BMC Cancer

RESEARCH

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Rapid identification of tumor patients with PG-SGA ≥ 4 based on machine learning: a prospective study

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Abstract

Background Malnutrition is common in cancer patients and worsens treatment and prognosis. The Patient-Generated Subjective Global Assessment (PG-SGA) is the best tool to evaluate malnutrition, but it is complicated has limited its routine clinical use.

Methods We reviewed 798 records from 416 cancer patients treated at our hospital from July 2022 to March 2024. We used machine learning methods like XGBoost and Random Forest to find important factors linked to PG-SGA scores of 4 or higher. We confirmed the most important factors with logistic regression analysis.

Results Among all models, XGBoost and Random Forest models perform the best, with the area under the curve (AUC) reaching of 0.75 and 0.77. Multivariate logistic regression analysis identified body mass index (BMI) (OR = 0.82, 95%CI 0.66–0.99; *P* = 0.045), handgrip strength (HGS) (OR = 0.89, 95%CI 0.82–0.96; *P* = 0.004), fat-free mass index (FFMI) (OR = 1.36, 95%CI 1.01–1.88; *P* = 0.045), and bedridden status (OR = 3.16, 95%CI 1.17–9.14; *P* = 0.026) as key predictors for PG-SGA scores of ≥ 4.

Conclusion BMI, HGS, FFMI, and bedridden status were identified as practical indicators to efficiently screen patients likely to have PG-SGA scores ≥ 4.

Keywords Cancer, Nutritional Assessment, Patient-Generated Subjective Global Assessment, Machine Learning

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Introduction

Malnutrition is a common and serious problem among cancer patients because more people are getting cancer worldwide. Studies show that between 22.6% and 94.6% of cancer patients are malnourished [1–4]. This high risk is caused by several things. Cancer patients have higher metabolic needs, cancer treatments have bad side effects, and they eat less because they lose their appetite. Malnutrition harms the immune system, weakens muscles, and affects how organs work. This makes quality of life worse, treatments less effective, and the overall outlook worse [5–7]. Studies also show that malnourished cancer patients have more treatment complications and live shorter lives, showing that good nutritional management

is very important in cancer care [2, 8]. It is important to check nutritional status quickly and accurately to provide the right nutritional help.

Among the existing tools for assessing nutritional status, the Patient-Generated Subjective Global Assessment (PG-SGA) is known as the best method for cancer patients because it has high sensitivity, specificity, and prediction ability [9, 10]. This tool looks at different parts of a patient's nutritional health, like what they eat, recent weight changes, symptoms, and how well they function. Even though it covers many areas, PG-SGA depends a lot on what patients say, which can lead to memory mistakes. Also, it takes time and needs trained professionals to do accurate assessments [11, 12]. These problems make it difficult to use it in places with limited resources, especially where rapid and extensive assessment methods are required.

Machine learning offers a promising alternative by leveraging automated, data-driven approaches to address these limitations. By training our model on large-scale clinical datasets, we identified latent key clinical features—such as laboratory indicators, tumor types, and treatment modalities—that are predictive of malnutrition. Compared with conventional PG-SGA assessments, our machine learning approach automates data extraction from electronic health records and minimizes human bias, thereby enhancing evaluation accuracy and consistency.

In our study, we adopted a PG-SGA cut-off score of 4—widely recognized in the literature as indicating significant nutritional risk [13]. Patients scoring 4 or higher are recommended for nutritional intervention or supportive care, and this threshold aligns well with established clinical study [14, 15]. Consequently, focusing on this group enhances the model's clinical relevance and applicability.

The main goal of this research is to create a simple and effective assessment method that helps clinicians identify malnourished cancer patients more easily and provide timely help. By combining traditional assessment methods with new machine learning approaches, this study aims to improve the accuracy, accessibility, and efficiency of nutritional evaluations in cancer care settings.

Materials and methods

This study looked at data from patients who had lab tests and physical function checks at the Comprehensive Special Care Department of Sichuan Cancer Hospital from July 2022 to March 2024. The detailed study workflow is shown in Fig. 1.

Inclusion and exclusion criteria

Patients were eligible if they were aged ≥18 years, diagnosed with malignant tumors, and had received at least one anti-cancer treatment (e.g., chemotherapy, radiotherapy, surgery, targeted therapy, or immunotherapy). Exclusion criteria were as follows: patients with missing key clinical data (such as laboratory results, nutritional status assessments, or essential demographic details); those with severe systemic diseases (e.g., advanced heart, liver, or kidney failure) that could affect nutritional status evaluation; pregnant patients; and individuals who died before initiating anti-cancer treatment or were referred to other medical institutions. Ethical approval for this study was obtained from the Ethics Committee of Sichuan Provincial Cancer Hospital. This study utilized routinely collected data. The Institutional Ethics Committee approved a waiver of informed consent for all participants. Approval Number: SCCHEC-02–2022-066.

Data collection and processing

Data were extracted from the Sichuan Cancer Hospital patient database. Two experienced staff members independently reviewed medical records using standardized data collection forms, with discrepancies resolved by a third reviewer. All laboratory tests were conducted promptly in the hospital's clinical laboratory. Nutritional assessments were carried out by certified dietitians, physicians, or nurses with substantial expertise in nutritional evaluation.

