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Predictive Model for Mild Cognitive Impairment Risk in Community-Dwelling Older Adults with Depressive Symptoms Based on Explainable Machine Learning: A Cross-Sectional Study

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Structured Abstract

Background:

Mild cognitive impairment (MCI) represents a high-risk prodromal stage of Alzheimer's disease, and its prevalence and conversion risk are higher among community-dwelling older adults presenting with depressive symptoms. Currently, there is a lack of interpretable and easily implementable risk stratification tools specifically tailored for this "high-risk within high-risk" population.

Methods:

This cross-sectional study enrolled 297 community-dwelling older adults with depressive symptoms (GDS-15 $\geq$ 5). Guided by the biopsychosocial model, 18 candidate predictors were collected. Core predictors were selected using LASSO regression and stepwise logistic regression, and four predictive models were developed: logistic regression, support vector machine, random forest, and XGBoost. Model performance was evaluated using five-fold cross-validation and an independent test set, and model interpretability was addressed using SHAP for both global and local explanations.

Results:

Five core predictive factors were ultimately identified: sleep quality, educational level, activities of daily living (ADL) ability, social support, and anxiety status. The XGBoost model exhibited the best performance on the test set, and both calibration and decision curve analyses indicated favorable clinical net benefit. SHAP analysis further revealed that poor sleep, ADL dependency, and anxiety substantially increased the risk of MCI, whereas higher education and strong social support acted as protective factors.

Conclusion :

We developed an interpretable MCI risk stratification model based on XGBoost and SHAP, capable of

effectively identifying individuals at high risk of MCI among community-dwelling older adults with depression. The model demonstrates strong discriminative performance and clinical interpretability, and has the potential to provide community healthcare workers with an intuitive and reliable tool for early screening and intervention decision support.

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Keywords: mild cognitive impairment; depressive symptoms; machine learning; explainable artificial intelligence; risk factors; cross-sectional study.

1 Introduction

Mild cognitive impairment (MCI) is a transitional state between normal aging and dementia^[1], characterized by objectively detectable cognitive decline while activities of daily living are largely preserved and the clinical diagnostic criteria for dementia are not met. MCI represents a high-risk prodromal stage of Alzheimer's disease, with a risk of progression to dementia that is 3–5 times higher than that of cognitively normal older adults^[2]. Approximately 10%–20% of elderly individuals worldwide have MCI, and conversion rates within five years can be as high as 70%^[3]. With the acceleration of population aging in China, the cognitive decline and dementia risk associated with MCI have become prominent public health concerns. Early identification of high-risk individuals in the community is key to secondary prevention^[4].

Depressive symptoms constitute a complex psychological state characterized by core features such as low mood, diminished interest, and loss of energy, and are highly prevalent among the elderly; community detection rates in China reach as high as 23.6%^[5]. They are not merely affective disturbances but also act to precipitate a variety of geriatric syndromes^[6]. From a pathophysiological perspective, depression and cognitive impairment share mechanisms including hypothalamic–pituitary–adrenal axis dysregulation, chronic low-grade inflammation, and reduced brain-derived neurotrophic factor, which provide a biological basis for their association^[7,8,9].

Although the causal relationship between MCI and depressive symptoms requires further confirmation through longitudinal studies, the frequent coexistence and mutual exacerbation of the two conditions in older adults is clinically significant and cannot be ignored^[10]. Substantial evidence indicates that depressive symptoms constitute an independent risk factor for MCI and accelerate its progression to dementia—MCI patients with concurrent depression face a 1.2–2.3-fold higher risk of converting to dementia compared with those without depression^[11,12]. This group forms a vicious "depression–MCI–dementia" cycle and can be regarded as a "high-risk within the high-risk" population^[13]. Therefore, screening for MCI among older adults with depressive symptoms is more urgent than screening in the general elderly population^[14,15].

To date, several studies have developed prediction models for MCI among community-dwelling older adults using traditional statistical approaches or machine learning algorithms^[16,17]. However, models specifically targeting MCI prediction in populations with late-life depressive symptoms remain very limited^[18]. Moreover, conventional models such as logistic regression have restricted capacity to capture complex nonlinear relationships, while machine learning models, despite superior performance, are hindered by their "black box" nature, which impedes clinical adoption^[19,20]. In community care, nurses and primary clinicians need not only to identify who is at high risk but also to understand why—whether risk stems from poor sleep, insufficient social

support, anxiety, or functional decline. Only by identifying modifiable driving factors can individualized intervention plans be devised^[21,22]. Therefore, there is a need for an integrative model that incorporates multidimensional factors, achieves strong predictive performance, and offers clinical interpretability^[23,24].

This study, grounded in the biopsychosocial medical model, employs cross-sectional data to construct an interpretable machine-learning model for stratifying the risk of mild cognitive impairment (MCI)^[25]. The aim is to develop an interpretable MCI risk stratification model based on machine-learning algorithms. We will compare four algorithms—Logistic Regression (LR), Support Vector Machine (SVM), Random Forest (RF), and eXtreme Gradient Boosting (XGBoost)—and apply SHAP (SHapley Additive exPlanations) to provide global and local explanations of the optimal model, thereby identifying key risk factors and their directions of effect to offer community care providers an intuitive and trustworthy decision-support tool^[26,27,28].

2 Methods

2.1 Study Subjects

This study employed a cross-sectional survey design. Between December 2025 and March 2026, using convenience sampling, communities under the jurisdiction of the Community Health Service Centers in Jian'guang, Jiannan, and Hezhou subdistricts of Fengcheng City, Yichun, Jiangxi Province, were selected as the study sites^[29]. Inclusion criteria were: (1) age ≥ 65 years; (2) continuous residence in the community for ≥ 6 months with plans to remain for at least one more year; (3) a score ≥ 5 on the 15-item Geriatric Depression Scale (GDS-15), indicating the presence of depressive symptoms^[19]; and (4) provision of informed consent and voluntary participation in the study. Exclusion criteria were: (1) clinically diagnosed neurodegenerative disorders such as dementia or Parkinson's disease, or a history of stroke with residual significant functional impairment (modified Rankin Scale >2)^[12]; (2) severe somatic illnesses, including hospitalization for major cardiovascular events such as myocardial infarction within the past 6 months, or current receipt of regular dialysis, radiotherapy, or chemotherapy; (3) a prior history of schizophrenia or bipolar disorder^[30]; and (4) severe visual or hearing impairment precluding completion of questionnaire interviews.

The sample size was estimated using the formula for cross-sectional studies: $N = [Z_{(\alpha/2)}^2 \times P \times (1 - P)] / \delta^2$. With $Z_{(\alpha/2)} = 1.96$ and allowable error $\delta = 0.05$. Because there are no precise reports of the prevalence of mild cognitive impairment (MCI) among older adults with depressive symptoms, a conservative estimate of $P = 0.5$ was used, yielding a calculated sample size of 247. Allowing for a 20% invalid questionnaire rate, the final required sample size was determined to be at least 297^[31]. The study ultimately included 297 valid samples, which were randomly stratified by MCI status and split into a training set ($n = 208$) and a test set ($n = 89$) at a 7:3 ratio. The training set was used for feature selection, model training, and 5-fold cross-validation; the test set was reserved solely for final model performance evaluation and remained “unseen” throughout model development^[32]. The sample selection flow is shown in Figure 1.

