanical ventilation: A prospective cohort study[J]. International journal of medical informatics,2025,199:105910. 10.1016/j.ijmedinf.2025.105910.
15. Yang J., Li G., Chen S., et al. Machine Learning-Assistant Colorimetric Sensor Arrays for Intelligent and Rapid Diagnosis of Urinary Tract Infection[J]. ACS sensors,2024,9(4):1945-1956. 10.1021/acssensors.3c02687.
16. Zhang Y., Wu Y., Gao H., et al. Machine Learning-Based Prediction of Central Line-Associated Bloodstream Infection in Children with Acute Leukemia[J]. The Journal of hospital infection,2026. 10.1016/j.jhin.2026.05.016.
17. Lundberg S. M., Erion G., Chen H., et al. From Local Explanations to Global Understanding with Explainable AI for Trees[J]. Nature machine intelligence,2020,2(1):56-67. 10.1038/s42256-019-0138-9.
18. Wu W. T., Li Y. J., Feng A. Z., et al. Data mining in clinical big data: the frequently used databases, steps, and methodological models[J]. Military Medical Research,2021,8(1):44. 10.1186/s40779-021-00338-z.

19. Johnson A. E., Pollard T. J., Shen L., et al. MIMIC-III, a freely accessible critical care database[J]. Scientific data,2016,3:160035. 10.1038/sdata.2016.35.
20. Moons K. G., Altman D. G., Reitsma J. B., et al. Transparent Reporting of a multivariable prediction model for Individual Prognosis or Diagnosis (TRIPOD): explanation and elaboration[J]. Annals of internal medicine,2015,162(1):W1-73. 10.7326/m14-0698.
21. Di Lodovico Silvia, Fasciana Teresa, Di Giulio Mara, et al. Spread of Multidrug-Resistant Microorganisms[J]. 2022,11(7):832.
22. Du F., Ji Q., Li Y., et al. Analysis of the etiological characteristics of multidrug-resistant organisms and prognostic factors in ICU patients[J]. Frontiers in physiology,2025,16:1658683. 10.3389/fphys.2025.1658683.
23. Hernández-Tejero M., Pavesi M., Aziz F., et al. Multidrug-resistant colonization in decompensated cirrhosis outside the ICU predicts infection and poor outcomes[J]. JHEP reports : innovation in hepatology,2026,8(3):101707. 10.1016/j.jhepr.2025.101707.
24. Beltrán J. C., Fernández-Sarmiento J., Orjuela-Cañón A. D., et al. Microvascular phenotypes in pediatric sepsis identified by machine learning: prognostic implications for organ dysfunction and mortality[J]. Critical care (London, England),2026,30(1):61. 10.1186/s13054-025-05785-x.
25. Mi T., Li X., Fang Q., et al. Machine learning models for predicting severe acute kidney injury in patients with sepsis-induced myocardial injury[J]. Scientific reports,2025,15(1):19563. 10.1038/s41598-025-04579-z.
26. Jiang W., Zhang Y., Weng J., et al. Explainable Machine Learning Model for Predicting Persistent Sepsis-Associated Acute Kidney Injury: Development and Validation Study[J]. Journal of medical Internet research,2025,27:e62932. 10.2196/62932.
27. Huang J., Chen H., Deng J., et al. Interpretable machine learning for predicting 28-day all-cause in-hospital mortality for hypertensive ischemic or hemorrhagic stroke patients in the ICU: a multi-center retrospective cohort study with internal and external cross-validation[J]. Frontiers in neurology,2023,14:1185447. 10.3389/fneur.2023.1185447.
28. Song B., Jiang G., Liu Y., et al. A clinical prediction model for central venous catheter-associated bloodstream infections: derivation and validation from the MIMIC-IV cohort[J]. European journal of medical research,2026,31(1):213. 10.1186/s40001-025-03817-4.
29. Luo G., He S., Stone B. L., et al. Developing a Model to Predict Hospital Encounters for Asthma in Asthmatic Patients: Secondary Analysis[J]. JMIR medical informatics,2020,8(1):e16080. 10.2196/16080.
30. Ferrão J. C., Oliveira M. D., Janela F., et al. Preprocessing structured clinical data for predictive modeling and decision support. A roadmap to tackle the challenges[J]. Applied clinical informatics,2016,7(4):1135-1153. 10.4338/aci-2016-03-soa-0035.
31. Kang X., Li T., Chen Q., et al. Construction and validation of a prediction model for developing type 2 diabetes mellitus in patients with chronic obstructive pulmonary disease[J]. Frontiers in endocrinology,2025,16:1560631. 10.3389/fendo.2025.1560631.