The collected data included: Demographic information (age, gender, and place of residence); Tumor characteristics (tumor location and TNM stage); Comorbidities (such as diabetes and hypertension); Anti-tumor treatment modalities (including chemotherapy, radiotherapy, targeted therapy, immunotherapy, and surgery); The collected laboratory indicators include Sodium (Na, mmol/L), Calcium (Ca, mmol/L), Potassium (K, mmol/L), Phosphate (PHOS, mmol/L), Iron (Fe, μmol/L), Triglycerides (TG, mmol/L), Uric Acid (URIC, μmol/L), C-Reactive Protein (CRP, mg/L), Total Bilirubin (TBIL, μmol/L), Albumin (ALB, g/L), Alanine Aminotransferase (ALT, U/L), Creatinine (Cr, μmol/L), White Blood Cell Count (WBC, ×10^9/L), Lymphocyte Count (LC, ×10^9/L), Hemoglobin (Hb, g/L), Platelets (PLT, ×10^9/L), and Glucose (GLU, mmol/L); Physical condition assessment included the following parameters: bedridden status (%), time spent walking less than 1 h per day (%), sleep duration less than 8 h per day (%), Oral Nutritional Supplement intake (ONS, %), Body Mass Index (BMI, kg/m^2), Fat-Free Mass Index (FFMI, kg/m^2), Handgrip Strength (HGS, kg), Energy Intake (EI, Cal/kg/day), and Protein Intake (PI, g/kg/day).

Prior to analysis, data were preprocessed and cleaned. Missing values were handled using median imputation for continuous variables or multiple imputation for complex patterns to maximize sample retention. Outliers

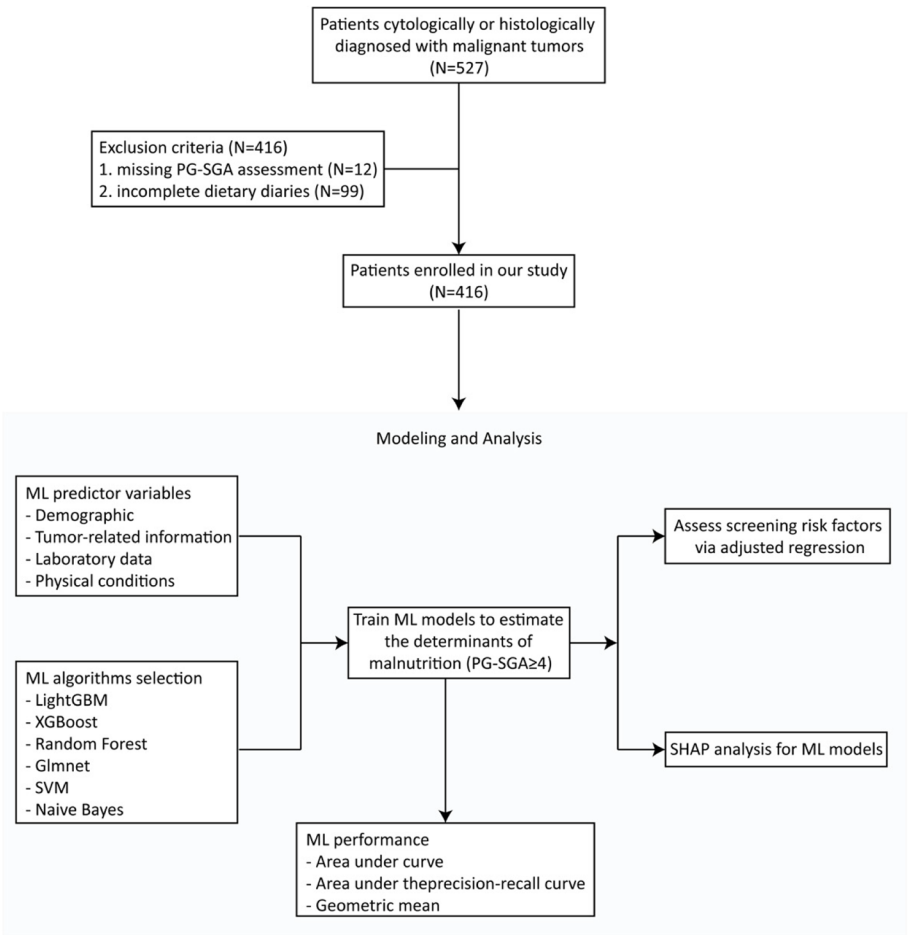

Fig. 1 Research flow chart. Abbreviation: ML, machine learning; SHAP, Shapley Additive Explanations; SVM, Support Vector Machine

were manually reviewed, and decisions to exclude or adjust them were based on clinical relevance. All patient data were anonymized and de-identified to ensure confidentiality. To meet machine learning algorithm requirements, categorical variables (e.g., anti-tumor treatment modalities, bedridden status) were one-hot encoded. For continuous variables (e.g., laboratory test metrics, BMI), standardization or normalization procedures were implemented according to their distribution properties and algorithmic requirements, thereby mitigating the confounding effects of scale differences during model training.

Model development

Feature selection and model optimization strategy

All available variables were initially included to avoid selection bias from pre-selection. Next, core parameters of tree-based models (e.g., tree depth, minimum node size, sample size, feature sampling rate) were fine-tuned to enhance feature engineering and model efficiency.