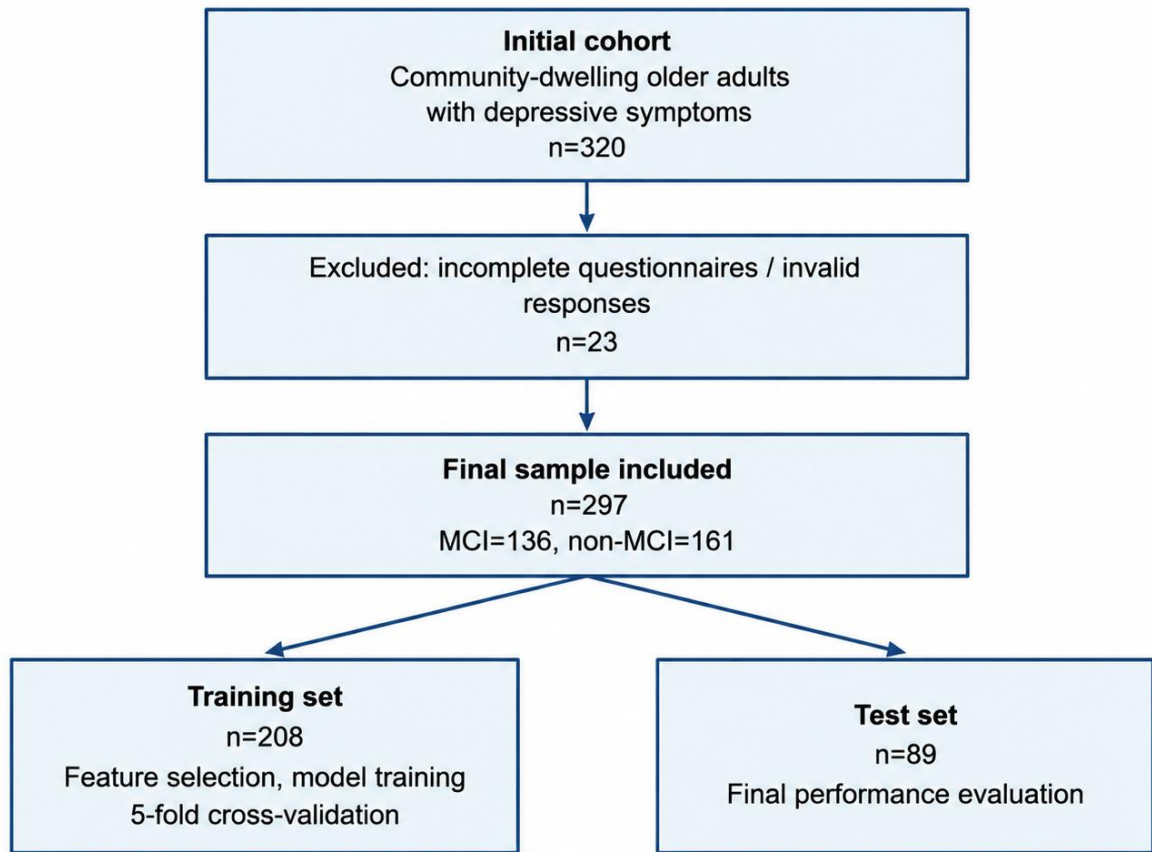


Figure 1 Sample selection flowchart

2.2 Outcome Measures: Assessment of Mild Cognitive Impairment

The outcome variable in this study was the presence of mild cognitive impairment (MCI) among community-dwelling older adults with depressive symptoms. MCI was determined using the Montreal Cognitive Assessment (MoCA)^[17,18]. The MoCA assesses seven cognitive domains—visuospatial and executive function, naming, attention, language, abstraction, delayed recall, and orientation—with a total score of 30 points; higher scores indicate better cognitive function. The instrument demonstrates high sensitivity and specificity for identifying MCI, with a Cronbach's α of 0.818, indicating good reliability and validity^[17]. Using the Chinese diagnostic cutoffs established by Professor Jia Jianping's research team, MCI thresholds for populations with different educational levels are: illiterate group ≤ 13 , primary school group ≤ 19 , and junior high school and above group ≤ 24 ^[18]. Based on these criteria, participants were classified into MCI and non-MCI groups. All MoCA assessments were conducted independently by uniformly trained researchers, with 10% of assessments randomly rechecked; the interrater agreement (Kappa) was 0.92^[13].

2.3 Predictor Variables and Dataset Construction

The predictive variables included in this study were selected according to the biopsychosocial medical model, yielding a total of 18 variables categorized into three dimensions: biological factors, psychological factors, and sociological factors^[24]. All variables were obtained directly through face-to-face questionnaires and physical measurements.

Biological factors include: age, sex, body mass index (BMI), number of chronic conditions, history of smoking, history of alcohol consumption, self-rated health status, and history of falls in the past six months^[40].

Psychological factors included: depressive symptoms, assessed using the 15-item Geriatric Depression Scale (GDS-15) with a total score range of 0–15, where a score ≥ 5 indicates the presence of depressive symptoms; for analysis this was treated as a continuous variable to retain dose–response information^[19]; anxiety status, assessed using the Generalized Anxiety Disorder 7-item scale (GAD-7), with a score ≥ 5 defining the presence of anxiety symptoms^[20]; sleep quality, assessed using the Pittsburgh Sleep Quality Index (PSQI), total score range 0–21^[21]; nutritional status, assessed using the Mini Nutritional Assessment—Short Form (MNA-SF), total score range 0–14^[22].

Sociological factors included: educational level; marital status; living arrangement; monthly income; ability to perform activities of daily living, assessed using the Activities of Daily Living (ADL) scale with a total score range of 14–56, where higher scores indicate greater dependency^[23]; and social support, assessed using the Social Support Rating Scale (SSRS) with a total score range of 12–66^[24].

Data preprocessing: For continuous variables with missingness $< 5\%$, missing values were imputed using the median; for categorical variables, the mode was used. Variables with missingness $> 15\%$ were excluded. Outliers were detected using boxplots; continuous values exceeding the mean ± 3 standard deviations were winsorized (truncated to the 5th and 95th percentiles). This procedure was performed only on the training set, and the resulting truncation thresholds were applied to the test set^[26].

All rating scales (GDS-15, GAD-7, PSQI, MNA-SF, ADL, SSRS and MoCA) adopted in this study are published standardized assessment tools from previously published studies, and corresponding references have been listed in the reference list. No self-designed questionnaires were developed for this cross-sectional research.

2.4 Feature Selection

To prevent data leakage and ensure objectivity in feature selection, all feature selection procedures were performed exclusively within the training set ($n=208$), and the test set ($n=89$) was not involved in any feature selection process^[31].

Phase 1: Univariate prescreening. Univariate analyses were performed on 18 variables in the training set: continuous variables were tested using independent-samples t tests, and categorical variables using χ^2 tests. Variables with $P < 0.20$ were selected for inclusion in the next phase. This lenient threshold was adopted to avoid excluding potentially important predictors^[25].

Stage 2: LASSO (Least Absolute Shrinkage and Selection Operator) regression. Variables with $P < 0.20$ in the univariate analysis were entered into the LASSO regression^[25]. Prior to performing LASSO regression, all continuous variables in the training set (age, BMI, PSQI, MNA-SF, ADL, SSRS, GDS-15) were standardized using Z-score normalization once; the normalization parameters (mean and standard deviation) were calculated and saved exclusively from the training set. A 10-fold cross-validation was used to determine the optimal penalty parameter λ for the LASSO regression, and the $\lambda_{\min}$ that minimized the cross-validation error was selected as the final parameter; variables with nonzero coefficients were retained for the candidate pool^[25,31].

Stage 3: Stepwise logistic regression for refined selection. Variables identified by LASSO were entered into a binary stepwise logistic regression (forward selection, entry criterion $\alpha=0.05$, removal criterion $\alpha=0.10$) to further identify features with independently significant predictive effects^[42]. It should be noted that stepwise regression has inherent theoretical limitations related to unstable variable selection; therefore, the selection results from this stage are primarily intended to reduce model complexity and generate a core feature set, and the ultimate performance of the predictive model will be rigorously evaluated on an independent test set^[26,42].

2.5 Model Development and Comparison

2.5.1 Data Normalization and Balancing Processing

We first applied Z-score normalization to all continuous variables in the training set; this normalization was performed independently of the prior standardization used for LASSO. The means and standard deviations for the normalization were computed exclusively from the training set, and the same parameters were then applied to standardize the test set^[42]

Regarding class imbalance, we did not perform any oversampling on the entire training set; instead, within each fold of the five-fold cross-validation we applied SMOTE (Synthetic Minority Over-sampling Technique) to the training subset to generate minority-class samples. The validation sets and the final test set retained their original distributions. This approach prevents data leakage^[27].

2.5.2 Model Training and Hyperparameter Tuning

This study constructed predictive models using four machine learning algorithms: logistic regression (LR), support vector machine (SVM), random forest (RF), and extreme gradient boosting (XGBoost)^[28,32]. Within the training set, hyperparameter tuning was performed using 5-fold cross-validation combined with grid search, and the hyperparameter combination yielding the highest mean AUC was selected as the optimal configuration for each model. In each fold of the cross-validation, the training folds were used to fit the model and the validation fold to assess performance; this procedure was repeated five times and the mean and standard deviation of each metric were calculated^[31,32].

2.5.3 Model Performance Evaluation

The final model's performance was evaluated on an independent test set to verify its generalizability^[41]. Evaluation metrics included accuracy, precision, recall/sensitivity, specificity, F1-score, and the area under the receiver operating characteristic curve (AUC) with its 95% confidence interval. Calibration curves were plotted and the Brier score was calculated to assess the accuracy of the model's predicted probabilities^[42]. Decision curve analysis (DCA) was employed to evaluate the model's net clinical benefit across different threshold probabilities^[38].