32. Strandberg R., Åberg F., Asteljoki J. V., et al. Use of new CORE risk score to predict 10 year risk of liver cirrhosis in general population: population based cohort study[J]. BMJ (Clinical research ed),2025,390:e083182. 10.1136/bmj-2024-083182.
33. Meinshausen Nicolai, Bühlmann Peter. Stability Selection[J]. Journal of the Royal Statistical Society Series B: Statistical Methodology,2010,72(4):417-473. 10.1111/j.1467-9868.2010.00740.x %J Journal of the Royal Statistical Society Series B: Statistical Methodology.
34. Yin Q. Y., Li J. L., Zhang C. X. Ensembling Variable Selectors by Stability Selection for the Cox Model[J]. Computational intelligence and neuroscience,2017,2017:2747431. 10.1155/2017/2747431.
35. Hu M., Zhang H., Wu B., et al. Interpretable predictive model for shield attitude control performance based on XGboost and SHAP[J]. Scientific reports,2022,12(1):18226. 10.1038/s41598-022-22948-w.
36. Závora J., Adámková V., Studená A., et al. The Role of Routine Surveillance Cultures in Optimising Sepsis Management in High-Risk Patient Groups[J]. Pathogens (Basel, Switzerland),2026,15(1). 10.3390/pathogens15010082.
37. Sirichayanugul T., Srisawat C., Thummakomut C., et al. Development and internal validation of simplified predictive scoring (ICU-SEPSA score) for mortality in patients with multidrug resistant infection[J]. Frontiers in pharmacology,2022,13:938028. 10.3389/fphar.2022.938028.
38. Ye Q., Chen X., Zhang J., et al. Meta-analysis of risk factors for infection by multi-drug-resistant organisms in intensive care unit patients[J]. The Journal of hospital infection,2025,158:1-10. 10.1016/j.jhin.2025.01.015.
39. Hatzianastasiou S., Vlachos P., Stravopodis G., et al. Incidence, risk factors and clinical outcome of multidrug-resistant organisms after heart transplantation[J]. World journal of transplantation,2024,14(2):93567. 10.5500/wjt.v14.i2.93567.
40. Climo M. W., Yokoe D. S., Warren D. K., et al. Effect of daily chlorhexidine bathing on hospital-acquired infection[J]. The New England journal of medicine,2013,368(6):533-542. 10.1056/NEJMoa1113849.
41. Martin-Mateos R., Martínez-Arenas L., Carvalho-Gomes Á, et al. Multidrug-resistant bacterial infections after liver transplantation: Prevalence, impact, and risk factors[J]. Journal of hepatology,2024,80(6):904-912. 10.1016/j.jhep.2024.02.023.
42. Heath M. R., Fan W., Leu C. S., et al. Gut colonization with multidrug resistant organisms in the intensive care unit: a systematic review and meta-analysis[J]. Critical care (London, England),2024,28(1):211. 10.1186/s13054-024-04999-9.
43. Frondelius T., Atkova I., Miettunen J., et al. Early prediction of ventilator-associated pneumonia with machine learning models: A systematic review and meta-analysis of prediction model performance(□)[J]. European journal of internal medicine,2024,121:76-87. 10.1016/j.ejim.2023.11.009.
44. Eyebe S., Wafeu G. S., Mbamyah E. L., et al. Risk factors for colonisation and infection with multidrug-resistant Pseudomonas aeruginosa in intensive care unit: a systematic review and meta-

analysis[J]. Systematic reviews,2026. 10.1186/s13643-025-02975-0.

45. O'Grady N. P. Prevention of Central Line-Associated Bloodstream Infections[J]. The New England journal of medicine,2023,389(12):1121-1131. 10.1056/NEJMra2213296.
46. Pitiriga V., Bakalis J., Theodoridou K., et al. Comparison of microbial colonization rates between central venous catheters and peripherally inserted central catheters[J]. Antimicrobial resistance and infection control,2023,12(1):74. 10.1186/s13756-023-01285-1.
47. Maia M. O., da Silveira C. D. G., Gomes M., et al. Multidrug-Resistant Bacteria on Critically Ill Patients with Sepsis at Hospital Admission: Risk Factors and Effects on Hospital Mortality[J]. Infection and drug resistance,2023,16:1693-1704. 10.2147/idr.S401754.
48. Wu C., Lu J., Ruan L., et al. Tracking Epidemiological Characteristics and Risk Factors of Multi-Drug Resistant Bacteria in Intensive Care Units[J]. Infection and drug resistance,2023,16:1499-1509. 10.2147/idr.S386311.
49. Wang Q., Yan T., Ma C., et al. Poor Glycemic Control in Carbapenem-Resistant Klebsiella pneumoniae Infections: Impact on Epidemiological Features, Mortality Risks, and Polymyxin Resistance[J]. Infection and drug resistance,2025,18:647-660. 10.2147/idr.S501632.
50. Noorunnahar M., Chowdhury A. H., Mila F. A. A tree based eXtreme Gradient Boosting (XGBoost) machine learning model to forecast the annual rice production in Bangladesh[J]. PloS one,2023,18(3):e0283452. 10.1371/journal.pone.0283452.
51. Pan Q., Zhou X., Zhang B., et al. Interpretable machine learning for early detection of carbapenem-resistant Klebsiella pneumoniae in ICUs: risk prediction using LASSO and XGBoost[J]. Frontiers in public health,2026,14:1798927. 10.3389/fpubh.2026.1798927.