Additionally, we introduced the glmnet generalized linear model to improve prediction performance. We also employed a Bayesian framework-based randomized algorithm as a control group. While the latter may not be the most practical choice without rigorous parameter optimization, it serves as a benchmark for comprehensively evaluating the effectiveness of our primary method.

Selection of machine learning models

We evaluated six machine learning algorithms with different strengths for predicting PG-SGA ≥ 4 in cancer patients. LightGBM and XGBoost: Gradient boosting decision tree algorithms selected for their efficiency and strong performance with large-scale, high-dimensional data. Random Forest is widely recognized for its robustness against overfitting and its capacity to model complex feature interactions, all while providing insights into feature importance. Glmnet is a regularized regression method, which effectively solves the multicollinearity problem, identifies the key predictors, and provides a simple and interpretable linear model. Support vector

machine (SVM) is especially suitable for analyzing high-dimensional and nonlinear relationships, so it is very suitable for data sets with limited sample size and many variables. At the same time, Naive Bayes algorithm is famous for its computational efficiency, and it is a practical tool for developing baseline model and testing algorithm performance.

Training of machine learning models

To guarantee reliable model evaluation, we randomly partitioned the dataset into a training set (80%) for model training and parameter optimization, and a hold-out test set (20%) for independent performance evaluation. During training, tenfold cross-validation was performed on the training set (80% of the dataset) to reduce overfitting and enhance model stability. Algorithms were compared based on accuracy, scalability, and computational speed to identify the optimal predictive model. To optimize model performance, we employed nested cross-validation combined with a grid search to fine-tune the hyperparameters of each algorithm.

To address class imbalance in the training set, the Synthetic Minority Over-sampling Technique (SMOTE) was applied. Ultimately, all fully trained models were evaluated on the previously unseen test set, representing the remaining 20% of the overall dataset, to verify their generalizability.

Measuring model performance

We have selected the Area Under the Receiver Operating Characteristic Curve (AUC), Area Under the Precision-Recall Curve (AUPRC), and Geometric Mean (Gmean) as our primary evaluation metrics for several critical reasons. AUC serves as a robust measure assessing the model's discriminative capability across all threshold values, particularly effective in managing class-imbalanced data [16]. AUPRC, by contrast, specifically targets the minority class (malnourished patients), yielding more insightful assessments in imbalanced scenarios [17]. Lastly, the Gmean evaluates the equilibrium between the model's capacity to accurately identify both positive and negative cases, thereby offering a holistic performance evaluation for malnutrition prediction in cancer patients [18]. To ensure the stability of the model, the 95% confidence interval is calculated according to the cross-validation results [19, 20].

Feature importance

The Shapley Additive Explanations (SHAP) method was used to interpret the best-performing model, improving its transparency and understanding [21]. Based on game theory, SHAP quantifies the contribution of each feature to the model's predictions while accounting for feature interactions. We performed SHAP analysis on the training dataset and computed the average absolute SHAP value for each feature to assess its overall importance. This approach identifies the most influential features for predictions and supports model simplification. The results of the SHAP analysis are visualized using a bar chart that displays the relative ranking of feature importance, thus providing the foundation for subsequent regression validation.

Statistical analysis

Continuous variables are displayed as interquartile mean (IQR), and categorical variables are displayed as counts and percentages. Using multivariate regression to further validate the association between features and malnutrition. Also, restricted cubic splines were used to look at possible nonlinear relationships between continuous risk factors and PG-SGA scores of 4 or higher [22]. All statistical tests were two-tailed with a significance level of $p < 0.05$. Model calibration was assessed using the Hosmer–Lemeshow test, with $p > 0.05$ indicating good fit between predicted probabilities and observed outcomes. Analyses were conducted using R version 4.3.1.

Results

Baseline characteristics of patients

The study included 416 cancer patients aged over 18 years, accounting for a total of 798 records. All participants were pathologically confirmed to have malignant tumors. Detailed baseline characteristics are provided in Table 1.

Performance of machine learning models

We evaluated the performance of six machine learning models. Table 1 presents the detailed performance metrics for each model, including AUC, AUPRC, and Geometric Mean (Gmean). As shown in Table 2, all models except Naive Bayes demonstrated good discriminative ability on the test set. The Random Forest model performed the best, with an AUC of 0.77 (95% CI: [0.69–0.84]), followed by the SVM model (AUC = 0.76, 95% CI: [0.69–0.83]), and both XGBoost and LightGBM models (AUC = 0.75). The Glmnet model had an AUC of 0.71 (95% CI: [0.63–0.79]). The Naive Bayes model performed notably worse, with an AUC of only 0.56 (95% CI: [0.47–0.65]).