All analyses were conducted in a Python 3.12 environment using packages including NumPy, pandas, scikit-learn, and XGBoost^[32].

3 Model Interpretation Based on SHAP

To address the "black-box" nature of machine learning models and enhance their clinical interpretability, this study employed the SHAP (SHapley Additive exPlanations) method to interpret the final selected optimal model^{[28][38]}. SHAP is a game-theoretic explanation framework that quantifies feature importance by computing the marginal contribution of each feature to the model's predictions^[28]. The specific analyses comprised: (1) global interpretability: generating a SHAP summary plot to display the distribution of SHAP values for each feature across all samples, thereby identifying the key factors that contribute most to MCI risk prediction and using color coding to indicate the relationship between feature value magnitude and prediction direction; (2) local interpretability: producing SHAP force plots for individual subjects to visually demonstrate how each feature shifts a subject's prediction from the baseline to the final predicted value, thereby explaining why the model assigns a high- or low-risk prediction to a particular individual^[38]. Through SHAP analysis, this study aims to make model predictions more understandable and acceptable to community healthcare providers^[20].

4 Results

4.1 Baseline Characteristics of the Study Population

The study initially enrolled 320 community-dwelling older adults meeting criteria for depressive symptoms. After excluding invalid questionnaires according to predefined exclusion criteria, a final sample of 297 participants was obtained, yielding an effective response rate of 92.8%. Based on MoCA scores and stratification by educational level, 136 participants were classified as having MCI, corresponding to a prevalence of 45.8%^[1,18]. The prevalence of MCI was 41.7% (45/108) in males and 48.1% (91/189) in females.

Table 1 presents the baseline characteristics of the MCI and non-MCI groups across all 18 variables. The two groups differed significantly in age, BMI, self-rated health status, prevalence of anxiety, total PSQI score, total MNA-SF score, education level distribution, proportion living alone, total ADL score, and total SSRS score (all $P < 0.05$). No significant differences were observed in sex, number of chronic diseases, smoking history, alcohol consumption history, history of falls, marital status, or monthly income distribution. Detailed comparisons are shown in Table 1.

Table 1 Baseline Characteristics of Study Participants (MCI Group vs. Non-MCI Group)

Variable	Total Sample (N=297)	MCI Group (n=136)	Non-MCI Group (n=161)	Statistic	P-value
Biological Factors					
Age (years, mean ± SD)	75.8 ± 6.2	78.8 ± 5.9	73.2 ± 5.2	t=8.67	<0.001
Sex, n (%)				$\chi^2=0.92$	0.338
Male	108 (36.4)	45 (33.1)	63 (39.1)		
Female	189 (63.6)	91 (66.9)	98 (60.9)		
BMI (kg/m ² , mean ± SD)	23.6 ± 3.2	21.8 ± 2.5	25.2 ± 2.8	t=-11.04	<0.001
Number of chronic diseases, n (%)				$\chi^2=4.75$	0.313
0	42 (14.1)	15 (11.0)	27 (16.8)		
1	78 (26.3)	32 (23.5)	46 (28.6)		
2	95 (32.0)	45 (33.1)	50 (31.1)		
3	58 (19.5)	32 (23.5)	26 (16.1)		

Variable	Total Sample (N=297)	MCI Group (n=136)	Non-MCI Group (n=161)	Statistic	P-value
≥ 4	24 (8.1)	12 (8.8)	12 (7.5)		
Smoking history, yes, n (%)	63 (21.2)	25 (18.4)	38 (23.6)	$\chi^2=0.91$	0.340
Alcohol consumption, yes, n (%)	87 (29.3)	35 (25.7)	52 (32.3)	$\chi^2=1.23$	0.267
Self-rated health status, n (%)				$\chi^2=13.01$	0.001
Good	65 (21.9)	18 (13.2)	47 (29.2)		
Fair	95 (32.0)	43 (31.6)	52 (32.3)		
Poor	137 (46.1)	75 (55.1)	62 (38.5)		
History of falls, yes, n (%)	98 (33.0)	52 (38.2)	46 (28.6)	$\chi^2=2.69$	0.101
Psychological Factors					
GDS-15 total score (mean $\pm$ SD)	8.3 $\pm$ 2.1	8.8 $\pm$ 2.1	7.8 $\pm$ 2.0	t=3.95	<0.001
Anxiety (GAD-7 ≥ 5), n (%)	129 (43.4)	79 (58.1)	50 (31.1)	$\chi^2=20.84$	<0.001
PSQI total score (mean $\pm$ SD)	11.1 $\pm$ 3.8	12.6 $\pm$ 3.4	9.8 $\pm$ 3.7	t=6.63	<0.001
MNA-SF total score (mean $\pm$ SD)	10.5 $\pm$ 2.1	9.2 $\pm$ 1.8	11.5 $\pm$ 1.8	t=-10.83	<0.001
Sociological Factors					

Variable	Total Sample (N=297)	MCI Group (n=136)	Non-MCI Group (n=161)	Statistic	P-value
Education level, n (%)				$\chi^2=11.70$	0.008
Illiterate/Semi-literate	89 (30.0)	52 (38.2)	37 (23.0)		
Primary school	128 (43.1)	58 (42.6)	70 (43.5)		
Junior high	52 (17.5)	18 (13.2)	34 (21.1)		
High school or above	28 (9.4)	8 (5.9)	20 (12.4)		
Marital status (not married), n (%)	121 (40.7)	61 (44.9)	60 (37.3)	$\chi^2=1.46$	0.227
Living status (living alone), n (%)	83 (27.9)	48 (35.3)	35 (21.7)	$\chi^2=6.07$	0.014
Monthly income, n (%)				$\chi^2=3.05$	0.218
<4000 CNY	156 (52.5)	78 (57.4)	78 (48.4)		
4000–6000 CNY	89 (30.0)	39 (28.7)	50 (31.1)		
≥6000 CNY	52 (17.5)	19 (14.0)	33 (20.5)		
ADL total score (mean ± SD)	18.5 ± 4.3	19.5 ± 4.8	17.6 ± 3.6	t=3.82	<0.001
SSRS total score (mean ± SD)	31.7 ± 7.7	28.2 ± 6.8	34.6 ± 7.2	t=-7.78	<0.001

Note: MCI: mild cognitive impairment; BMI: body mass index; GDS-15: 15-item Geriatric Depression Scale; PSQI: Pittsburgh Sleep Quality Index; MNA-SF: Mini Nutritional Assessment-Short Form; ADL: Activities of Daily Living Scale; SSRS: Social Support Rating Scale. Continuous variables are expressed as mean ± standard deviation; between-group comparisons were performed using independent-samples t tests. Categorical variables are presented as n (%); between-group comparisons were conducted using χ^2 tests.

Educational level, monthly income, and number of chronic diseases are ordinal categorical variables; between-group comparisons were performed using χ^2 tests on the original categories.

4.2 Feature Selection Results

In the training cohort (n=208), univariable analyses were first performed for all 18 variables, and variables with $P<0.20$ were selected, yielding 15 candidate predictors. The candidate predictors were entered into a LASSO regression model, and the optimal penalty parameter $\lambda_{\min}$ was determined by 10-fold cross-validation (see Fig. 2, left). Eight predictors with nonzero coefficients were retained: age, educational level, BMI, number of chronic diseases, self-rated health status, anxiety (GAD-7), sleep quality (PSQI total score), and social support (SSRS total score). The LASSO coefficient trace and cross-validation error curve are shown in Fig. 2.

Subsequently, the eight aforementioned variables were entered into a binary stepwise logistic regression (forward selection, entry criterion $\alpha = 0.05$, removal criterion $\alpha = 0.10$)^[42]. As shown in Table 2, after seven iterations, five variables remained in the final regression model (all $P < 0.05$) and were identified as the core feature set for this predictive model: educational level (middle school or above), sleep quality (PSQI), anxiety status (present), activities of daily living (ADL), and social support (SSRS)^[23,24]. Collinearity diagnostics indicated that the variance inflation factor (VIF) for all variables was less than 2, suggesting no multicollinearity^[42]. Notably, although age and BMI were retained in the initial LASSO screening (nonzero coefficients), they were subsequently excluded from the stepwise logistic regression because they did not meet the entry criterion (age $P = 0.087$, BMI $P = 0.124$), indicating that their independent predictive effects were not significant after adjustment for other variables.