Figures

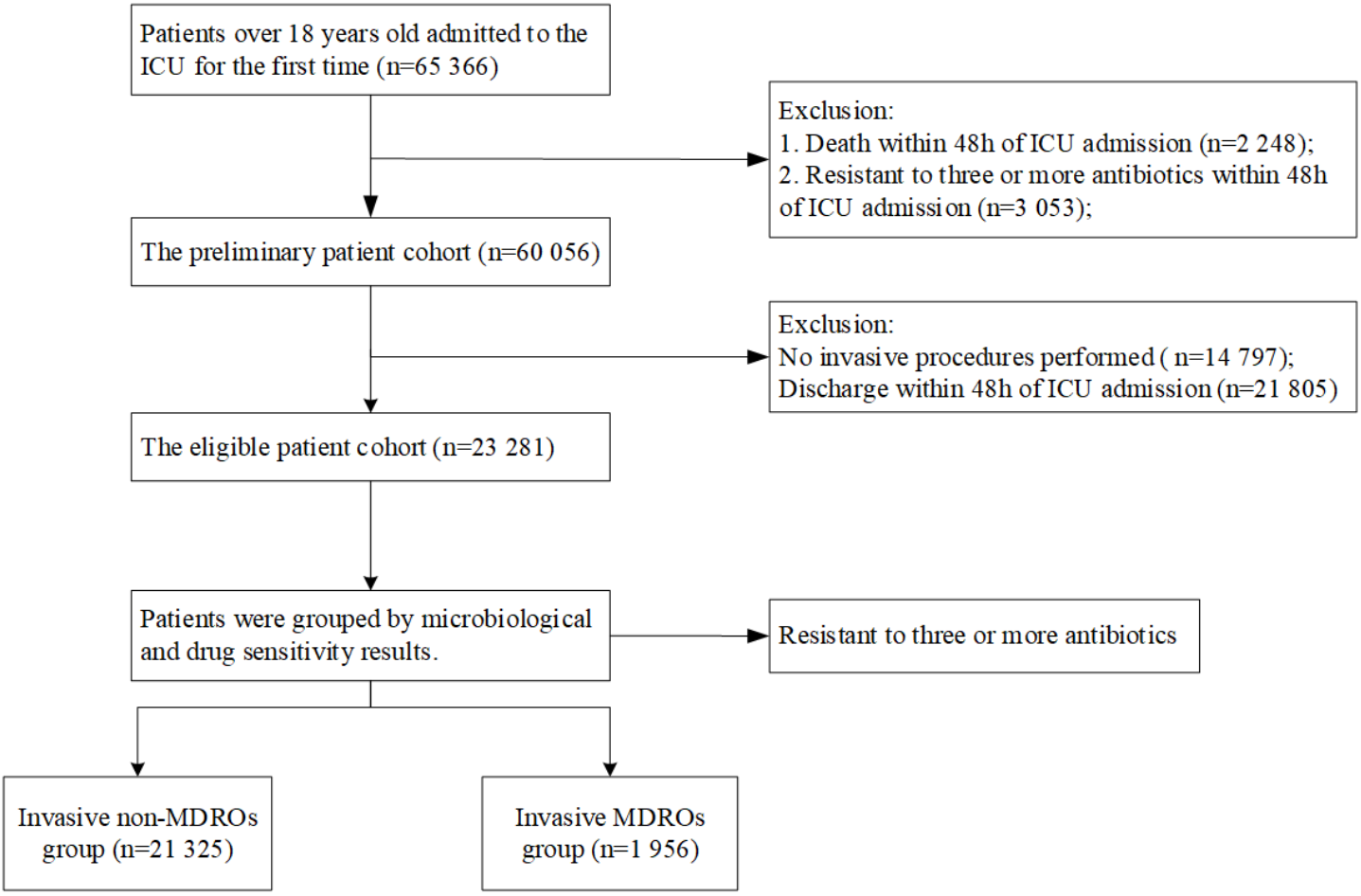


Figure 1

Flowchart of participants selection.