In terms of the AUPRC metric, which assesses performance on imbalanced datasets, the LightGBM model performed the best (0.73, 95% CI: [0.62–0.82]), followed by SVM (0.72) and Random Forest (0.71). For Gmean, the XGBoost model achieved the highest score (0.71), with Random Forest and Glmnet following closely behind (both 0.70). Figure 2 illustrates the calibration

Table 1 Baseline profile of patients in our study

Variables	Patients($N=416$)	Entries($N=798$)
Age, year (median [IQR])	59.46(52.53–67.63)	59.45(52.57–66.63)
Gender, n(%)		
Female	167(40.1)	317(39.7)
Male	249(59.9)	481(60.3)
Address, n(%)		
City	237(57.0)	468(58.6)
Country/Urban	179(43.0)	330(41.4)
Tumor site, n(%)		
lung	145(34.9)	285(35.7)
upper gastrointestinal	53(12.7)	93(11.7)
hepatobiliary and pancreatic	24(5.8)	43(5.4)
colorectal	88(21.2)	182(22.8)
urogenital	26(6.2)	59(7.4)
blood system	20(4.8)	31(3.9)
breast	19(4.6)	36(4.5)
head and neck	22(5.3)	27(3.4)
others	19(4.6)	42(5.3)
TNM_stage (%)		
I/II	18(4.3)	35(4.4)
III/IV	117(28.1)	272(34.1)
Unknown	281(67.5)	491(61.5)
Comorbidity, n(%)		
diabetes	35(8.4)	67(8.4)
hypertension	54(13.0)	120(15.0)
CHD	6(1.4)	27(3.4)
Ongoing anti-tumor treatment, n(%)		
chemotherapy	144(34.6)	402(50.4)
radiotherapy	8(1.9)	16(2.0)
surgery	61(14.7)	66(8.3)
targeted	26(6.2)	49(6.1)
immunotherapy	10(2.4)	48(6.0)
Laboratory indicators (median [IQR])		
Na, mmol/L	140.20(139.40–142.00)	140.20(139.00–141.85)
Ca, mmol/L	2.30(2.23–2.36)	2.33(2.25–2.39)
K, mmol/L	4.09(3.87–4.30)	4.08(3.86–4.31)
PHOS, mmol/L	1.09(0.95–1.21)	1.09(0.96–1.19)
Fe, μmol/L	12.90(9.60–18.10)	12.30(8.90–16.80)
TG, mmol/L	1.31(1.00–1.76)	1.55(1.09–2.00)
URIC, μmol/L	324.50(288.75–375.25)	314.00(264.75–379.00)
CRP, mg/dL	0.39(0.14–1.44)	0.46(0.19–1.94)
TBIL, μmol/L	10.02(6.82–13.73)	8.60(6.20–12.05)
ALB, g/L	41.00(37.75–43.40)	40.80(37.70–43.40)
ALT, U/L	27.00(16.00–41.38)	25.00(17.00–39.50)
Cr, μmol/L	70.00(59.00–84.00)	65.00(55.50–78.75)
WBC, $\times 10^9$/L	5.66(4.04–6.94)	5.21(4.09–6.85)
LC, $\times 10^9$/L	1.10(0.89–1.42)	1.10(0.77–1.43)
Hb, g/L	126.00(115.00–136.00)	123.00(112.00–135.00)
PLT, $\times 10^9$/L	175.00(138.00–235.50)	192.50(135.00–244.00)
GLU, mmol/L	5.08(4.72–5.69)	5.10(4.67–5.59)

Table 1 (continued)

Variables	Patients(*N* = 416)	Entries(*N* = 798)
Physical condition		
bedridden (%)	76(18.3)	176(22.1)
Walk time less than 1 h (%)	49(11.8)	102(12.8)
Sleep time less than 8 h (%)	33(7.9)	73(9.1)
ONS (%)	72(17.3)	165(20.7)
BMI, kg/m^2 (median [IQR])	22.77(20.76–24.66)	22.84(20.63–25.10)
FFMI, kg/m^2 (median [IQR])	16.23(14.92–17.94)	16.23(14.92–18.12)
HGS, kg (median [IQR])	26.10(19.00–33.00)	26.05(19.80–32.92)
EI, Cal/kg/day (median [IQR])	19.73(15.68–24.71)	19.14(15.15–24.29)
PI, g/kg/day (median [IQR])	1.17(0.89–1.47)	1.15(0.90–1.46)

Abbreviation: TNM tumor/node/metastasis, *PHOS* phosphorus, *GLU* glucose, *TG* triglyceride, *URIC* uric acid, *CRP* C-reactive protein, *TBIL* total bilirubin, *ALB* albumin, *ALT* alanine transaminase, *Cr* creatinine, *WBC* white blood cell, *LC* lymphocyte counts, *Hb* hemoglobin, *PTL* platelet, *BMI* body mass index, *FFMI* fat free mass index, *HGS* hand grip strength, *EI* energy intake, *PI* protein intake, *ONS* oral nutritional supplement

Table 2 Machine learning models performance

Models	AUC (95% CI)	AUPRC (95% CI)	Gmean
LightGBM	0.75 (0.67 to 0.82)	0.73 (0.62 to 0.82)	0.68
XGBoost	0.75 (0.67 to 0.83)	0.69 (0.56 to 0.80)	0.71
Random Forest	0.77 (0.69 to 0.84)	0.71 (0.59 to 0.82)	0.70
Glmnet	0.71 (0.63 to 0.79)	0.68 (0.57 to 0.77)	0.70
SVM	0.76 (0.69 to 0.83)	0.72 (0.60 to 0.82)	0.68
Naive Bayes	0.56 (0.47 to 0.65)	0.51 (0.40 to 0.62)	0.44

AUC = Area Under the Curve. AUPRC = Area Under the Precision-Recall Curve. Gmean means the sqrt (sensitivity * specificity). 95% CI shows the uncertainty for AUC and AUPRC metrics

performance of the models. The calibration curves reflect the consistency between predicted probabilities and actual outcomes, with the diagonal representing perfect calibration. The Hosmer–Lemeshow test results showed that the LightGBM and XGBoost models exhibited the best calibration performance, with no significant differences between predicted probabilities and actual outcomes. Figure 3 Comparison of Receiver Operating Characteristic (ROC) curves for various machine learning models evaluated on the test dataset, demonstrating the performance of these models in classification tasks. Figure 4 presents a comparison of feature importance between the XGBoost and Random Forest models.

