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ORIGINAL ARTICLE

# Construction and validation of prognostic models for acute kidney disease and mortality in patients at risk of malnutrition: an interpretable machine learning approach

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## ABSTRACT

**Background.** Acute kidney injury (AKI) is a prevalent complication in patients at risk of malnutrition, elevating the risks of acute kidney disease (AKD) and mortality. AKD reflects the adverse events developing after AKI. This study aimed to develop and validate machine learning (ML) models for predicting the occurrence of AKD, AKI and mortality in patients at risk of malnutrition.

**Methods.** We retrospectively reviewed the medical records of patients at risk of malnutrition. Eight ML algorithms were employed to predict AKD, AKI and mortality. The performance of the best model was evaluated using various metrics and interpreted using the SHapley Additive exPlanation (SHAP) method. An artificial intelligence (AI)-driven web application was also created based on the best model.

**Results.** A total of 13 395 patients were included in our study. Among them, 1751 (13.07%) developed subacute AKD, 1253 (9.35%) were transient AKI, and 1455 (10.86%) met both AKI and AKD criteria. The incidence rate of mortality was 6.74%. The light gradient boosting machine (LGBM) outperformed other models in predicting AKD, AKI and mortality, with area under curve values of 0.763, 0.801 and 0.881, respectively. The SHAP method revealed that AKI stage, lactate dehydrogenase, albumin, aspirin usage and serum creatinine were the top five predictors of AKD. An online prediction website for AKI, AKD and mortality was developed based on the final models.

**Conclusions.** The LGBM models provide an effective method for predicting AKD, AKI and mortality at an early stage in patients at risk of malnutrition, enabling prompt interventions. Compared with the AKD model, the models for predicting AKI and mortality perform better. The AI-driven web application can significantly aid in creating personalized preventive measures. Future work will aim to expand the application to larger, more diverse populations, incorporate additional biomarkers and refine ML algorithms to improve predictive accuracy and clinical utility.

**Keywords:** acute kidney disease, hospital mortality, machine learning, patients at risk of malnutrition, risk prediction

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## KEY LEARNING POINTS

**What was known:**

- Acute kidney injury (AKI) is a common complication in patients at risk of malnutrition, increasing the risks of acute kidney disease (AKD) and mortality.
- AKD reflects adverse events occurring after AKI, and there was a need to develop predictive models for AKD, AKI, and mortality.
- This research aimed to fill that gap by applying machine learning (ML) to predict these outcomes in patients at risk of malnutrition.

**This study adds:**

- The light gradient boosting machine model outperformed other algorithms in predicting AKD, AKI and mortality, with high accuracy.
- SHapley Additive exPlanation (SHAP) analysis identified AKI stage, lactate dehydrogenase, albumin, aspirin usage and serum creatinine as top predictors for AKD.
- A user-friendly, artificial intelligence (AI)-driven web application was developed, offering personalized risk predictions for AKI, AKD and mortality.

**Potential impact:**

- Early identification of AKI and AKD risks in patients at risk of malnutrition enables timely interventions, potentially improving outcomes.
- The AI-driven tool enhances decision-making for healthcare providers, aiding in personalized treatment strategies.
- This research supports the broader adoption of ML models in clinical practice to improve patient care and preventive measures.

## INTRODUCTION

Malnutrition is defined as a state of insufficient intake or uptake of nutrients, leading to higher healthcare costs and mortality rates [1, 2]. A 2015 study found a rate of 27.8%, using the nutritional risk screening (NRS-2002) score [3]. Importantly, the association between illness and nutritional status seems to be bidirectional [3, 4]. Acute kidney injury (AKI) and chronic kidney disease (CKD) are affected by metabolic changes and malnutrition [5]. Additionally, patients at risk of malnutrition are at a higher risk of renal impairment [4]. Most research focuses on AKI and CKD, with limited studies on renal function changes in the 7–90 days following kidney injury.

Current evidence indicates that AKI can progress to an intermediate stage called acute kidney disease (AKD), defined by the 16th Acute Disease Quality Initiative (ADQI) meeting as acute or subacute damage and/or loss of kidney function persisting for 7–90 days following an AKI-triggering event [6]. While AKI represents a sudden decline in kidney function, AKD encompasses a broader timeframe and includes patients who do not fully recover from an episode of AKI [7]. Therefore, distinguishing between AKD and AKI in clinical practice is crucial, as the management strategies and prognostic implications for these conditions differ.

Recently, several studies have demonstrated that the superior predictive capabilities of machine learning (ML) models over traditional statistical methods in predicting diseases. For instance, in pediatric critical care, the prediction of Stage 2/3 AKI by a ML model showed an area under curve (AUC) of the receiver operating characteristic (ROC) curve of 0.89 [8]. Wang *et al.* developed ML models to assist in diagnosing malnutrition [9]. Despite ML's complexity, the SHapley Additive exPlanation (SHAP) method has been developed to make these models more interpretable [10, 11].

Hence, this study aimed to achieve the following objectives: (i) investigate the incidence rates of AKD, AKI and mortality among patients at risk of malnutrition to fill a gap in the epidemiology of kidney injury trajectories; (ii) develop predictive ML models for AKD, AKI and mortality, using SHAP analysis to clarify the contributions of individual features and provide insights into the model's decision-making process; and (iii) create an innovative, user-friendly online risk calculator based on ML algorithms.

## MATERIALS AND METHODS

### Data collection

We conducted a retrospective review of the medical records of all 21 964 hospitalized patients at risk of malnutrition from our hospital between October 2012 and October 2019. Patients were excluded if they met any of the following criteria: undergoing continuous dialysis, having undergone renal transplantation prior to the diagnosis of AKI or AKD, having fewer than two serum creatinine (Scr) tests during hospitalization, missing inpatient data, being under 18 years of age or having a hospitalization duration of $<$48 h.

The risk of malnutrition during hospitalization was evaluated by the NRS-2002 scale within the first 24 h after admission, which consists of a score for impaired nutritional status, a score for the severity of disease and an additional score if age $\geq$70 years. Malnutrition risk is identified if the total NRS-2002 score is $\geq$3 [12]. Impaired nutritional status is rated from 0 to 3 based on changes in body mass index, weight and food intake, while disease severity is graded from 0 to 3 depending on the type and history of diseases.