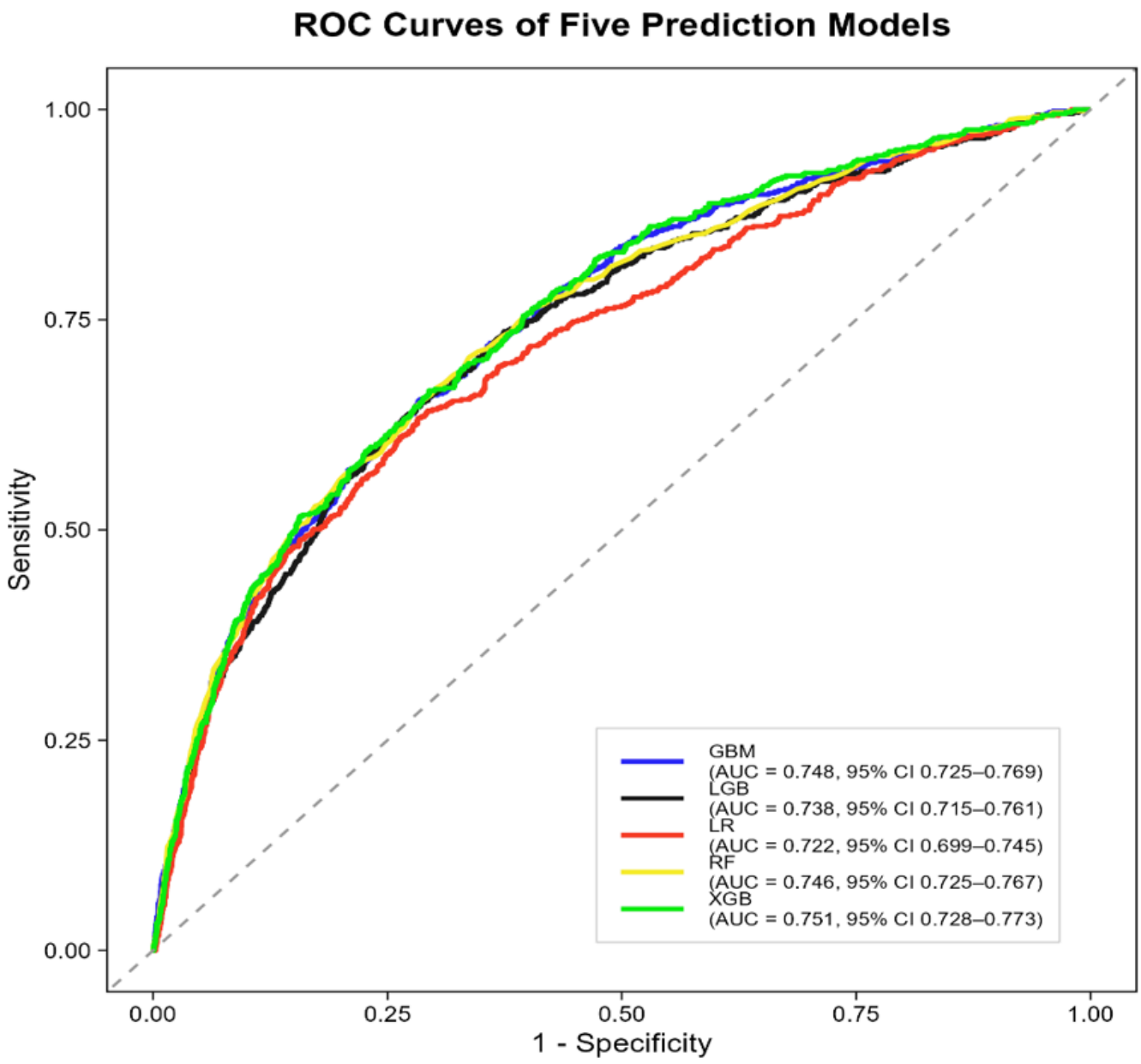


Figure 2

Receiver operating characteristic (ROC) curves of the five models. LR: logistic regression, RF: random forest, LGB: light gradient boosting Machine, GBM: gradient boosting machine, XGB: extreme gradient boosting