Table 2 Stepwise Logistic Regression Feature Selection Results

Variable	Reference Group	OR	95% CI	P-value
Education level				
(Junior high or above)	Below junior high	0.513	0.272–0.968	0.039
Sleep quality (PSQI total score)	Continuous variable	1.210	1.113–1.316	<0.001
Anxiety status (Yes)	No anxiety	3.170	1.782–5.641	<0.001

Variable	Reference Group	OR	95% CI	P-value
Activities of daily living (ADL total score)	Continuous variable	1.135	1.057–1.220	<0.001
Social support (SSRS total score)	Continuous variable	0.875	0.836–0.915	<0.001

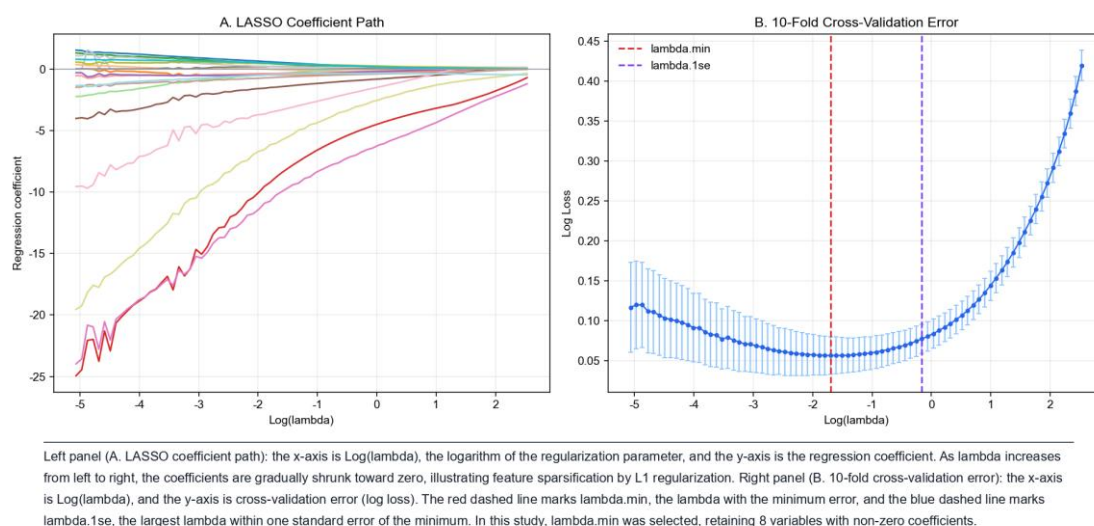


Figure 2 LASSO coefficient paths and 10-fold cross-validation

4.3 Model Development and Comparison

Based on the five selected core features, four machine learning prediction models were constructed^[32]. Within the training set ($n=208$), model performance was evaluated using 5-fold cross-validation. As shown in Table 3, the XGBoost model achieved the highest mean AUC (0.968 ± 0.037), slightly outperforming random forest (RF, 0.960 ± 0.035) and logistic regression (LR, 0.961 ± 0.034); the support vector machine (SVM) yielded a mean AUC of 0.955 ± 0.038 .

Table 3 Model performance with 5-fold cross-validation on the training set (mean $\pm$ standard deviation)

Model	Accuracy	Precision	Recall / Sensitivity	Specificity	F1 Score	AUC
Logistic Regression (LR)	0.909 ± 0.061	0.907 ± 0.129	0.916 ± 0.047	0.904 ± 0.132	0.905 ± 0.057	0.961 ± 0.034
Support Vector Machine (SVM)	0.899 ± 0.061	0.916 ± 0.117	0.874 ± 0.071	0.922 ± 0.108	0.890 ± 0.063	0.955 ± 0.038
Random Forest (RF)	0.890 ± 0.068	0.888 ± 0.118	0.884 ± 0.069	0.896 ± 0.113	0.882 ± 0.068	0.960 ± 0.035
XGBoost	0.918 ± 0.043	0.921 ± 0.072	0.905 ± 0.078	0.930 ± 0.066	0.910 ± 0.047	0.968 ± 0.037

Note: Values in the table represent the mean ± standard deviation from 5-fold cross-validation.

In the final performance evaluation on the independent test set (n=89) (Table 4, Figure 3 left), the XGBoost model achieved an AUC of 0.982 (95% CI: 0.952–0.997), accuracy of 0.888, precision of 0.943, recall of 0.805, specificity of 0.958, and F1 score of 0.868, demonstrating overall superior performance compared with logistic regression (AUC = 0.947), support vector machine (AUC = 0.955) and random forest (AUC = 0.959). In terms of calibration (Figure 3 right), the Brier score for XGBoost was 0.075, slightly better than the other models (logistic regression 0.110, support vector machine 0.079, random forest 0.104). It should be noted that the test-set AUC exceeds the cross-validated mean (0.968), which may be attributable to random fluctuation due to the small test-set sample size (n=89); therefore, the model’s generalizability requires external validation.

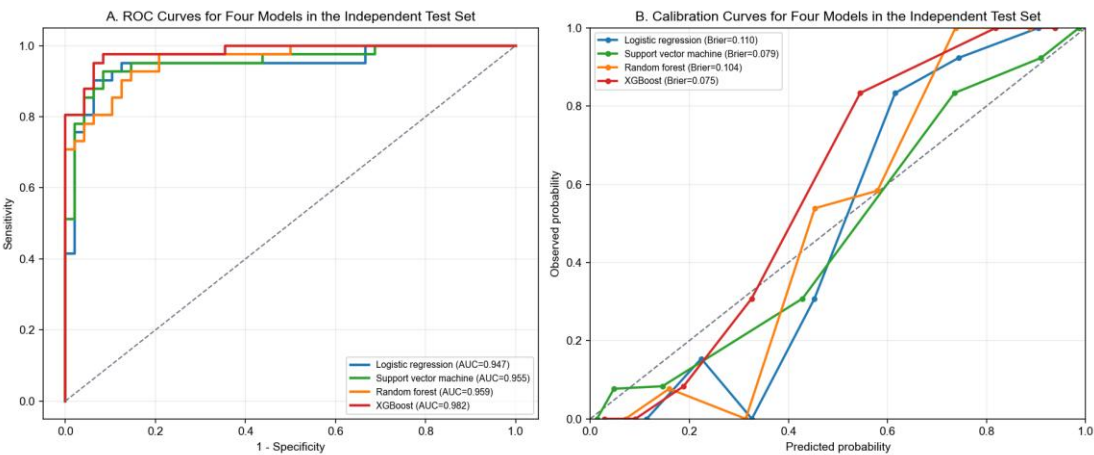
In the final performance evaluation on the independent test set (n = 89) (Table 4, Figure 3, left), the XGBoost model achieved an AUC of 0.982 (95% CI: 0.952–0.997), accuracy of 0.888, precision of 0.943, recall of 0.805, specificity of 0.958, and F1 score of 0.868, demonstrating overall superior performance compared with logistic regression (AUC = 0.947), support vector machine (AUC = 0.955), and random forest (AUC = 0.959). Regarding calibration (Figure 3, right), XGBoost yielded a Brier score of 0.075, slightly better than the other models. It should be noted that the test-set AUC exceeds the cross-validated mean value (0.968),

which may reflect random variation due to the relatively small test-set sample size (n = 89); thus, the model’s generalizability requires external validation.

Decision curve analysis (DCA) results (Figure 4) indicate that the XGBoost model provides higher net benefit across a broad range of risk thresholds (threshold probability 0.2–0.7), markedly outperforming the extreme strategies of “intervene on all” and “intervene on none,” demonstrating favorable clinical applicability^[38].

Table 4 Comparison of Final Model Performance on the Independent Test Set

模型	准确率	精确率	召回率/灵敏度	特异度	F1 分数	AUC (95% CI)	Brier 评分
逻辑回归(LR)	0.910	0.884	0.927	0.896	0.905	0.947 (0.890–0.991)	0.110
支持向量机 (SVM)	0.843	0.765	0.951	0.750	0.848	0.955 (0.897–0.992)	0.079
随机森林(RF)	0.865	0.968	0.732	0.979	0.833	0.959 (0.919–0.989)	0.104
XGBoost	0.888	0.943	0.805	0.958	0.868	0.982 (0.952–0.997)	0.075



Left panel (A. ROC curves for four models in the independent test set): the x-axis is 1 - specificity (false-positive rate), and the y-axis is sensitivity (true-positive rate). The four curves represent the discrimination of each model in the independent test set. XGBoost (red) has the highest AUC (0.982); a larger area under the curve indicates better discrimination between MCI and non-MCI. Right panel (B. calibration curves): the x-axis is predicted probability, and the y-axis is observed probability. The diagonal dashed line is the ideal calibration line, where predicted probability equals observed probability. Curves closer to this line indicate better calibration. XGBoost (red) has the lowest Brier score (0.075), indicating the best calibration.