Complete blood counts and blood chemistry analyses were performed within 3 days of admission. Additionally, we collected data on demographic characteristics, comorbidities and medications from the hospital information system. The comorbidities mentioned in this study were defined according to the International Classification of Diseases, 10th Revision. The study was approved by the Institutional Review Board (QYFY WZLL 28942). As a retrospective study, it adhered to ethical guidelines by

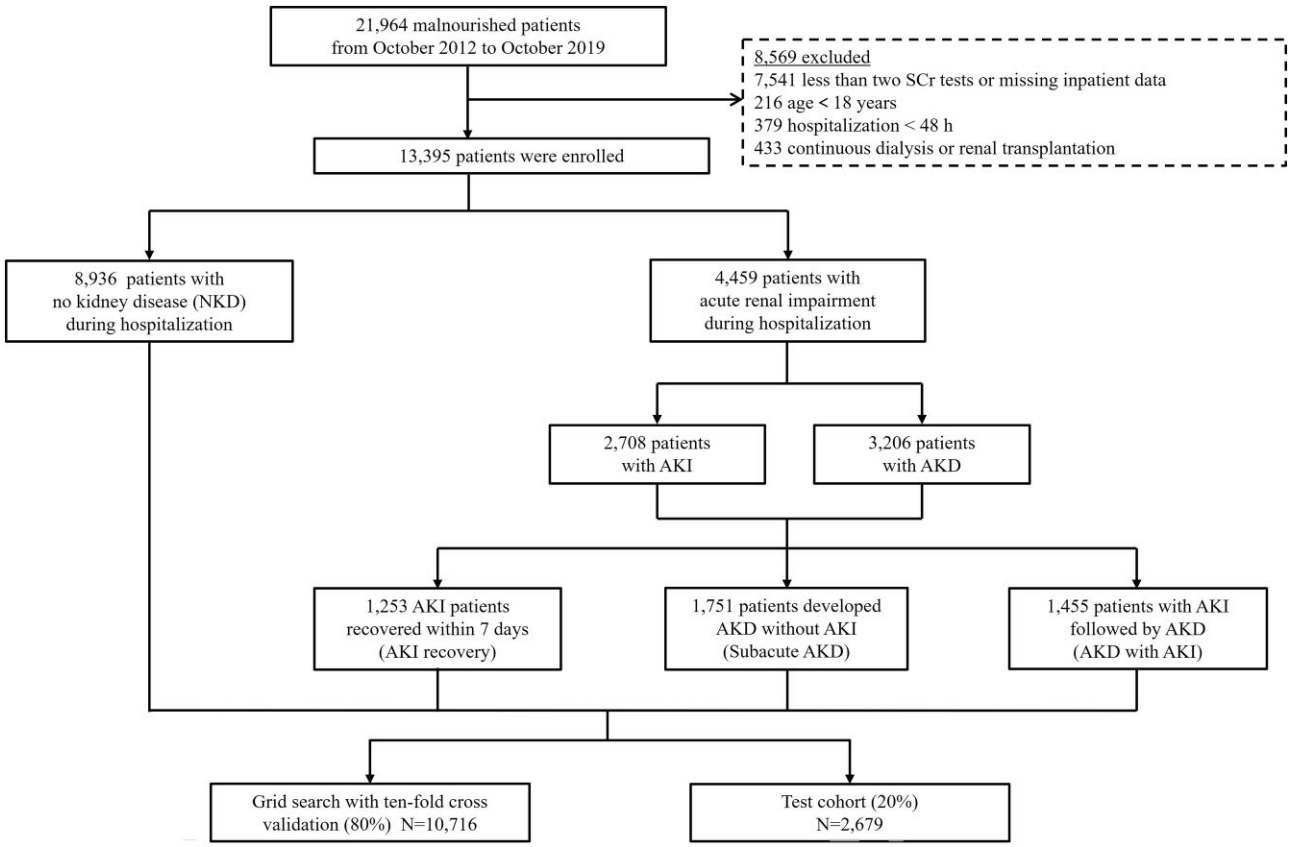


**Figure 1:** Flow diagram of patient selection.

ensuring patient confidentiality through anonymized data collection. All data usage and processes complied with relevant privacy protocols and ethical regulations to safeguard participant rights and meet legal and regulatory requirements.

## Definition

The primary outcome was the occurrence of AKD, with secondary outcomes including AKI and mortality. AKI was diagnosed based on Kidney Disease: Improving Global Outcomes (KDIGO) 2012 as follows: Scr level >26.5 mmol/L (0.3 mg/dL) within 48 h; an increase in Scr to >1.5-fold the baseline-confirmed value or an increase presumed to have occurred within 7 days; or urine output <0.5 mL/kg/h for >6 h [13]. AKD was defined following the 2017 ADQI as acute or subacute damage and/or loss of kidney function for a duration of between 7 and 90 days after exposure to an AKI initiating event. Subacute AKD is characterized by a gradual decline in kidney function during the first 7 days that does not meet the KDIGO criteria for AKI but progresses to AKD after 7 days [6]. Diagnosis and staging of AKI and AKD were determined at the first fulfillment of these criteria.

Based on the diagnostic criteria for AKI and AKD, patients were categorized into four groups. (i) Transient AKI, included patients who met the criteria for AKI but experienced a decline in Scr levels within 7 days and did not subsequently meet the criteria for AKD after 7 days. (ii) Subacute AKD, comprised patients whose Scr levels increase gradually over the first 7 days, not meeting the KDIGO criteria for AKI but progressing to AKD after 7 days (AKD without AKI). (iii) AKD with AKI, included patients who experienced stage ≥1 AKI that persisted for at least 7 days following the initial AKI event, indicating a continuous progression from AKI to AKD (persistent AKI). (iv) No kidney disease (NKD), consisted of patients who had an estimated glomerular filtration rate (eGFR) of 60 mL/min/1.73 $m^2$ or higher and no detectable albuminuria, and who did not meet the criteria for either AKI or AKD. To thoroughly assess the impact of evolving kidney injury patterns on mortality among patients at risk of malnutrition, we integrated AKI and AKD into a unified metric termed "trajectory" during the construction of the mortality model. The "trajectory" variable adopted values of 0, 1, 2 and 3, corresponding to NKD, transient AKI, subacute AKD, and AKD with AKI, respectively. Baseline Scr was defined as the first Scr value measured during hospitalization, and the baseline eGFR was calculated using the Chronic Kidney Disease Epidemiology Collaboration formula [14].

## Feature selection

In this study, we employed the Recursive Feature Elimination (RFE) method for feature selection. The principle of feature selection was to retain essential predictors while eliminating redundant ones, thereby identifying a minimal set of predictors that could enhance model accuracy while reducing complexity. Starting with the entire dataset, the RFE method evaluates features based on AUC of the ROC curve. In each iteration, RFE calculates ranking scores, with higher rankings given to predictors more strongly associated with the outcome. Lower-ranked predictors are subsequently eliminated in a recursive manner until an optimal predictor set is obtained. In this study, we used the light