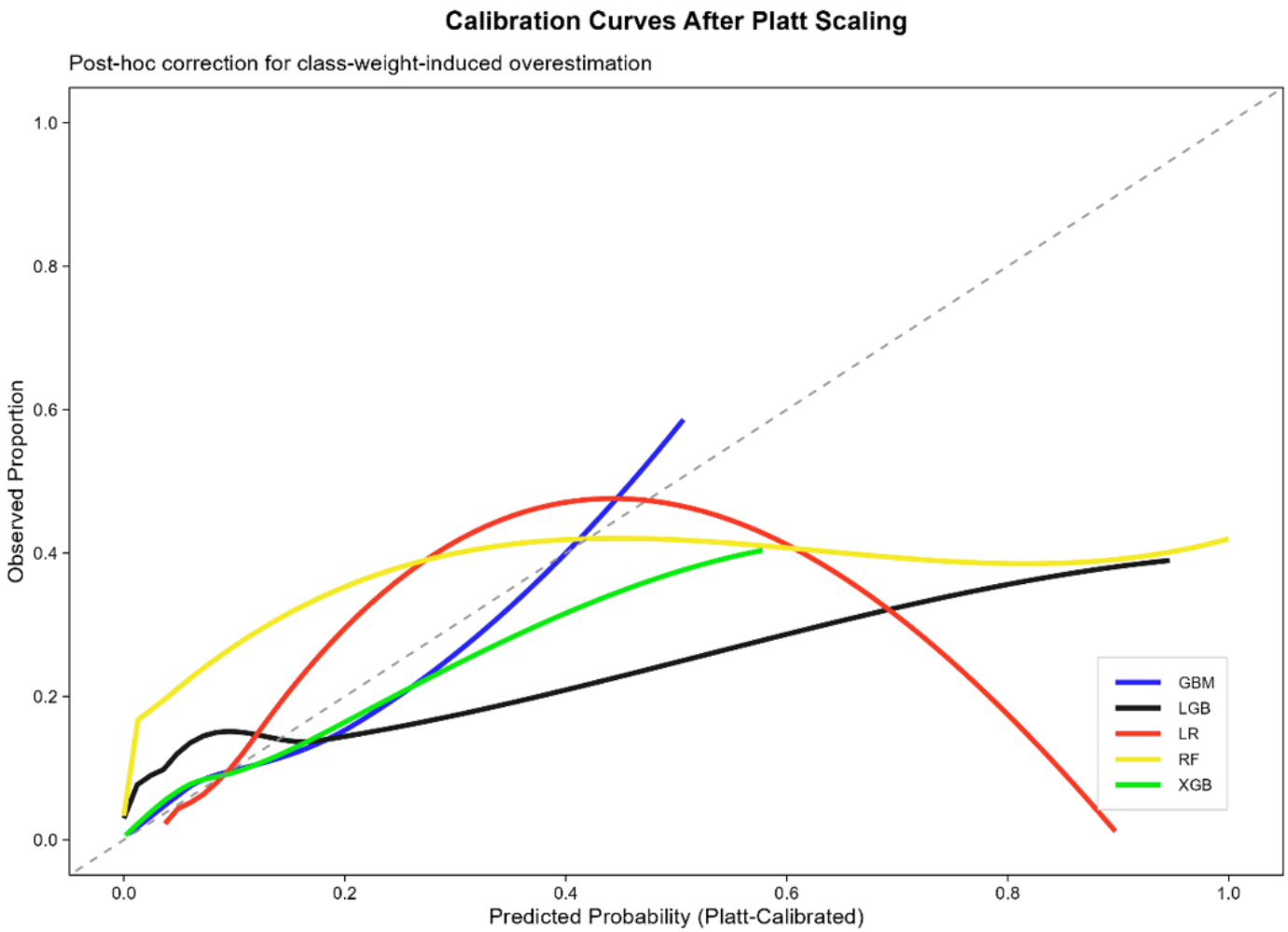


Figure 3

Calibration curves of the five models. LR: logistic regression, RF: random forest, LGB: light gradient boosting Machine, GBM: gradient boosting machine, XGB: extreme gradient boosting