Figure 3 ROC curve and calibration curve

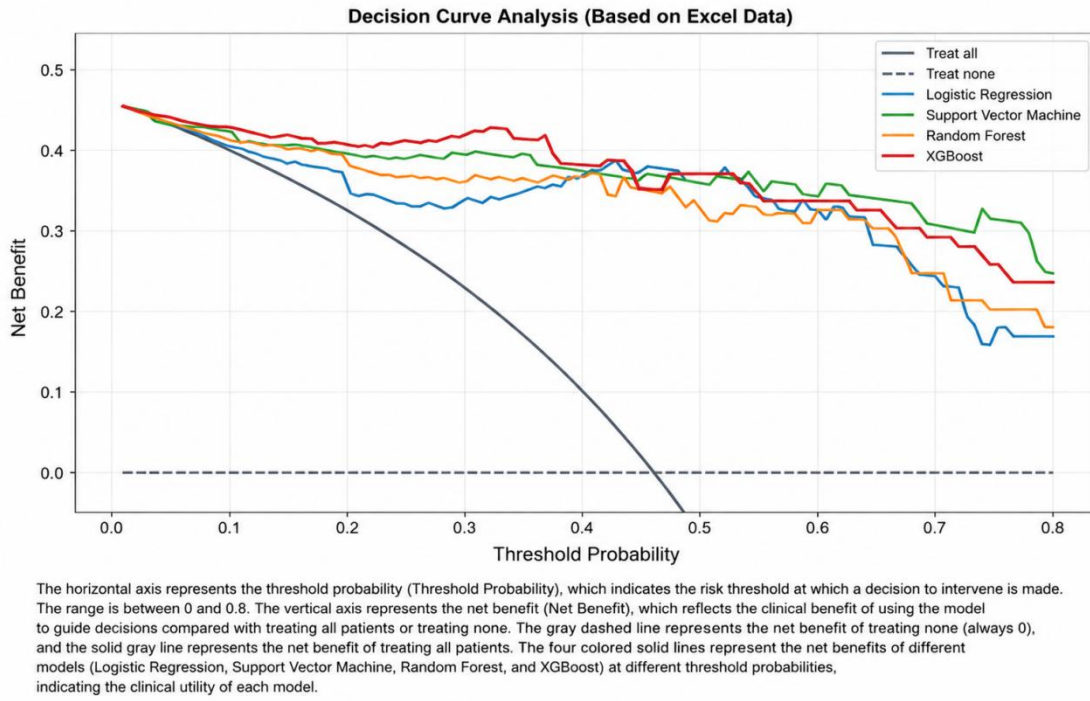


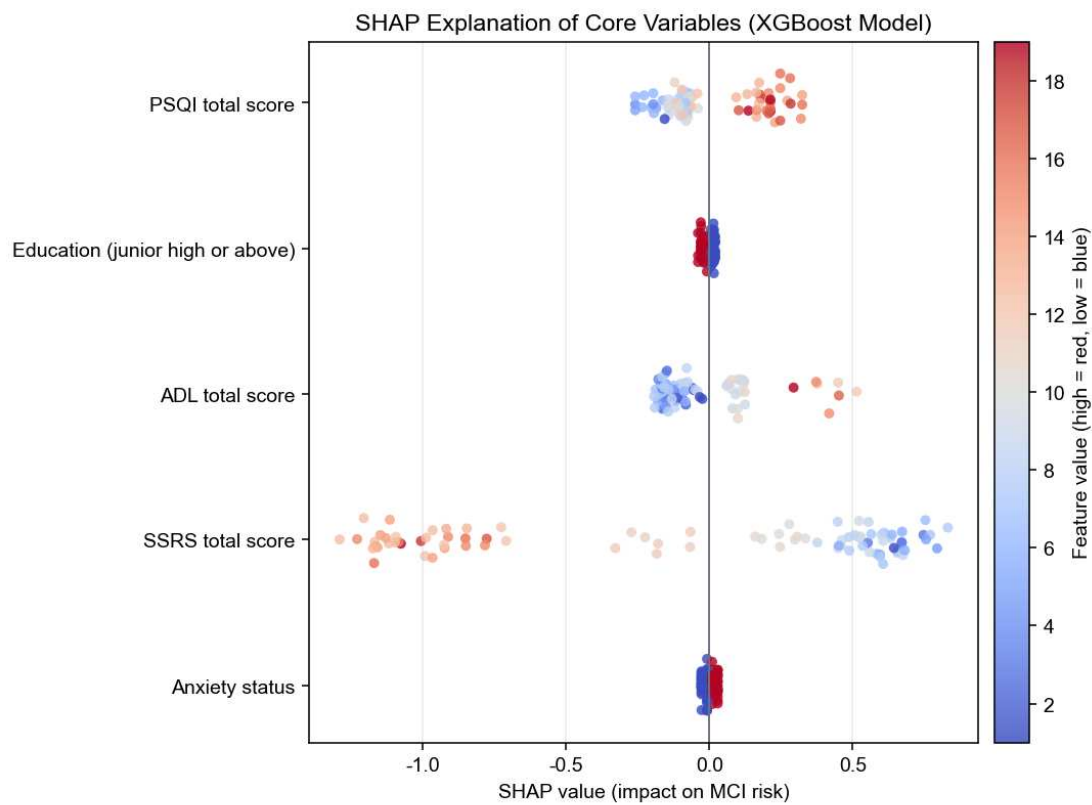
Figure 4 Decision curve analysis

4.4 Model Interpretation

To enhance the interpretability of the model, the SHAP method was applied to provide both global and local explanations for the best-performing XGBoost model^[28,38].

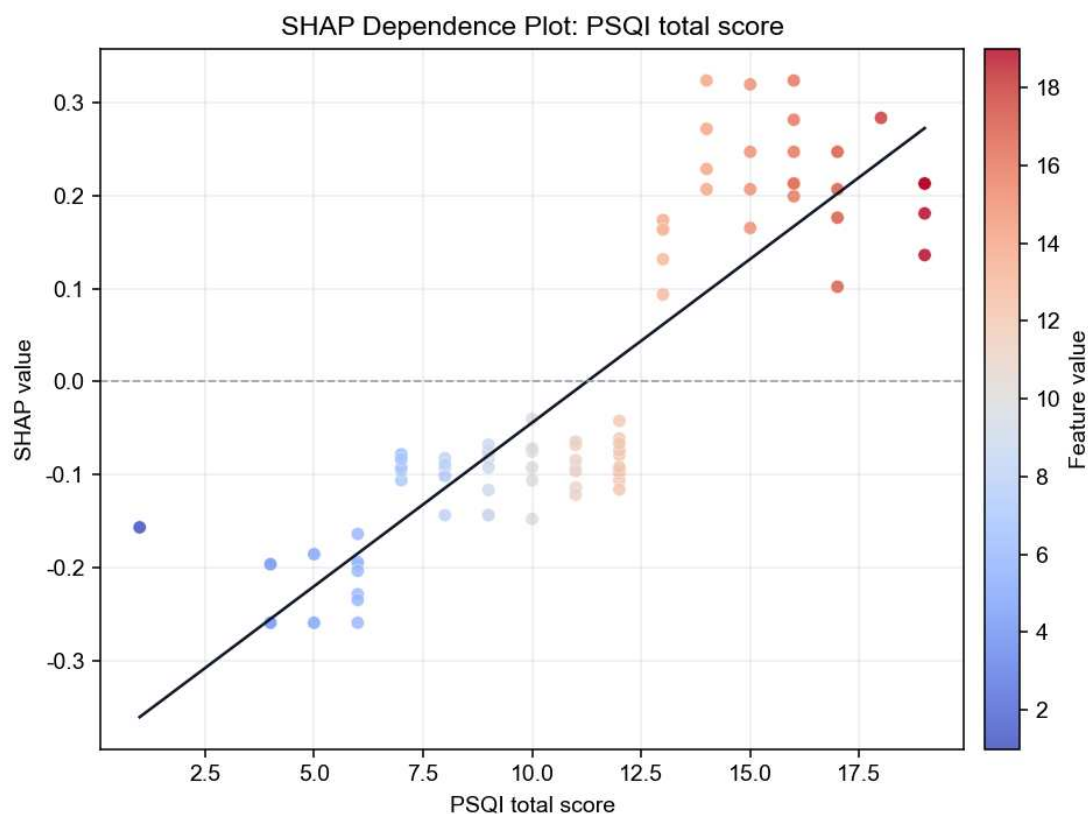
Global explanation (Figure 5A): The SHAP summary plot indicates that, ranked by feature importance, the top five contributors to MCI risk prediction are sleep quality (PSQI), educational level, ability in activities of daily living (ADL), social support (SSRS), and anxiety status^[23,24]. Color coding shows that higher PSQI scores, higher ADL scores, and presence of anxiety markedly increase MCI risk, whereas higher educational level and higher SSRS scores markedly decrease MCI risk (positive SHAP values)^[34,35]. Conversely, higher educational level (red, junior high school and above) and higher SSRS scores (red, good social support) significantly reduce MCI risk (negative SHAP values). SHAP dependence plots (Figures 5B–5F) further elucidate the directional effects of each factor.