**Table 1: Baseline characteristics of patients.**

| Features | Total ($n = 13\,395$) | NKD ($n = 8936$) | Acute/subacute renal impairment ($n = 4459$) | | | |
|---|---|---|---|---|---|---|
| | | | Transient AKI ($n = 1253$) | Subacute AKD ($n = 1751$) | AKD with AKI ($n = 1455$) | *P*-value |
| Demographics | | | | | | |
| Age (years) | 65.05 ± 14.63 | 64.87 ± 14.28 | 64.02 ± 16.7 | 67.17 ± 14.72 | 64.43 ± 14.54 | **<.01** |
| Male, *n* (%) | 8344 (62.29) | 5696 (63.74) | 765 (61.05) | 989 (56.48) | 894 (61.44) | **<.01** |
| Smokers, *n* (%) | 4991 (37.26) | 3534 (39.55) | 417 (33.28) | 543 (31.01) | 497 (34.16) | **<.01** |
| Drinkers, *n* (%) | 4067 (30.36) | 2853 (31.93) | 348 (27.77) | 443 (25.3) | 423 (29.07) | **<.01** |
| BMI ($kg/m^2$) | 22.73 ± 3.95 | 22.63 ± 3.82 | 23.19 ± 4.28 | 22.38 ± 4.10 | 23.37 ± 4.11 | **<.01** |
| SBP (mmHg) | 130.07 ± 22.04 | 129.55 ± 20.84 | 131.95 ± 25.6 | 130.38 ± 22.46 | 131.28 ± 25.03 | **<.01** |
| DBP (mmHg) | 76.40 ± 12.84 | 76.49 ± 12.16 | 76.84 ± 14.75 | 75.87 ± 13.07 | 76.11 ± 14.75 | .15 |
| NRS-2002 score | 3.00 (1.00) | 3.00 (1.00) | 3.00 (1.00) | 3.00 (1.00) | 4.00 (1.00) | **<.01** |
| Laboratory tests | | | | | | |
| RBC ($\times 10^{12}$/L) | 3.93 ± 0.79 | 4.01 ± 0.75 | 3.91 ± 0.87 | 3.76 ± 0.8 | 3.73 ± 0.89 | **<.01** |
| WBC ($\times 10^9$/L) | 8.61 ± 11.91 | 8.06 ± 11.18 | 10.05 ± 11.96 | 8.99 ± 11.51 | 10.27 ± 15.77 | **<.01** |
| Scr (μmol/L) | 92.7 ± 74.97 | 86.19 ± 46.82 | 112.19 ± 124.5 | 92.57 ± 72.12 | 116.06 ± 132.51 | **<.01** |
| Glucose (mmol/L) | 6.69 ± 3.24 | 6.34 ± 2.87 | 7.8 ± 4.21 | 6.8 ± 3.26 | 7.75 ± 3.91 | **<.01** |
| Na (mmol/L) | 139.56 ± 5.28 | 139.93 ± 4.73 | 139.15 ± 6.73 | 138.74 ± 5.53 | 138.63 ± 6.4 | **<.01** |
| Hemoglobin (g/L) | 116.28 ± 25.38 | 118.01 ± 24.55 | 116.74 ± 27.6 | 110.9 ± 24.81 | 111.77 ± 27.62 | **<.01** |
| Platelets ($10^9$/L) | 229.19 ± 108.43 | 238.27 ± 107.9 | 204.7 ± 97.16 | 223.87 ± 110.59 | 200.94 ± 109.86 | **<.01** |
| ALT (U/L) | 54.15 ± 240.81 | 39.4 ± 118.46 | 88.59 ± 359.53 | 53.5 ± 225.24 | 115.85 ± 519.06 | **<.01** |
| GGT (U/L) | 94.43 ± 231.09 | 82.95 ± 214.22 | 102.21 ± 241.7 | 102.97 ± 248.07 | 147.98 ± 285.91 | **<.01** |
| ADA (U/L) | 13.9 ± 12.27 | 13.21 ± 10.03 | 14.84 ± 20.13 | 15.09 ± 14.46 | 15.92 ± 12.59 | **<.01** |
| Total bilirubin (umol/L) | 32.46 ± 71.34 | 23.56 ± 45.95 | 47.35 ± 109.38 | 34.82 ± 69.7 | 71.44 ± 124.72 | **<.01** |
| AST (U/L) | 56.71 ± 323.14 | 34.73 ± 106.19 | 120.08 ± 507.5 | 51.49 ± 243.94 | 143.43 ± 764.99 | **<.01** |
| Cholesterol (mmol/L) | 4.49 ± 1.57 | 4.56 ± 1.39 | 4.31 ± 1.92 | 4.38 ± 1.62 | 4.34 ± 2.14 | **<.01** |
| HDL (mmol/L) | 1.14 ± 0.44 | 1.18 ± 0.4 | 1.08 ± 0.53 | 1.09 ± 0.43 | 0.97 ± 0.53 | **<.01** |
| LDL (mmol/L) | 2.6 ± 1.22 | 2.65 ± 1.06 | 2.46 ± 1.42 | 2.53 ± 1.27 | 2.56 ± 1.75 | **<.01** |
| Triglycerides (mmol/L) | 1.27 ± 1.06 | 1.21 ± 0.98 | 1.38 ± 1.22 | 1.29 ± 0.92 | 1.5 ± 1.47 | **<.01** |
| LDH (U/L) | 226.69 ± 253.47 | 199.7 ± 179.85 | 301.0 ± 382.71 | 241.79 ± 224.85 | 310.22 ± 435.45 | **<.01** |
| UA (umol/L) | 272.61 ± 131.41 | 267.53 ± 112.95 | 289.76 ± 162.99 | 269.86 ± 145.15 | 292.4 ± 177.9 | .89 |
| ALP (U/L) | 114.38 ± 151.06 | 106.89 ± 132.27 | 118.23 ± 180.22 | 124.28 ± 161.99 | 145.14 ± 204.23 | **<.01** |
| Total protein (g/L) | 62.03 ± 8.96 | 63.1 ± 8.5 | 59.46 ± 9.72 | 60.8 ± 9.0 | 59.16 ± 9.75 | **<.01** |
| Albumin (g/L) | 33.58 ± 6.41 | 34.44 ± 6.15 | 32.32 ± 6.68 | 31.93 ± 6.35 | 31.38 ± 6.69 | **<.01** |
| Albumin globulin ratio | 1.23 ± 0.34 | 1.25 ± 0.33 | 1.23 ± 0.4 | 1.16 ± 0.34 | 1.16 ± 0.33 | **<.01** |
| Prothrombin time (s) | 11.55 ± 3.96 | 11.08 ± 2.56 | 12.56 ± 5.17 | 12.06 ± 6.22 | 12.9 ± 5.53 | **<.01** |
| Fibrinogen (g/L) | 3.61 ± 1.19 | 3.63 ± 1.14 | 3.56 ± 1.28 | 3.57 ± 1.21 | 3.52 ± 1.36 | .01 |
| Thrombin time (s) | 15.42 ± 7.0 | 15.01 ± 4.58 | 16.13 ± 10.01 | 16.04 ± 9.14 | 16.62 ± 11.5 | **<.01** |
| Comorbidities, *n* (%) | | | | | | |
| CKD | 717 (5.35) | 241 (2.7) | 157 (12.53) | 115 (6.57) | 204 (14.02) | **<.01** |
| Pneumonia | 1516 (11.32) | 1143 (12.79) | 91 (7.26) | 188 (10.74) | 94 (6.46) | **<.01** |
| Bronchitis | 238 (1.78) | 178 (1.99) | 11 (0.88) | 34 (1.94) | 15 (1.03) | .01 |
| Asthma | 232 (1.73) | 161 (1.8) | 17 (1.36) | 27 (1.54) | 27 (1.86) | .42 |
| COPD | 597 (4.46) | 387 (4.33) | 46 (3.67) | 98 (5.6) | 66 (4.54) | .34 |
| ICH | 884 (6.6) | 508 (5.68) | 116 (9.26) | 163 (9.31) | 97 (6.67) | **<.01** |
| Cerebral infarction | 1052 (7.85) | 611 (6.84) | 124 (9.9) | 182 (10.39) | 135 (9.28) | **<.01** |
| Hepatic cirrhosis | 443 (3.31) | 217 (2.43) | 38 (3.03) | 63 (3.6) | 125 (8.59) | **<.01** |
| DM | 2824 (21.08) | 1776 (19.87) | 272 (21.71) | 410 (23.42) | 366 (25.15) | **<.01** |
| HUA | 207 (1.55) | 123 (1.38) | 22 (1.76) | 38 (2.17) | 24 (1.65) | .03 |
| Hyperthyroidism | 57 (0.43) | 36 (0.4) | 4 (0.32) | 11 (0.63) | 6 (0.41) | .67 |
| Atrial fibrillation | 291 (2.17) | 102 (1.14) | 47 (3.75) | 73 (4.17) | 69 (4.74) | **<.01** |
| ACS | 1076 (8.03) | 536 (6.0) | 137 (10.93) | 213 (12.16) | 190 (13.06) | **<.01** |
| CHD | 2874 (21.46) | 1679 (18.79) | 285 (22.75) | 535 (30.55) | 375 (25.77) | **<.01** |
| Hypertension | 4864 (36.31) | 3000 (33.57) | 519 (41.42) | 768 (43.86) | 577 (39.66) | **<.01** |
| Medications, *n* (%) | | | | | | |
| $\beta$-blockers | 5073 (37.87) | 3171 (35.49) | 528 (42.14) | 633 (36.15) | 741 (50.93) | **<.01** |
| ACEI | 1032 (7.7) | 540 (6.04) | 108 (8.62) | 210 (11.99) | 174 (11.96) | **<.01** |
| ARB | 1947 (14.54) | 1223 (13.69) | 169 (13.49) | 320 (18.28) | 235 (16.15) | **<.01** |
| Statins | 2044 (15.26) | 1224 (13.7) | 200 (15.96) | 336 (19.19) | 284 (19.52) | **<.01** |
| CCB | 3946 (29.46) | 2348 (26.28) | 426 (34.0) | 588 (33.58) | 584 (40.14) | **<.01** |
| PPIs | 11 522 (86.02) | 7616 (85.23) | 1049 (83.72) | 1523 (86.98) | 1334 (91.68) | **<.01** |
| $\beta$-lactam antibiotics | 5747 (42.9) | 3550 (39.73) | 545 (43.5) | 820 (46.83) | 832 (57.18) | **<.01** |