Considering multiple performance metrics, both XGBoost and Random Forest models performed most robustly in this study. XGBoost excelled in calibration performance and Gmean, while Random Forest slightly outperformed in terms of AUC.

Multivariate analysis

Univariate logistic regression identified 14 variables as significant predictors. Subsequent multivariate analysis indicated that independent risk factors for PG-SGA scores ≥ 4 included bedridden status, low BMI, low FFMI, and reduced HGS. Table 3 provides detailed odds ratios (ORs) and 95% confidence intervals (CIs) for both univariate and multivariate analyses.

To further explore these associations, restricted cubic splines were used to visualize nonlinear relationships between continuous independent variables and the dependent variable, stratified by gender. The resulting visualizations are shown in Fig. 5.

Discussion

Our comparative analysis of machine learning models revealed that ensemble-based methods provided promising predictive performance for malnutrition risk. Specifically, Random Forest achieved the highest AUC of 0.77 (95% CI: 0.69–0.84), while XG Boost demonstrated the best balance between sensitivity and specificity with the highest Gmean value of 0.71. These two models were ultimately selected for our final analysis due to their robust performance and complementary strengths. The superior performance of these ensemble models can be attributed to their ability to capture complex, non-linear relationships between nutritional indicators without overfitting.

Through feature importance analysis, both models consistently identified BMI, HGS, FFMI, and bedridden status as key predictors of malnutrition in cancer patients. This machine learning approach demonstrated strong predictive accuracy in identifying patients with PG-SGA scores ≥ 4, with the integration of these multidimensional indicators significantly enhancing the identification of high nutritional risk patients [23].While the traditional PG-SGA remains a comprehensive assessment tool [24],it requires active patient involvement for subjective evaluations and depends heavily on professional medical

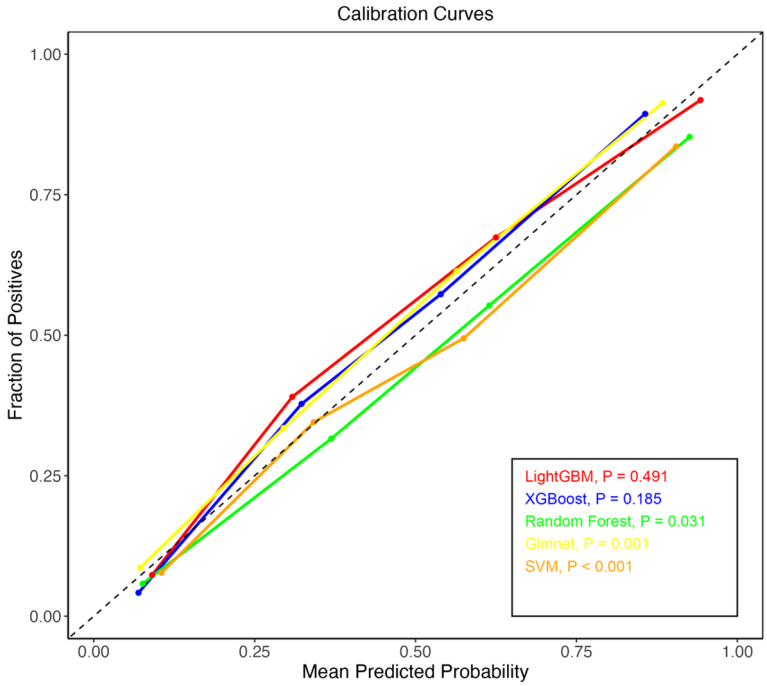

Fig. 2 Comparison of calibration curves for different machine learning models

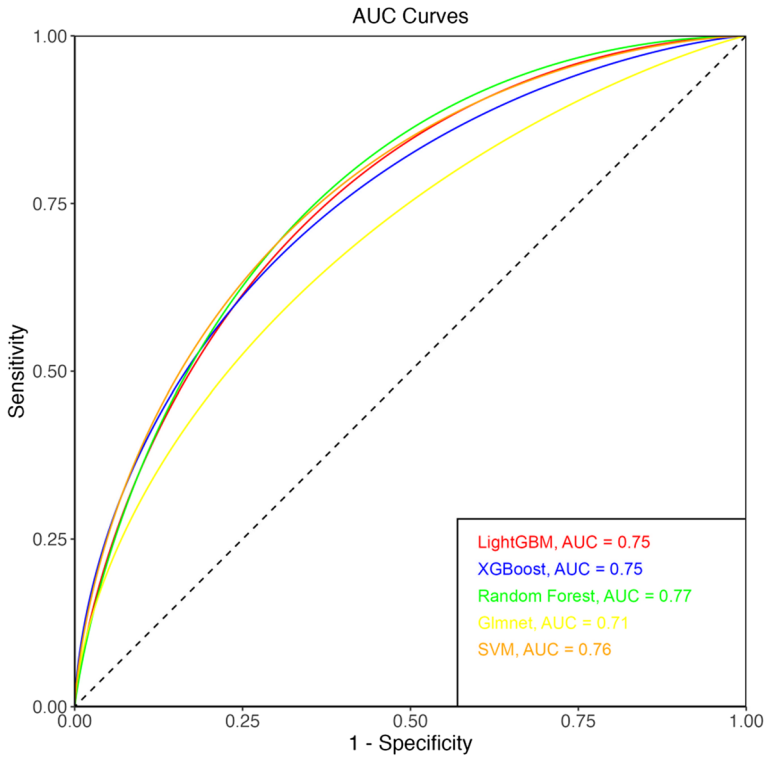

Fig. 3 Comparison of Receiver Operating Characteristic (ROC) curves of different machine learning models on the test set