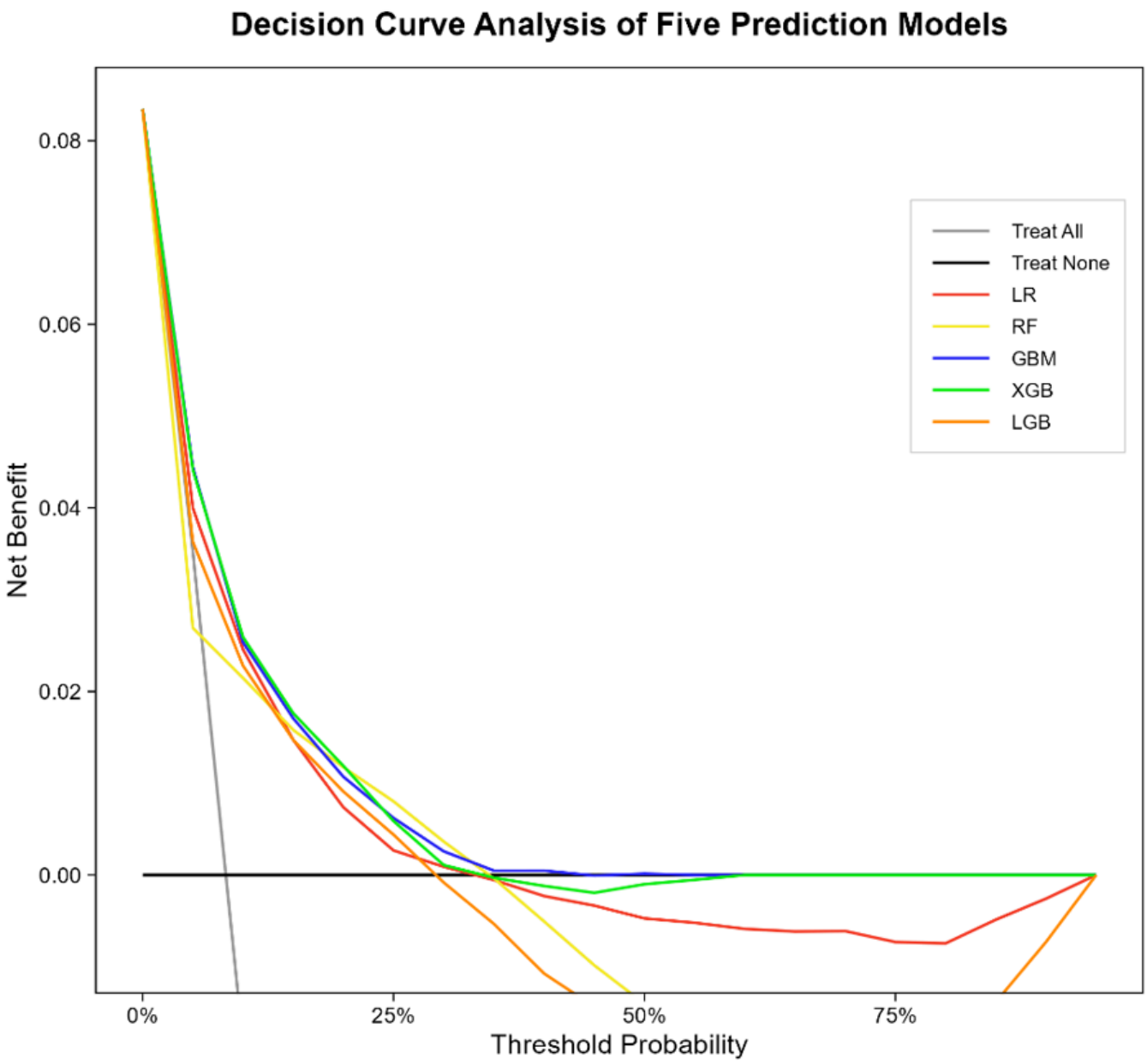


Figure 4

Decision curve analysis of the five models. LR: logistic regression, RF: random forest, LGB: light gradient boosting Machine, GBM: gradient boosting machine, XGB: extreme gradient boosting