**Table 1: Continued**

| Features | Total ($n = 13\,395$) | NKD ($n = 8936$) | Acute/subacute renal impairment ($n = 4459$) | | | P-value |
|---|---|---|---|---|---|---|
| | | | Transient AKI ($n = 1253$) | Subacute AKD ($n = 1751$) | AKD with AKI ($n = 1455$) | |
| Macrolides antibiotics | 383 (2.86) | 278 (3.11) | 26 (2.08) | 38 (2.17) | 41 (2.82) | .02 |
| Aminoglycoside antibiotics | 556 (4.15) | 350 (3.92) | 39 (3.11) | 86 (4.91) | 81 (5.57) | .06 |
| Quinolone antibiotics | 3795 (28.33) | 2431 (27.2) | 288 (22.98) | 568 (32.44) | 508 (34.91) | **<.01** |
| Cardiac glycosides | 7598 (56.72) | 4763 (53.3) | 808 (64.49) | 933 (53.28) | 1094 (75.19) | **<.01** |
| Aspirin | 4606 (34.39) | 2709 (30.32) | 442 (35.28) | 684 (39.06) | 771 (52.99) | **<.01** |
| Outcome | | | | | | |
| Mortality, *n* (%) | 903 (6.74) | 202 (2.26) | 213 (17.0) | 125 (7.14) | 363 (24.95) | **<.01** |
| Length of stay (days) | 21.74 ± 15.72 | 20.86 ± 13.33 | 17.75 ± 20.95 | 24.13 ± 13.52 | 27.7 ± 22.93 | **<.01** |

P values < .05 were considered statistically significant and were calculated between the NKD group and the acute/subacute renal impairment groups.
Results are presented as mean ± SD, *n* (%) or median (IQR).
SD: standard deviation; BMI: body mass index; SBP: systolic blood pressure; DBP: diastolic blood pressure; RBC: red blood cell; WBC: white blood cell; ALT: alanine transaminase; GGT: gamma-glutamyl transferase; ADA: adenosine deaminase; AST: aspartate transaminase; HDL: high-density lipoprotein; LDL: low-density lipoprotein; UA: uric acid; ALP: alkaline phosphatase; COPD: chronic obstructive pulmonary disease; ICH: Intracranial hemorrhage; DM: diabetes mellitus; HUA: hyperuricemia; ACS: acute coronary syndrome; CHD: coronary heart disease; ACEI: angiotensin-converting enzyme inhibitor; ARB: angiotensin receptor blocker; CCB: calcium channel blocker; PPIs: proton pump inhibitors.

gradient boosting machine (LGBM) as the base classifier for RFE and performed feature selection on the training set. This process was implemented using the "RFE" module in Python 3.10.

## Model development and evaluation

We engineered predictive models for AKD, AKI and mortality. Scikit-learn (https://github.com/scikit-learn/scikitlearn) package was used to build models including logistic regression (LR), support vector machine (SVM), random forest (RF), naive bayes (NB), k-nearest neighbor (KNN), multi-layer perceptron (MLP), gradient boosting machine (GBM) and LGBM. In the realm of ML, a diverse array of algorithms has been employed to address complex predictive tasks. Among these, tree-based models such as RF, GBM and LGBM have garnered significant attention [15]. RF employs an ensemble of decision trees to average predictions, effectively reducing overfitting and variance. Conversely, LGBM and GBM incrementally develop trees through successive boosting iterations [16]. LGBM is particularly distinguished for its adept handling of large-scale and complex datasets, underpinned by its fast training capabilities and efficient data processing mechanisms [17]. LR offers a traditional, yet robust model for binary classification, widely appreciated for its interpretability [18]. SVM excels in high-dimensional spaces by finding the optimal hyperplane for classification [19]. MLP, a fundamental neural network, captures complex patterns through its layered structure [20]. KNN classifies samples based on the majority class among its closest neighbors, embodying simplicity and effectiveness [21]. Lastly, NB classifier based on Bayes' Theorem, assumes feature independence. This simple yet powerful assumption enables NB to perform effectively, especially in high-dimensional datasets [22]. These algorithms, with their distinct capabilities, form a robust toolkit for complex predictive modeling tasks.

The data were divided, with 80% utilized for training and 20% for testing. Grid search method with 10-fold cross-validation was used in the training set to prevent overfitting and to identify the optimal hyperparameters for each model. To address the disparity in the distribution of positive and negative samples, we implemented a strategy of class weight adjustment during the training phase of the ML model [23].

The performance of our predictive models was further evaluated on the test set, focusing on their discriminative ability and clinical utility. Discrimination was evaluated using several metrics, including: AUC, which measures the model's ability to distinguish between positive and negative outcomes [24]; sensitivity, which assesses the model's ability to correctly identify positive cases; specificity, which measures the model's ability to correctly identify negative cases; recall, which indicates the proportion of actual positives correctly identified; accuracy, which represents the overall proportion of correct predictions; F1 score, the harmonic mean of precision and recall; Brier score, which evaluates the accuracy of probabilistic predictions; and Matthews correlation coefficient (MCC), a balanced metric that takes into account both true and false positives and negatives. For clinical applicability, decision curve analysis (DCA) was employed, which calculated the net benefit of the final model by contrasting the predicted benefits against the expected risks associated with the outcomes [25]. Furthermore, the performance of the final model was showed through precision-recall (PR) curves, Kolmogorov–Smirnov (KS) plots and confusion matrix.