Local explanation (Figure 5G): A representative high-risk individual was selected for SHAP force plot analysis. The results indicate that this individual's elevated predicted risk of MCI is primarily driven by a high PSQI score (severe sleep disturbance) and a low SSRS score (lack of social support)^[33,36]. This visualization clearly demonstrates how the model arrives at a specific risk prediction based on the combination of individual features, providing concrete targets for community care personnel to develop individualized intervention plans.



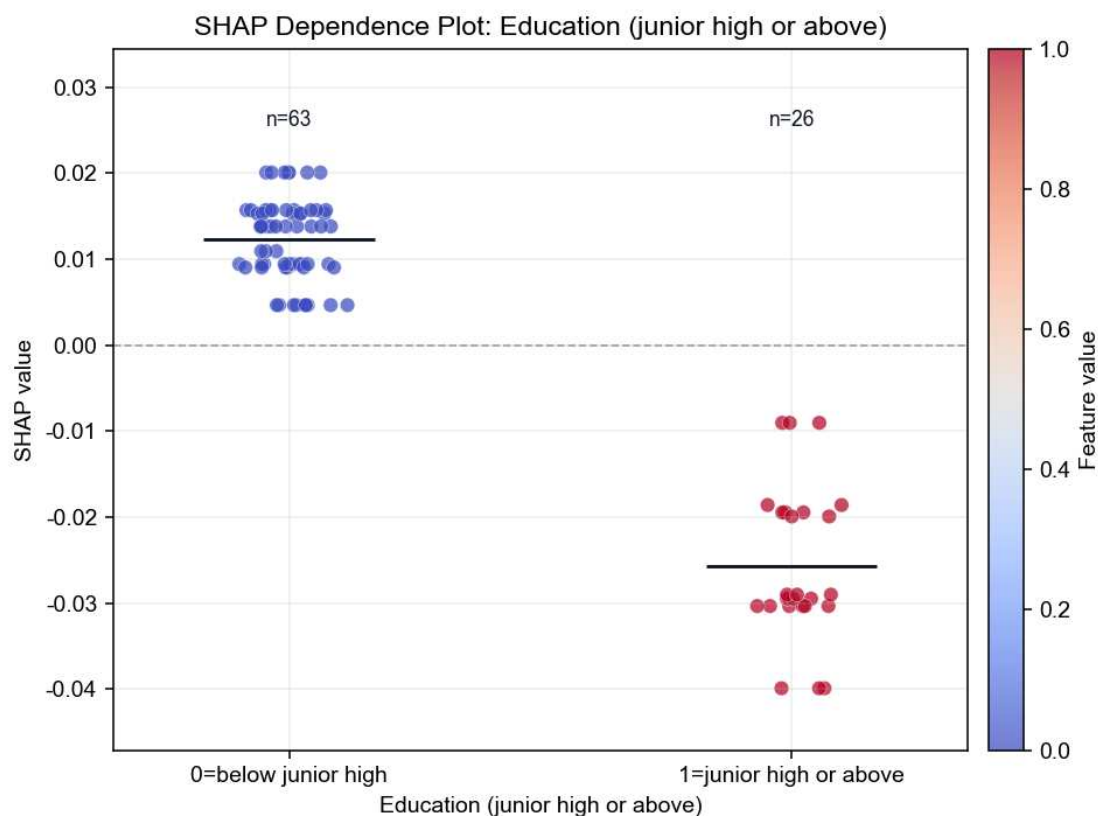
The x-axis is the SHAP value, representing each feature's contribution to MCI risk. Positive values on the right indicate increased MCI risk, whereas negative values on the left indicate reduced risk. The y-axis ranks features by importance from top to bottom: PSQI total score, education (junior high or above), ADL total score, SSRS total score, and anxiety status. The color bar indicates feature value (red = high, blue = low). Higher PSQI scores (red points on the right) markedly increase risk, whereas higher education and higher social support (red points on the left) act as protective factors. Each point represents one participant.

Figure 5A SHAP model explanation



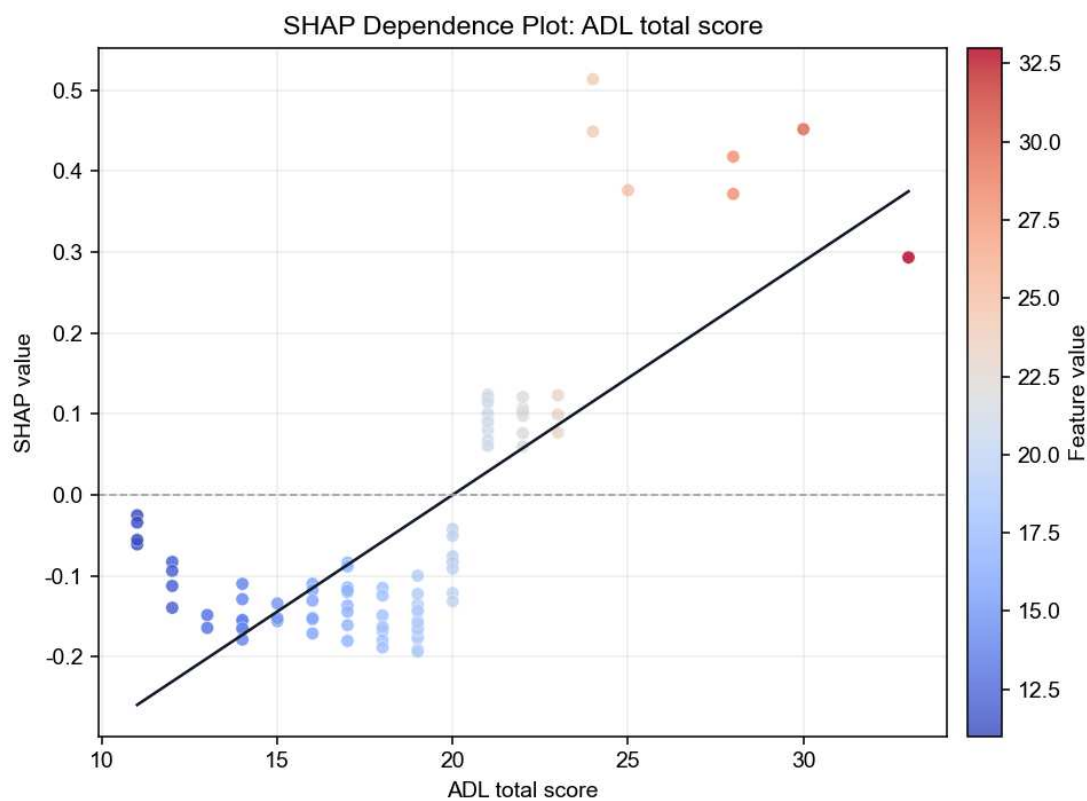
The x-axis is the PSQI total score (Pittsburgh Sleep Quality Index; approximately 2-18 points, with higher scores indicating poorer sleep quality), and the y-axis is the SHAP value. The color bar indicates feature value. The black trend line shows a strong positive association: lower PSQI scores (blue points, better sleep) have negative SHAP values and reduce MCI risk, whereas higher PSQI scores (red points, poorer sleep) have clearly positive SHAP values and substantially increase MCI risk. PSQI is the most important predictor in the model; participants with severe sleep disturbance (PSQI > 12) can have SHAP values above 0.3.