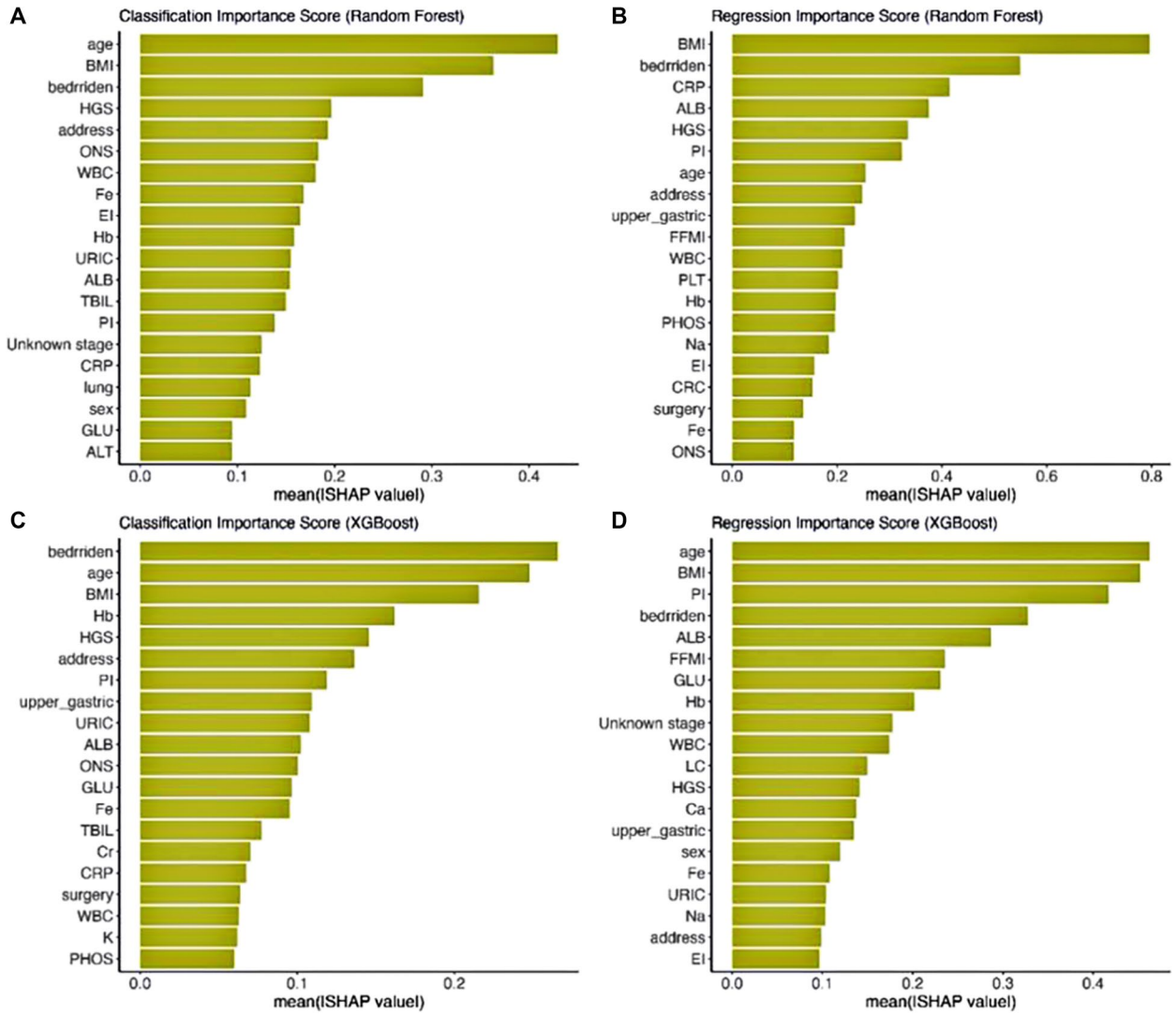

Fig. 4 Shapley Additive Explanations (SHAP) analysis for two models

personnel, making it both time-intensive and operationally complex [25]. To address these limitations, researchers have sought to modify the PG-SGA to preserve its accuracy while streamlining the process and reducing time demands. Although simplifying PG-SGA entries can shorten evaluation time, this approach often compromises the accuracy of nutritional assessments, limiting the tool to preliminary screening rather than comprehensive evaluation [12, 26]. Although some single-center studies have reported favorable outcomes regarding the stability and sensitivity of modified PG-SGA versions, these adaptations have yet to gain traction in broader clinical practice [27, 28]. The objective indicators identified in our study may offer a more practical and efficient alternative to support healthcare professionals in identifying patients at high nutritional risk, although further clinical validation is needed.