## Model interpretation

SHAP method was designed to address the "black box" issue in prediction models by providing a means to rank the importance of input features and explain model results [11, 26]. SHAP values are derived from cooperative game theory, where each feature is considered as a "player" contributing to the prediction outcome. This method offers both global and local explanations. Globally, SHAP values provide consistent attribution scores for each feature, revealing the overall influence of features on the model's predictions. Locally, SHAP values explain the contribution of each feature to specific predictions for individual cases, thus improving the interpretability of the model. Higher SHAP values indicate that a feature has a larger impact on the predicted outcome, either by increasing or decreasing the probability of a certain prediction. The SHAP method was implemented using the Python shap package.

### Online prediction website

We developed an online risk calculator using the Streamlit Python framework, incorporating the model with the optimal set of features. Once the relevant feature values are input, the website can predict the probability of AKD and mortality. This tool showcases the practical application of our research in a clinical setting and can additionally be used for external validation.

### Subgroup analysis

Given that patients with AKD stages 2–3 may have worse prognoses compared with the overall AKD population, we independently developed a ML prediction model specifically for AKD stages 2–3 and validated its predictive performance.

### Statistical analysis

Variables with >15% missing values were excluded from the analysis. For those with <15% missing data, the Multivariate Imputation by Chained Equations (MICE) algorithm was applied for imputation [27]. Utilizing LR to compute the required sample size with mortality as the outcome, we ascertained that a minimum of 2101 patients is essential to achieve a statistical power of 90% for the detection of an effect size of 0.10 at a two-sided significance level ($\alpha$) of 0.05. Continuous variables were presented as mean with standard deviation, or median with interquartile range, and compared using the independent-sample T test or Wilcoxon rank-sum test. Categorical variables were reported as counts and percentages and compared using the Chi-square test. All statistical analyses were performed using Python version 3.10.11, R version 4.3.1 and SPSS version 25.0. A two-tailed $P$-value of <.05 was deemed statistically significant.

## RESULTS

### Patient characteristics

A retrospective review of medical records encompassed 21 964 patients at risk of malnutrition, of whom 13 395 were selected for further analysis (Fig. 1). Table 1 presents the baseline characteristics of the study population. The incidence rates of AKI, AKD and mortality were 20.22% (2708/13 395), 23.93% (3206/13 395) and 6.74% (903/13 395), respectively. In total, 4459 patients (33.29%) developed acute/subacute kidney dysfunction, with 1751 (13.07%) developing subacute AKD, 1253 (9.35%) recovering from AKI, and 1455 (10.86%) meeting both AKI and AKD criteria. In summary, the acute/subacute renal impairment group exhibited statistically significant differences in baseline laboratory tests, including Scr, glucose, lipid profiles and uric acid, compared with the NKD group ($P < .01$). Additionally, significant differences were observed between the two groups in outcome variables such as mortality and length of hospital stay ($P < .01$).

### Feature selection and model performance

A comprehensive set of 60 features were included as predictor variables. Eight ML models were developed to predict AKD occurrence in patients at risk of malnutrition using all available feature. Among these models, the LGBM model

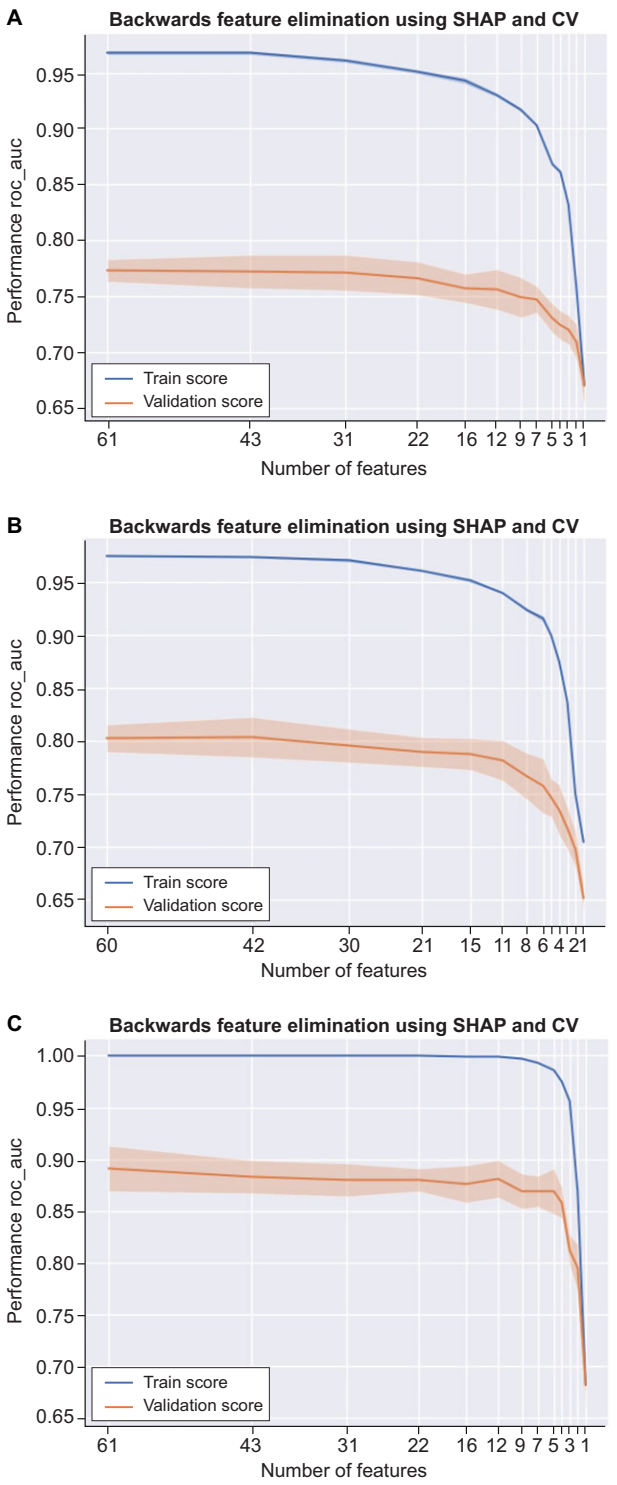


**Figure 2:** The RFE method was used for feature selection, displaying the AUC variations with the number of features for the LGBM model in predicting three different outcomes. (**A**) The AUC corresponding to the number of features included in LGBM for predicting AKD. (**B**) The AUC corresponding to the number of features included in LGBM for predicting AKI. (**C**) The AUC corresponding to the number of features included in LGBM for predicting mortality.