Figure 5B SHAP dependence plot



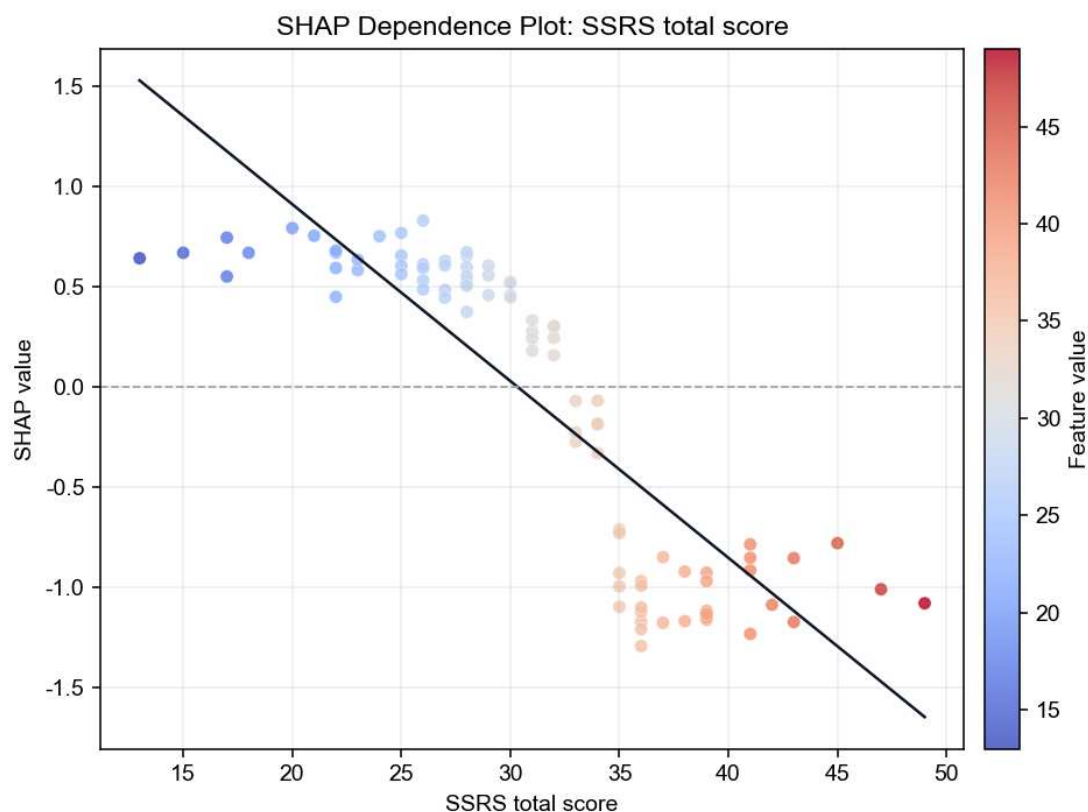
The x-axis is education as a binary variable (0 = below junior high school, 1 = junior high school or above), and the y-axis is the SHAP value for MCI risk. The color bar indicates feature value (red = 1, junior high or above; blue = 0, below junior high). The blue cluster on the left (n = 63) represents participants below junior high school, with positive SHAP values (approximately 0.005 to 0.02), indicating increased MCI risk. The red cluster on the right (n = 26) represents participants with junior high school education or above, with negative SHAP values (approximately -0.01 to -0.04), indicating a protective effect. The black horizontal lines are group mean SHAP values. In the final model, junior high school education or above was associated with lower MCI risk (OR = 0.513, 95% CI: 0.272-0.968).

Figure 5C SHAP dependence plot Education level



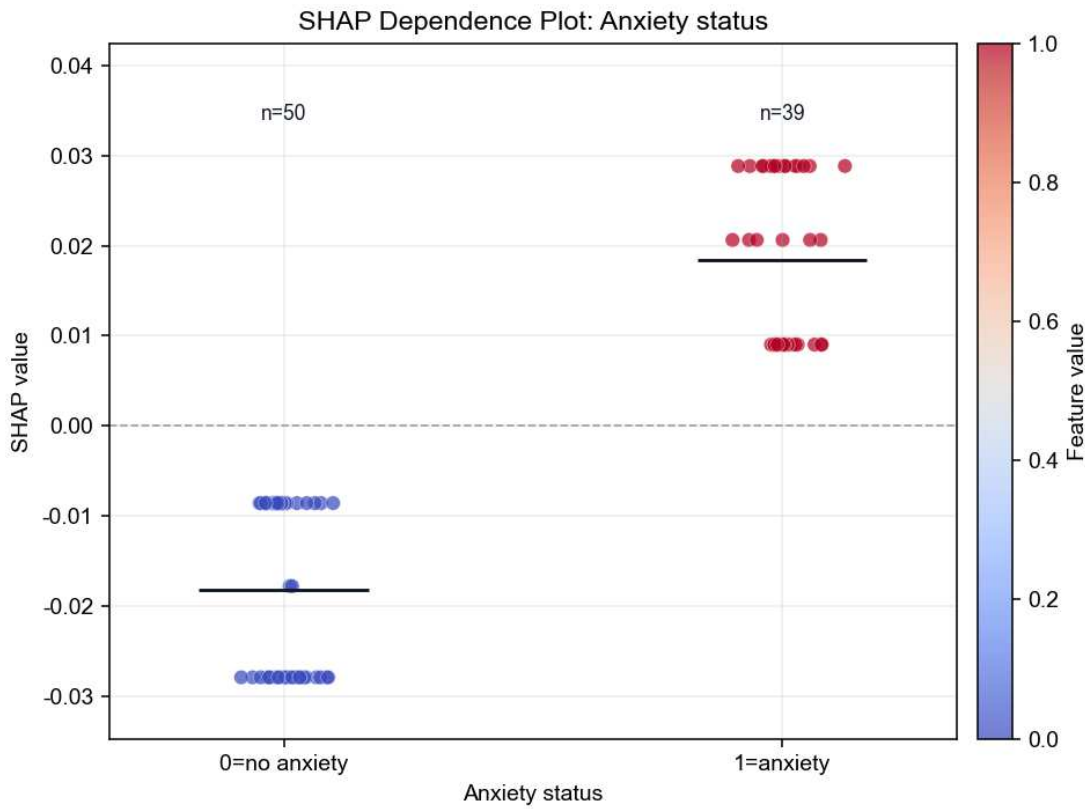
The x-axis is ADL total score (activities of daily living; approximately 10-34 points, with higher scores indicating greater functional dependence and poorer daily living ability), and the y-axis is the SHAP value for MCI risk. The color bar indicates feature value (red = higher score and poorer function, blue = lower score and better function). The black trend line shows a strong positive association: lower ADL scores have negative SHAP values and reduce risk, whereas higher ADL scores have positive SHAP values and increase risk. When ADL total score exceeds 20, SHAP values begin to shift from negative to positive, suggesting that functional dependence increases cognitive risk. In the final model, each 1-point increase in ADL score was associated with higher MCI risk (OR = 1.135, 95% CI: 1.057-1.220).

Figure 5D SHAP dependence plot for total ADL score



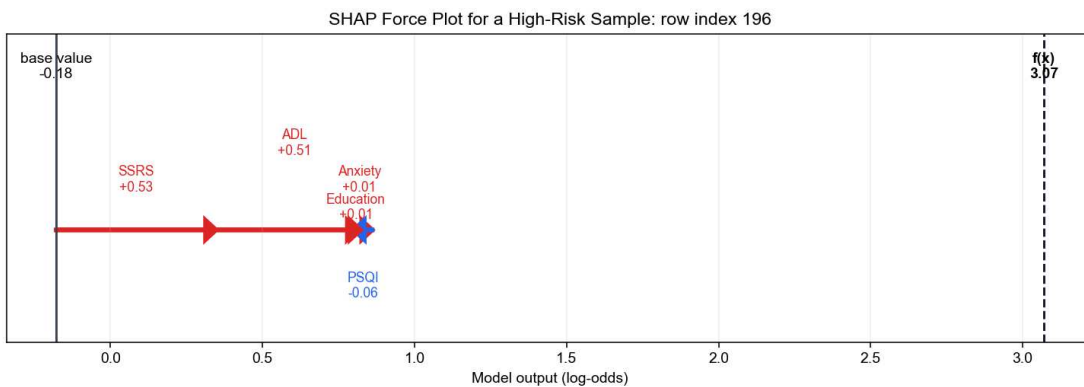
The x-axis is SSRS total score (Social Support Rating Scale; approximately 12-50 points, with higher scores indicating better social support), and the y-axis is the SHAP value for MCI risk. The color bar indicates feature value (red = higher score and better social support, blue = lower score and poorer social support). The black trend line shows a strong negative association: lower SSRS scores have positive SHAP values and increase MCI risk, whereas higher SSRS scores have negative SHAP values and reduce risk. When SSRS total score is below 30, SHAP values are mostly positive, suggesting that inadequate social support increases cognitive risk; when SSRS total score exceeds 35, SHAP values become negative and social support becomes protective. In the final model, each 1-point increase in SSRS score was associated with lower MCI risk (OR = 0.875, 95% CI: 0.836-0.915).