BMI and FFMI play complementary roles in reflecting malnutrition risk. Metabolic changes in cancer patients, including enhanced protein catabolism and reduced muscle synthesis driven by inflammation (e.g., TNF-α, IL-6), often lead to early FFMI decline, even when BMI remains within the normal range [29–31]. For patients with normal BMI, who may otherwise be overlooked for malnutrition, FFMI addresses the limitations of BMI alone, enabling the early detection of malnutrition [32]. Previous studies have also demonstrated that FFMI decline serves as a reliable predictor of nutritional status in patients with malignant tumors [33]. Our FFMI cut-off values differed slightly from prior research [34],

Table 3 Regression results for screening variables

Variables	Univariate		Multivariate	
	Odds ratio (95% CI)	*P* value	Odds ratio (95% CI)	*P* value
Age, years	1.03 (1.02–1.04)	< 0.001	0.99 (0.94–1.03)	0.568
Address				
City	Reference		Reference	
Country/urban	1.54 (1.16–2.05)	0.003	0.89 (0.29–2.67)	0.830
Bedridden (No/Yes)	2.79 (1.98–3.96)	< 0.001	3.16 (1.17–9.14)	0.026
ONS (No/Yes)	1.70 (1.21–2.41)	0.003	1.86 (0.63–5.59)	0.259
EI, Cal/kg/day	0.99 (0.96–1.01)	0.283		
PI, g/kg/day	0.69 (0.47–1.01)	0.057		
BMI, kg/m^2	0.84 (0.79–0.89)	< 0.001	0.82 (0.66–0.99)	0.045
FFMI, kg/m^2	0.82 (0.74–0.90)	< 0.001	1.36 (1.01–1.88)	0.045
HGS, kg	0.93 (0.91–0.96)	< 0.001	0.89 (0.82–0.96)	0.004
WBC, × 109/L	1.00 (0.93–1.06)	0.920		
Hb, g/L	0.96 (0.94–0.97)	< 0.001	0.97 (0.93–1.00)	0.057
ALB, g/L	0.85 (0.80–0.91)	< 0.001	0.99 (0.85–1.16)	0.939
Na, mmol/L	0.90 (0.82–0.97)	0.013	0.95 (0.80–1.16)	0.603
Fe, umol/L	1.01 (0.97–1.05)	0.622		

Abbreviation: ONS oral nutritional supplement, *EI* energy intake, *PI* protein intake, *BMI* body mass index, *FFMI* fat free mass index, *HGS* hand grip strength, *WBC* white blood cell; *Hb* hemoglobin, *ALB* albumin

likely due to variations in population characteristics and research aims. However, they reinforce FFMI's value in early detection of muscle depletion and hidden malnutrition, especially in patients with normal BMI.

HGS, a key indicator of overall muscle strength, exhibits its predictive value across molecular, cellular, and systemic levels. At the molecular level, cancer patients often experience abnormal muscle fiber protein expression, mitochondrial dysfunction, and increased oxidative stress, which directly impair muscle strength production [35, 36]. At the cellular level, reductions in muscle fiber cross-sectional area and altered neuromuscular junction functionality further exacerbate these effects [37]. At the systemic level, decreased nutrient utilization efficiency and endocrine dysfunction contribute to a self-reinforcing cycle of decline [38]. HGS effectively evaluates muscle function and physical condition, with its decline not only associated with PG-SGA scores [39–41] but also predictive of recovery potential [42]. Building on this, the sex-specific cut-off values established in our study offer more refined standards compared to previously suggested thresholds [43]. Such gender-specific references are crucial, considering biological differences in muscle composition and strength, and thus can significantly enhance the precision of nutritional assessments in clinical practice.

Bedridden state plays an important role in leading to disused muscle atrophy, accelerating bone loss and decreasing cardiopulmonary function. It also affects the nutritional status of patients by increasing stress response and inflammatory markers, thereby disrupting normal metabolism and aggravating malnutrition [44]. Bedridden patients often face psychosocial challenges such as anxiety, depression and anorexia. These challenges cause a mixture of physical and psychological factors, resulting in higher PG-SGA scores.

Our study also emphasized the importance of considering gender differences in nutritional assessment. Our analysis by gender shows that there are significant differences between men and women in key indicators (Fig. 5). This suggests that we need to consider gender specific factors when identifying patients with a PG-SGA score of 4 or higher. These results support the concept of precision medicine and personalized care and provide a more personalized and practical method for clinical practice.