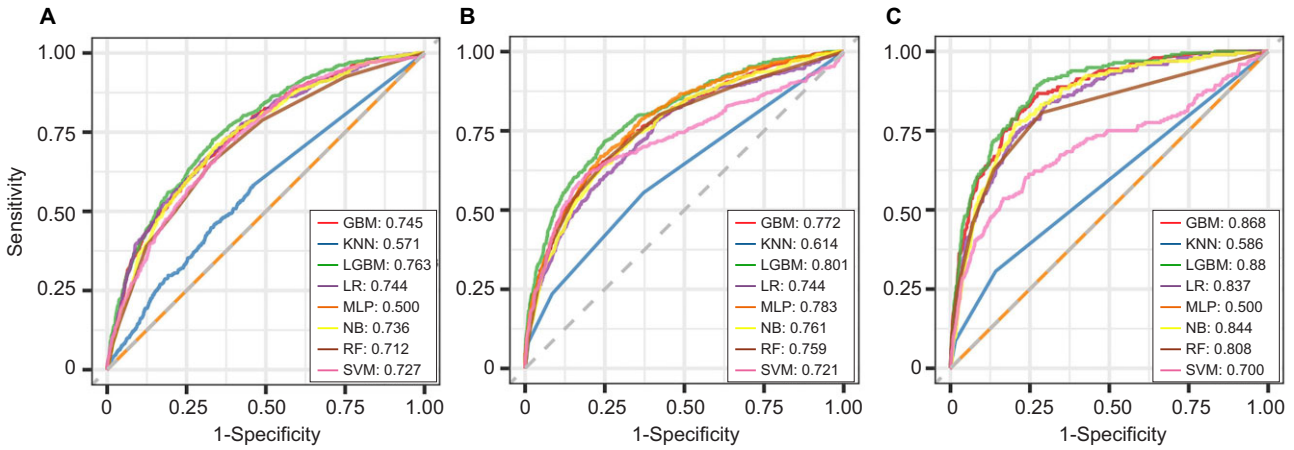


**Figure 3:** Performance of eight ML models for different outcomes with selected features. (**A**) ROC curves for AKD prediction. (**B**) ROC curves for AKI prediction. (**C**) ROC curves for mortality prediction.

demonstrated the highest efficacy in predicting AKD, achieving an AUC of 0.778. The performance metrics of these eight ML models in predicting AKD were comprehensively summarized in Supplementary data, Table S1. Notably, the LGBM model exhibited the highest AUC, F1 score and MCC, indicating its ability to accurately predict the occurrence of AKD in patients with malnutrition. Therefore, LGBM emerged as the optimal model for AKD prediction. Similarly, we have developed ML models for both AKI and mortality prediction. The LGBM models for AKI and mortality, utilizing all features, achieved AUCs of 0.814 and 0.892, respectively, which were the best performances among all models. Therefore, the LGBM algorithm was also identified as the optimal model for predicting both AKI and mortality (Supplementary data, Table S2 and S3).

Given LGBM's superior performance, we subsequently conducted a feature selection process specifically within the LGBM model framework. Optimize feature selection by performing RFE to identify the most predictive subset of features for enhancing model performance. Figure 2 displays the feature selection results of the LGBM model in predicting three different outcomes. The model used 12, 15 and 12 features for predicting AKD, AKI and mortality, respectively, achieving a high AUC while minimizing computational processes and enhancing the efficiency of the predictive model.

After filtering the indicators, we reconstructed a streamlined model to facilitate practical application. For the prediction of AKD, the ROC curves for each model are displayed in Fig. 3A. The LGBM model stood out with the highest AUC of 0.763 (Table 2). Following LGBM, the models, in descending order of AUC, were GBM, LR, NB, SVM, RF, KNN and MLP, with respective AUCs of 0.745, 0.744, 0.736, 0.727, 0.712, 0.571 and 0.500, with the MLP model scoring the lowest. Furthermore, the KS plot and PR curve demonstrated that the model exhibited satisfactory classification capabilities and maintained a favorable balance between precision and recall (Supplementary data, Fig. S1). To assess the clinical relevance of the top-performing LGBM model, we presented its DCA curve in Supplementary data, Fig. S1C, which suggested favorable clinical utility.

The LGBM model achieved the highest AUC for both AKI (0.801) and mortality (0.881) predictions, as shown in Fig. 3B and C. The evaluation metrics of the model constructed after filtering indicators are provided in Supplementary data, Tables S4 and S5. DCA curves (Supplementary data, Figs S2C and S3C) confirmed its clinical utility. The supplementary materials summarized performance metrics, and additional evaluations like KS plots and PR curves demonstrated robust classification capabilities, highlighting the model's reliability in practical applications.

## Model interpretation

The SHAP summary plot (Fig. 4A) highlighted the contributions of each feature to the model's predictions for AKD. The top five features associated with AKD included AKI stage, lactate dehydrogenase (LDH), albumin, aspirin usage and Scr. Among these, AKI stage showed the highest influence, with more severe stages significantly increasing the likelihood of AKD, underscoring the progression of kidney injury as a critical determinant. The SHAP interaction plot (Supplementary data, Fig. S4) visually clarified the interplays among these features within the AKD model. SHAP dependence plots (Supplementary data, Fig. S5) facilitated the understanding of how individual features influenced the model's output while simultaneously showing the relationship between two features. Furthermore, local explanations provided insights into how specific features contributed to individual predictions. The force plots depicted the personalized prediction processes for two representative patients (Fig. 4C and D). The cases depicted in decision plots (Supplementary data, Fig. S6) demonstrate patients who share similar predicted probabilities, yet their underlying feature compositions leading to these predictions vary.

The SHAP method was also applied to the AKI and mortality models, with detailed results provided in the supplementary files. In the AKI model, Scr emerged as the predominant contributing factor, consistent with expectations (Supplementary data, Fig. S7). In the mortality model, the "trajectory" variable ranked second in terms of significance (Supplementary data, Fig. S8). Increasing grades of the "trajectory" were associated with higher SHAP values, indicating elevated mortality risk. This underscores the substantial influence of kidney injury trajectory on survival outcomes among patients at risk of malnutrition.

## Subgroup analysis

The LGBM model demonstrated robust predictive accuracy for AKD stages 2–3, achieving an AUC of 0.806 in the test set

Table 2: Evaluation of the performance of eight ML models using selected features to predict AKD.