Figure 5E SHAP dependence plot SSRS total score



The x-axis is anxiety status as a binary variable (0 = no anxiety, 1 = anxiety), and the y-axis is the SHAP value for MCI risk. The color bar indicates feature value (red = anxiety, blue = no anxiety). The blue cluster on the left (n = 50) represents participants without anxiety, with negative SHAP values (approximately -0.01 to -0.03), indicating a protective effect. The red cluster on the right (n = 39) represents participants with anxiety, with positive SHAP values (approximately 0.01 to 0.03), indicating increased MCI risk. The black horizontal lines are group mean SHAP values. In the final model, anxiety was associated with higher MCI risk (OR = 3.170, 95% CI: 1.782-5.641).

Figure 5F SHAP dependence plot Anxiety state



The x-axis is the model output in log-odds, ranging from 0 to 3.0. The base value on the left is -0.18, representing the average log-odds in the study population. Red arrows push the prediction to the right and increase MCI risk: SSRS total score (+0.53, insufficient social support), ADL total score (+0.51, functional dependence), anxiety status (+0.01), and education (junior high or above, +0.01). The blue arrow pushes the prediction to the left and reduces risk: PSQI total score (-0.06, better sleep quality). After accumulating feature contributions, the final model output is $f(x) = 3.07$, corresponding to a high-risk prediction.

Figure 5G High-risk Samples SHAP

5 Discussion

We compared the ability of four machine learning models to identify MCI among community-dwelling older adults with depressive symptoms. XGBoost demonstrated the most stable performance, achieving an AUC

of 0.982, a Brier score of 0.075, and a calibration curve closest to the diagonal^[32,38]. With SHAP-based interpretation, the model is no longer a black box; community nurses can directly observe each predictor's direction and magnitude of contribution^[28,38]. The results indicate that XGBoost exhibits superior robustness in both discriminative performance and calibration metrics. Given its strong discrimination (AUC = 0.982), low Brier score (0.075), and excellent calibration, this model is suitable for community-level risk stratification applications^[38]. Moreover, integrating the model with SHAP values substantially enhances clinical interpretability^[28]. Therefore, XGBoost has the potential to serve as an effective tool for community healthcare personnel to identify high-risk individuals for MCI among older adults with depressive symptoms, enabling timely targeted interventions to improve cognitive outcomes^[14,15].

According to the present study, sleep quality (PSQI) was the strongest predictor associated with MCI risk, ranking first in SHAP contribution^[21,33]. Compared with previous studies^[33,41], a possible explanation is that sleep fragmentation reduces clearance of β -amyloid, exacerbates tau phosphorylation, and activates the HPA axis leading to elevated cortisol levels, all of which damage the hippocampus^[35]. Anxiety also entered the model, ranking fifth in contribution; it impairs cognition via chronic stress and inflammatory pathways^[37]. These findings suggest that, within depressed populations, sleep disturbance and anxiety may affect cognition more directly than depression per se^[9,10].

This study found that educational attainment is a protective factor: individuals with at least a junior high school education have approximately half the risk of MCI compared with those with less than a junior high education. One possible explanation is that higher education provides greater cognitive reserve, enabling individuals to maintain normal cognitive performance in the face of early neuropathological changes^[2,3]. Cognitive reserve theory posits that education delays the clinical manifestation of cognitive impairment by enhancing the efficiency and plasticity of neural networks^[3,18]. This is highly consistent with previous findings^[16]: older adults with education at or above the college level had only 0.4 times the risk of developing depressive symptoms compared to those who never attended school. Individuals with lower educational levels may lack sufficient cognitive stimulation and health literacy, leading to more rapid depletion of cognitive reserve^[4,16]. The SHAP dependence plot clearly shows that higher educational attainment corresponds to larger negative SHAP values and thus lower risk^[18].

Social support is equally important. For each one-point increase in SSRS, the risk of MCI decreases to 0.875-fold^[24]. Although marital status was not significant in univariate analysis, a continuous social support score better reflects the actual level of support than the binary “married or not” variable^[24,30]. A possible mechanism is that marital relationships provide sustained emotional support, social interaction, and health surveillance, all of which help maintain cognitive engagement^[29,30]. Unmarried individuals, including widowed and divorced older adults, may face social isolation, lack of regular daily rhythms, and lower motivation to seek medical care, thereby accelerating cognitive decline^[6,29]. This is consistent with existing evidence that marital status influences the social, behavioral, and nutritional environment of older adults, which in turn affects cognitive health^[24,36].

Greater dependency in activities of daily living (ADL) was associated with a higher risk of MCI^[23]. This finding is consistent with prior studies: ADL impairment may indirectly compromise cognitive function via pathways such as reduced cognitive stimulation, diminished self-efficacy, and increased risk of depression^[23,39]. Individuals with higher ADL scores require more assistance in daily life, which may reflect underlying cognitive decline already affecting instrumental activities of daily living^[39]. Notably, ADL ranked third in

SHAP contribution, suggesting that, among older adults with depression, asking “Have you had difficulty taking care of yourself recently?” may provide greater cognitive warning value than measuring blood pressure^[39].

The study also found that BMI and age did not enter the final predictive model. Although both were significant in univariate analyses, their P values decreased to 0.087 and 0.124, respectively, after stepwise regression^[40,42]. A possible explanation is that sleep quality and ADL level partially mediated the effect of age, while BMI overlapped with information on nutritional status; moreover, the relationship between BMI and cognition in older adults may be U-shaped and therefore not well captured by a linear model^[22,40]. Conversely, this indicates that among elderly individuals with depressive symptoms, modifiable factors such as sleep, anxiety, social support, and functional training are more important than nonmodifiable characteristics like age and body habitus^[37].

In summary, the five core factors identified in this study (PSQI, educational level, ADL, SSRS, and anxiety), together with the XGBoost model, demonstrated good performance in detecting MCI among community-dwelling older adults with depressive symptoms^[1,14]. In other words, modifiable domains such as sleep, mood, daily functioning, and social support may represent priority targets for future care interventions^[21,24]. However, several limitations of the study should be acknowledged: first, the cross-sectional design constrained our ability to infer causal relationships between predictive factors and MCI; the present model provides “concurrent risk identification” rather than prospective prediction, and its predictive validity requires confirmation in longitudinal cohort studies^[41]. Second, the single-center setting and small sample size—together with a test-set AUC exceeding the mean from cross-validation—suggest potential optimistic bias and underscore the need for external validation^[31,43]. Third, feature selection relied on stepwise logistic regression, a method that is sensitive to sample fluctuations and therefore theoretically prone to instability in variable selection; the core predictors (educational level, PSQI, anxiety, ADL, SSRS) require verification of their robustness in independent datasets^[26,42]. Fourth, cognitive assessment in this study was primarily scale-based without imaging or biomarker data, which may have constrained the model’s performance ceiling^[25,43].

6 Conclusions

This study successfully developed an interpretable machine-learning–based hierarchical model to identify the risk of mild cognitive impairment (MCI) among community-dwelling older adults exhibiting depressive symptoms^[28,38]. The model integrates five core predictors across biological, psychological, and sociological domains, with sleep quality emerging as the most influential risk indicator^[21,33]. The XGBoost model demonstrated superior predictive accuracy and clinical utility; when coupled with SHAP-based interpretability, it holds promise as an effective tool for community healthcare providers to perform early screening and deliver targeted interventions to high-risk individuals, thereby contributing to secondary prevention of Alzheimer’s disease and the promotion of healthy aging^[2,14]. Future research should focus on multicenter, prospective cohort studies to further validate, optimize, and disseminate the model^[41,44].

Declarations

Abbreviations

ADL: Activities of Daily Living; **AUC:** Area under receiver operating characteristic curve; **DCA:** Decision Curve Analysis; **GAD-7:** Generalized Anxiety Disorder-7; **GDS-15:** 15-item Geriatric Depression Scale; **LASSO:** Least Absolute Shrinkage and Selection Operator; **MCI:** Mild Cognitive Impairment; **MNA-SF:** Mini Nutritional Assessment-Short Form; **MoCA:** Montreal Cognitive Assessment; **PSQI:** Pittsburgh Sleep Quality Ind

ex; **RF**: Random Forest; **SHAP**: SHapley Additive exPlanations; **SMOTE**: Synthetic Minority Over-sampling Technique; **SVM**: Support Vector Machine; **SSRS**: Social Support Rating Scale; **XGBoost**: Extreme Gradient Boosting.

Ethics approval and consent to participate

This study was approved by the Ethics Committee of Xinjiang Medical University (Approval No.XJYKD XR20260428001) and was conducted in accordance with the Declaration of Helsinki. All participants provided their written informed consent.

Consent for publication

Not applicable.

Availability of data and materials

The raw data supporting the conclusions of this article will be made available by the author, without undue reservation.

Competing Interests

The authors have no conflict of interest to declare.

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