The predictive value of BMI, FFMI, and HGS for malnutrition in this study matches previous research [33, 45–47]. Nevertheless, several limitations warrant attention. First, our prospective single-center design ensured consistent data collection and minimized selection bias; however, it limits generalizability, as variations in patient demographics, clinical practices, and resource availability across institutions may affect the applicability of our findings. Second, due to challenges in acquiring comparable external datasets, our conclusions rely solely on internal data, potentially introducing bias and optimistic performance estimates—thus, caution is warranted until

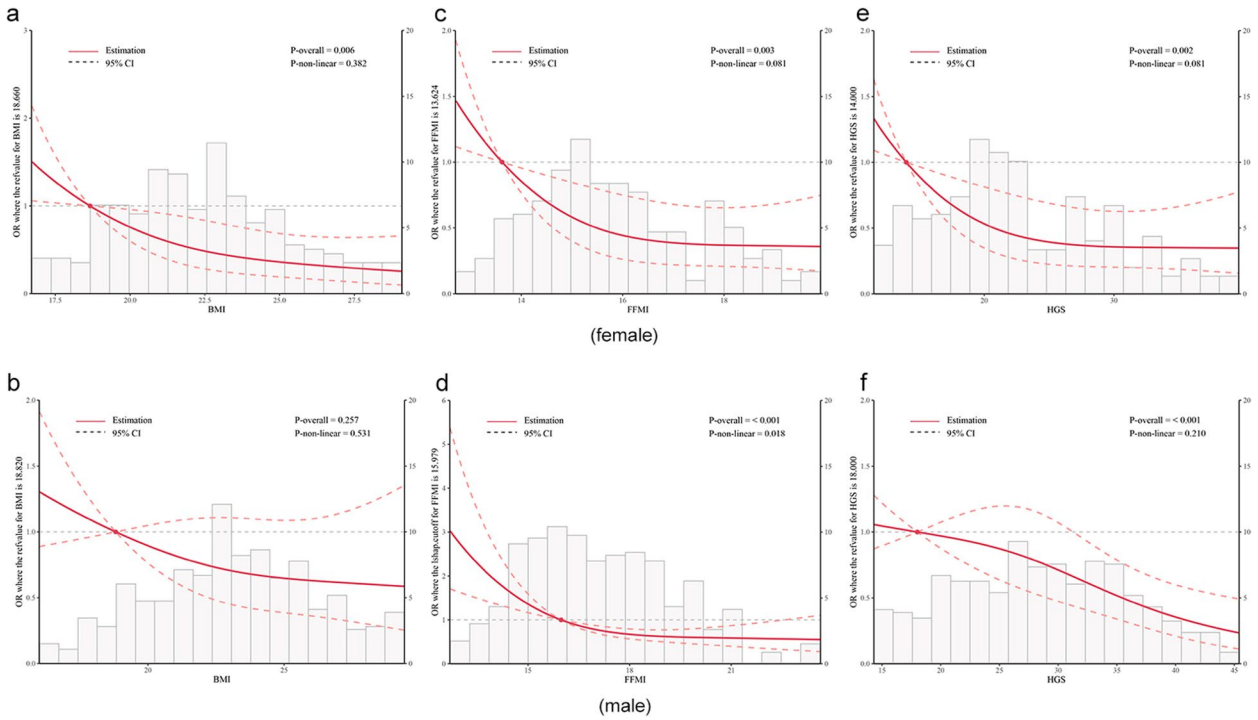

Fig. 5 The restrict cubic spline plots for continuous variables. The horizontal dashed line represents the reference OR of 1.0. 95% CI 95% confidence interval

multicenter external validations can confirm our results. Third, the limited sample size and algorithmic constraints restricted our ability to produce detailed SHAP beeswarm plots that might have provided deeper insights into feature relationships; nevertheless, our SHAP analysis effectively identified the primary predictors. Fourth, while SMOTE balanced the dataset, it may have introduced synthetic bias or artificial noise, impacting model robustness. These limitations underscore the need for future multicenter, prospective studies with larger, more diverse samples to validate and refine our findings, and for exploring advanced analytical methods, such as deep learning or hybrid models, to further enhance predictive accuracy and clinical utility.

Conclusion

This study identified four objective factors—BMI, FFMI, HGS, and bedridden status—as significant predictors for identifying high-risk malnutrition groups with PG-SGA scores ≥ 4. Gender-stratified analysis further provided optimal cutoff values for BMI, FFMI, and HGS specific to males and females, offering a more refined and targeted reference for rapidly identifying at-risk patients. The findings address some of the subjectivity and complexity associated with the traditional PG-SGA scoring system, presenting an efficient and objective approach for malnutrition assessment in clinical settings. We recommend prioritizing these indicators in practice to quickly identify patients at high risk for malnutrition, enable timely nutritional interventions, and ultimately improve both prognosis and quality of life.

Acknowledgements

There is not.

Authors' contributions

QG participated in all processes and completed the final paper writing; HJ completed data collection and analysis; CM is responsible for the conception and quality control of the study; LB, LY, HG and YM completed data collection; TX and YH completed the quality control of the study and revised the manuscript.

Funding

This research did not receive any specific grant from funding agencies in the public, commercial, or not-for-profit sectors.

Data availability

Data is provided within the manuscript or supplementary information files.

Declarations

Ethics approval and consent to participate

All experiments involving human participants and/or human tissue samples in this study were performed in accordance with the Declaration of Helsinki and relevant institutional guidelines and regulations. Ethical approval was obtained from the Ethics Committee of Sichuan Provincial Cancer Hospital (Approval Number: SCCHEC-02–2022-066). Written informed consent was obtained from all participants prior to enrollment.

Consent for publication
We confirm our consent for the manuscript titled "Rapid Identification of Tumor Patients with PG-SGA ≥ 4 Based on Machine Learning: A prospective Study" to be submitted for publication in BMC cancer. We agree to the submission of the manuscript and its contents to be published in the journal if accepted.

Competing interests
The authors declare no competing interests.

Received: 18 January 2025 Accepted: 24 April 2025
Published online: 20 May 2025

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