| Models | AUC | Precision | Recall | Accuracy | F1 score | Brier score | MCC |
|---|---|---|---|---|---|---|---|
| Training set | | | | | | | |
| SVM | 0.731 (0.723–0.738) | 0.575 (0.538–0.611) | 0.156 (0.135–0.177) | 0.772 (0.767–0.777) | 0.245 (0.217–0.273) | 0.160 (0.158–0.162) | 0.208 (0.181–0.234) |
| KNN | 0.585 (0.563–0.607) | 0.347 (0.323–0.372) | 0.224 (0.204–0.244) | 0.715 (0.708–0.723) | 0.272 (0.250–0.294) | 0.219 (0.211–0.226) | 0.109 (0.084–0.135) |
| NB | 0.737 (0.732–0.742) | 0.506 (0.490–0.521) | 0.385 (0.366–0.405) | 0.764 (0.758–0.770) | 0.437 (0.421–0.453) | 0.194 (0.191–0.198) | 0.296 (0.278–0.314) |
| MLP | 0.630 (0.532–0.727) | 0.239 (0.018–0.461) | 0.096 (0.001–0.192) | 0.770 (0.762–0.777) | 0.134 (0.005–0.264) | 0.168 (0.157–0.178) | 0.109 (0.006–0.212) |
| RF | 0.716 (0.703–0.729) | 0.506 (0.492–0.520) | 0.385 (0.368–0.403) | 0.764 (0.759–0.769) | 0.437 (0.422–0.452) | 0.164 (0.161–0.168) | 0.296 (0.279–0.312) |
| GBM | 0.753 (0.741–0.765) | 0.805 (0.767–0.844) | 0.038 (0.032–0.043) | 0.769 (0.767–0.770) | 0.072 (0.062–0.082) | 0.157 (0.155–0.159) | 0.141 (0.127–0.155) |
| LR | 0.750 (0.740–0.761) | 0.457 (0.444–0.470) | 0.597 (0.577–0.617) | 0.735 (0.727–0.743) | 0.518 (0.504–0.531) | 0.196 (0.193–0.200) | 0.345 (0.327–0.364) |
| LGBM | 0.761 (0.751–0.772) | 0.455 (0.442–0.468) | 0.611 (0.584–0.638) | 0.733 (0.725–0.742) | 0.521 (0.504–0.539) | 0.182 (0.178–0.186) | 0.349 (0.326–0.373) |
| Test set | | | | | | | |
| SVM | 0.727 | 0.587 | 0.176 | 0.768 | 0.270 | 0.163 | 0.224 |
| KNN | 0.571 | 0.341 | 0.212 | 0.707 | 0.262 | 0.227 | 0.095 |
| NB | 0.736 | 0.527 | 0.371 | 0.765 | 0.435 | 0.198 | 0.300 |
| MLP | 0.500 | 0.000 | 0.000 | 0.756 | 0.000 | 0.185 | 0.000 |
| RF | 0.712 | 0.505 | 0.389 | 0.757 | 0.440 | 0.172 | 0.292 |
| GBM | 0.745 | 0.690 | 0.031 | 0.760 | 0.058 | 0.162 | 0.108 |
| LR | 0.744 | 0.447 | 0.580 | 0.722 | 0.505 | 0.200 | 0.321 |
| LGBM | 0.763 | 0.445 | 0.603 | 0.719 | 0.512 | 0.185 | 0.328 |

(Supplementary data, Fig. S9). This indicated the model's enhanced capability in predicting more severe cases of AKD, which was crucial to improve patient outcomes.

### Online prediction website

Employing LGBM for AKD and mortality prediction, we have created an artificial intelligence (AI)-driven web application within the Streamlit framework. Limiting the model to the number of features selected by RFE did not significantly diminish its predictive performance; instead, it optimized both the F1 score and MCC. The calculator is accessible at Streamlit (lumos-design-app-app-rqm8wh.streamlit.app), and is specifically designed for practical application in clinical settings. Healthcare providers can input relevant patient data to instantly generate risk estimations, enabling real-time assessment and personalized clinical decision-making. By offering a user-friendly interface and rapid computation, this calculator empowers clinicians to make timely, evidence-based decisions, ultimately improving patient management and outcomes.

## DISCUSSION

To the best of our knowledge, our study is the first to establish ML models for AKD, AKI and mortality in patients at risk of malnutrition identified through the NRS-2002, offering valuable tools for risk assessment and clinical decision-making. This retrospective cohort study involved the development and validation of ML algorithms to predict AKD, AKI and mortality among this vulnerable population. Among the various algorithms tested, the LGBM algorithm demonstrated the highest discrimination capability for all three outcomes. To enhance the interpretability of the "black box" model, we utilized diverse SHAP plots at both global and local levels. Moreover, we created an AI-driven web application based on the LGBM model, designed to predict AKI, AKD and mortality in patients at risk of malnutrition, facilitating early prediction and intervention.

Several investigations have explored the relationship between malnutrition and AKI, establishing a significant link between nutritional status and patient prognosis. For instance, Sun *et al*. found that poor preoperative nutritional status was associated with an increased risk of postoperative AKI [28]. Similarly, Yu *et al*. identified that the risk of malnutrition, assessed using NRS-2002, was effective in identifying high-risk patients with AKI and predicting mortality [29]. Li *et al*. further illustrated that malnutrition not only heightens the risk of developing AKI, but also worsens patient outcomes [4]. Yamaguchi *et al*. found that patients with NKD, AKI and CKD demonstrated an association between malnutrition and increased mortality [30]. Building on these findings, and currently lacking research on the incidence rates and risk assessment of AKI, AKD and mortality among malnourished populations, our study aims to fill this gap, with the goal of informing clinical decision-making and improving patient prognosis.

It is worth emphasizing that in predicting mortality, we incorporated the renal function trajectory variable into our mortality prediction model. This underscores the importance of monitoring renal function trajectories from 7 to 90 days for prognosis. The ADQI 16 report proposed definitions and classifications that integrate these stages to provide a comprehensive view of hypothetical trajectories of AKD [6]. According to the consensus, our study divided the population into four groups: NKD, transient