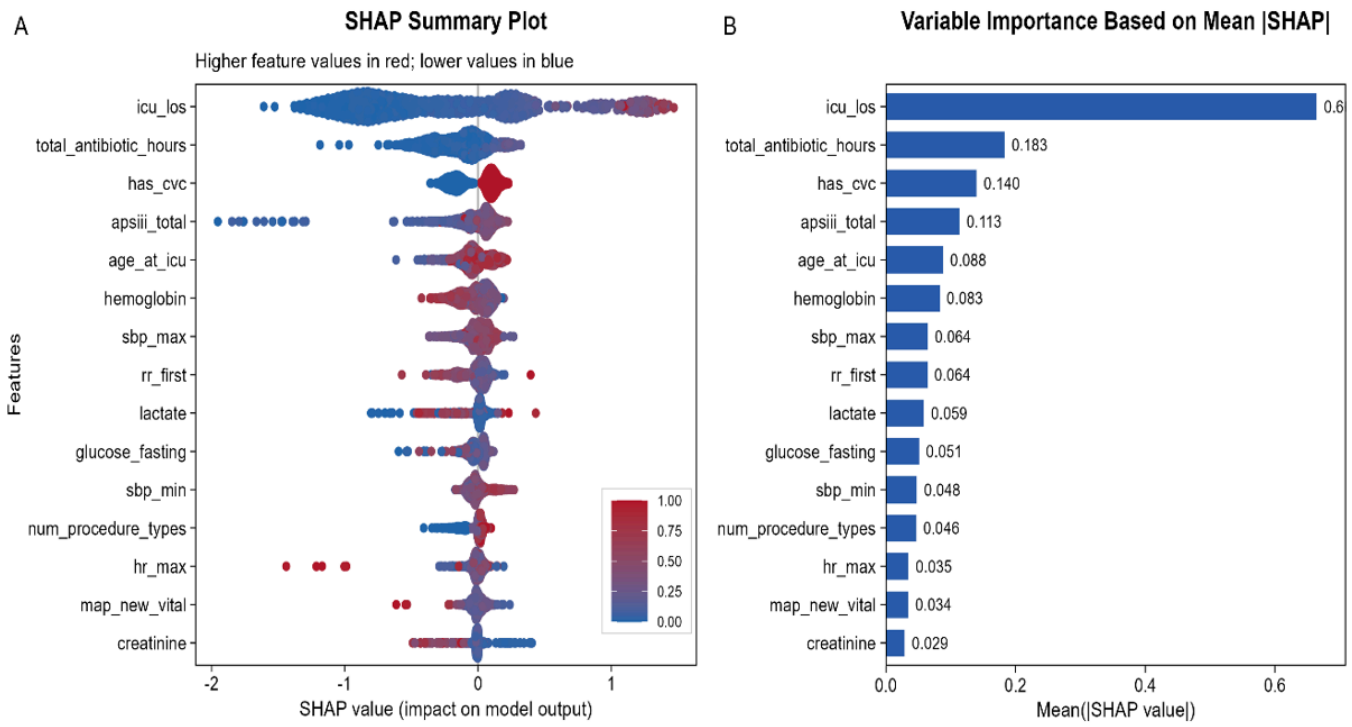


Figure 5

(A) Summary plot of the SHAP values for the XGB model. (B) SHAP variable importance ranking. icu_los, the length of ICU stay; total_antibiotic_hours, total antibiotic using hours; apsii_total, APS Ⅱ score; sbp, systolic blood pressure; hr, heart rate; map, mean arterial pressure