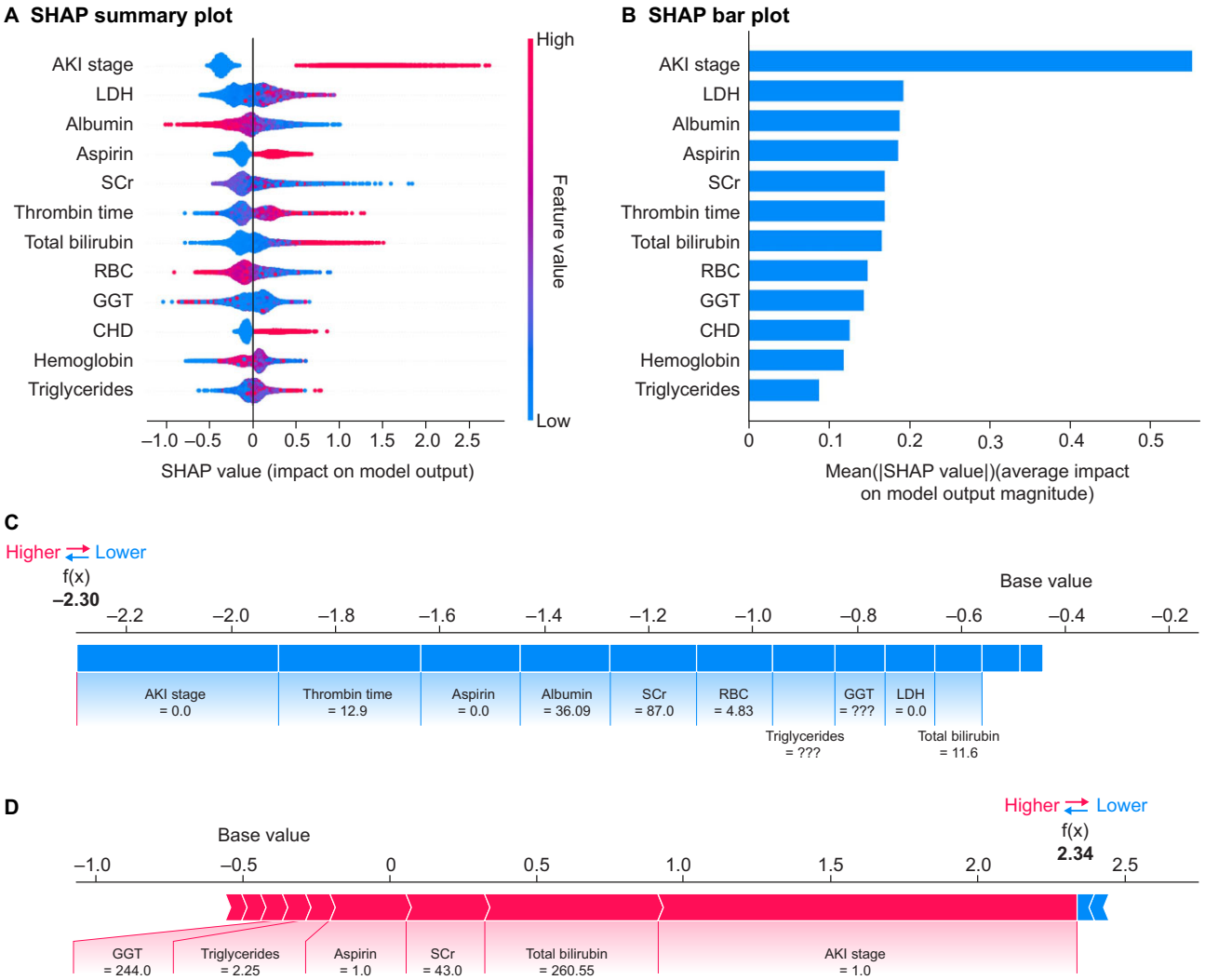


**Figure 4:** SHAP summary plot, feature importance matrix plot and force plots of the final LGBM model for predicting AKD. (**A**) The SHAP summary plot demonstrates the general importance of each feature in the LGBM model. The color bar on the right indicates the relative value of a feature in each case. Red dots indicate high values and blue dots indicate low values. The violin graph lining up on the midline is the aggregation of dots representing each case in the train set. The distance between the upper and lower margin of the violin graph represents the amount of the cases that end up with the same SHAP values offered by this feature. (**B**) The importance ranking of selected features of the LGBM model. (**C, D**) Force plots that illustrate the individualized prediction composition for two representative patients. The patient in (C) has a mortality probability below 10%, while the patient in (D) has a probability exceeding 90%. The base value represents the averaged predicted results. At the bottom of each plot, feature values and their corresponding names are listed. Categorical features including AKI stage and CHD were represented by 0 and 1, while "0" means "No" and "1" means "Yes." *LDH, lactate dehydrogenase; CHD, coronary heart disease; RBC, red blood cell count; GGT, gamma-glutamyl transferase.

AKI, subacute AKD, and AKD with AKI, to study the dynamic trajectories of renal function impairment. Analyzing the differences in baseline characteristics, mortality rates and length of hospital stay among these four groups helps in understanding the continuum from acute to subacute kidney disease and is useful for creating a unified variable that captures dynamic changes in kidney function. Moreover, the inclusion of these categories into a single trajectory variable can help in assessing the impact on clinical outcomes, such as mortality, as demonstrated in various population-based cohort studies [31]. This approach provides a more holistic view of kidney disease progression and aids in the development of more accurate predictive models for patient outcome.

In recent years, ML methods have been widely employed in predicting AKI [32–35]. However, there is comparatively limited research on predicting AKD, particularly in patients at risk of malnutrition. Li *et al.* employed the SVM algorithm to predict early prognosis in elderly patients with AKD [7]. Wang *et al.* developed ML models, including LGBM, to assist in diagnosing malnutrition [9]. LGBM outperforms traditional regression models by providing higher accuracy, faster training times, and better handling of large datasets, making it a more effective tool for clinical applications. In our investigation, we expanded upon this approach by comparing various ML algorithms using rigorous metrics such as AUC, F1 scores and others. Notably, our study revealed that LGBM consistently outperformed other models in predicting nutritional status. Moreover, the application of ML techniques in nutritional assessment opens new avenues for understanding complex health outcomes in malnourished populations. Currently, there is a notable absence of studies utilizing ML to assess the specific risks of AKI, AKD or mortality in patients at risk of malnutrition, underscoring the novelty and

importance of our research endeavor in bridging this gap in the literature.

This study presents several crucial clinical implications. Initially, it constitutes the first attempt to compare baseline characteristics and hospital mortality among three different renal function trajectories post-injury. Secondly, we have successfully developed concise yet highly effective LGBM models for predicting AKD, AKI and mortality. Moreover, our approach involved a diverse array of SHAP plots to tackle the "black box" issue in risk assessment. The SHAP summary plot ranked features by their importance, while SHAP force plots and decision plots illustrated the variations in feature contributions for patients with similar predicted outcomes, thus enhancing the personalization and transparency of the decision-making process. Additionally, to achieve a balance between model complexity and clinical relevance, we used the RFE method for feature selection, focusing on features that are readily accessible in standard clinical practice. Furthermore, our models are designed for immediate clinical application, highlighted by the development of a web-based risk calculator that evaluates the risk of AKD and mortality in patients at risk of malnutrition, offering physicians a valuable tool to improve decision-making.

Our study encountered several limitations. Firstly, it was constrained by a single-center design and lacked ethnic diversity, potentially limiting the generalizability of our findings. Secondly, the follow-up period was too brief to ascertain whether patients developed CKD. Thirdly, while we relied on the NRS-2002 tool to screen patients for nutritional risk, we did not incorporate professional nutritional assessments to confirm malnutrition. This reliance on a screening tool without subsequent evaluation might have influenced the accuracy of our findings. Fourthly, our model's performance in predicting AKD was relatively modest compared with its prediction of mortality, indicating the need for further optimization of features and algorithms to improve accuracy. Additionally, it may also be due to some patients having sarcopenia. Assessing sarcopenia in every patient is challenging in clinical practice, making it difficult to exclude this group, and this could lead to reduced creatinine levels, potentially affecting the model's predictive accuracy. Fifthly, there is a potential for overfitting in ML models; however, we mitigated this risk through feature selection with RFE and rigorous validation, though the lack of external validation limits the model's generalizability. Additionally, the retrospective nature of our data collection introduced potential recall and selection biases. To address these challenges, future research should prioritize multi-center, prospective trials with diverse ethnic populations, incorporate professional nutritional assessments, and explore higher-quality features and advanced algorithms. This will validate and enhance the reliability of predictive models and improve the predictive performance of the AKD model. Additionally, future studies should extend the follow-up period to better assess the development of CKD.

## CONCLUSIONS

In conclusion, we developed LGBM models to forecast AKD, AKI and mortality at the time of admission, with the models for predicting AKI and mortality showing superior performance compared with the AKD model, which warrants further improvement. Additionally, we created a web tool to assist in clinical decision-making. For future research, we aim to conduct nationwide, multi-center trials with a diverse participant base, and to extend the follow-up period to better evaluate the progression of CKD.

## SUPPLEMENTARY DATA

Supplementary data are available at *Clinical Kidney Journal* online.

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## AUTHORS' CONTRIBUTIONS

X.W. and Y.X. designed research; X.W., C.L. and L.X. conducted research; S.J., L.C., Y.W. and X.M. analyzed data; and X.W. wrote the paper. Y.X. had primary responsibility for final content. All authors read and approved the final manuscript.

## DATA AVAILABILITY STATEMENT

Data described in the manuscript, code book and analytic code will be made available upon request pending (e.g. application and approval, payment, other).

## CONFLICT OF INTEREST STATEMENT

None declared.

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