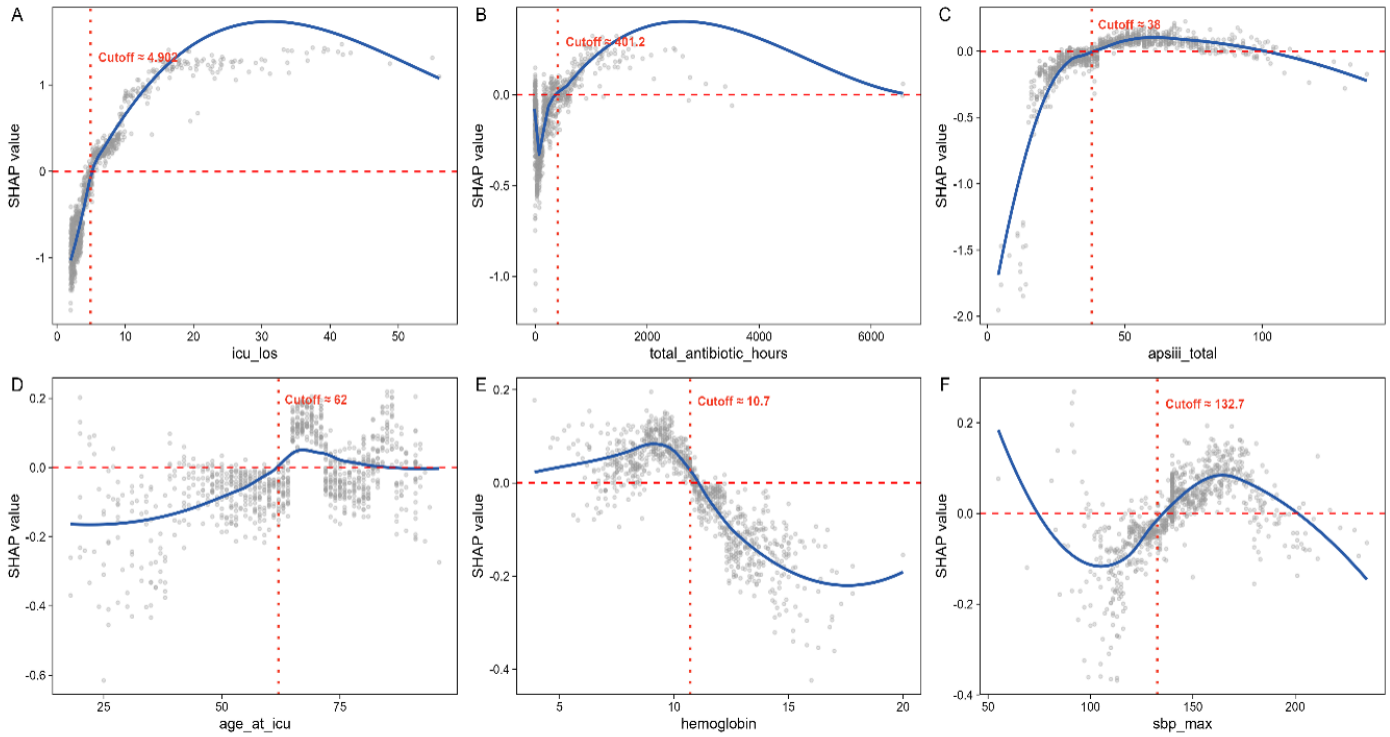


Figure 6

SHAP dependence plots for the top six continuous variables in the XGB model. (A)Length of ICU stay SHAP dependence plot, (B)Total antibiotic use hours SHAP dependence plot, (C) APS Ⅲ score SHAP dependence plot, (D)Age at ICU SHAP dependence plot, (E)Hemoglobin count SHAP dependence plot, (F) Maximum Systolic Blood Pressure in the first 24 hours SHAP dependence plot

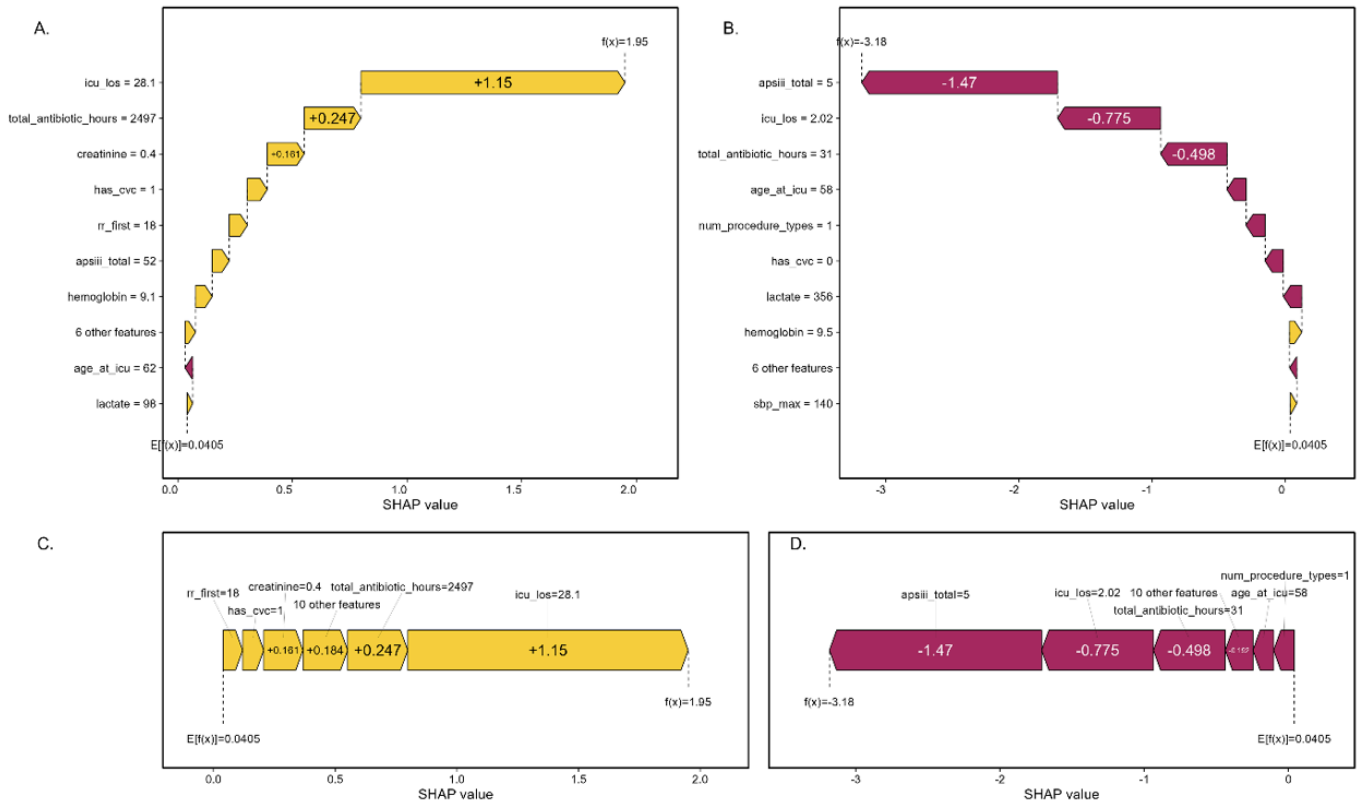


Figure 7

Individual predictions for two patients underwent invasive procedures

Supplementary Files

This is a list of supplementary files associated with this preprint. Click to download.

- TableS2CharacteristicsofMDROspatientsandNonMDROpatientsoftheMIMICIVdatabase.docx
- FigureS2TheLassoregressionresults.pdf
- TableS1relevantprocessdata.docx
- FigureS1CorrelationMatrixHeatmap.pdf