

Original Article

Construction and clinical validation of a nomogram-based predictive model for diabetic retinopathy in type 2 diabetes

Yonghong Liu^{1*}, Zhaoling Zhou^{2*}, Zhiyong Wang³, Huan Yang⁴, Feifei Zhang⁴, Qinhu Wang⁴

¹Department of Ophthalmology, Gansu Provincial Hospital of TCM, No. 418 Guazhou Road, Qilihe District, Lanzhou 730050, Gansu, China; ²Department of Electrocardiogram, Gansu Provincial Hospital of TCM, No. 418 Guazhou Road, Qilihe District, Lanzhou 730050, Gansu, China; ³Trauma Disease Diagnosis and Treatment Center, Gansu Provincial Hospital of TCM, No. 418 Guazhou Road, Qilihe District, Lanzhou 730050, Gansu, China; ⁴Department of Endocrinology, The Third People's Hospital of Gansu Province, No. 763 Duanjiatan Road, Chengguan District, Lanzhou 730020, Gansu, China. *Equal contributors.

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Abstract: Objective: This study aimed to identify risk factors for diabetic retinopathy (DR) in patients with type 2 diabetes mellitus (T2DM) and construct a nomogram prediction model for DR. Methods: T2DM patients (n = 520) who underwent fundoscopic examinations from June 2020 to June 2022 were included. Of these patients, 220 had DR, yielding a disease rate of 40.38%. Patients were divided into a training set (n = 364) and a validation set (n = 156) at a 7:3 ratio. Feature variables were selected using LASSO regression, random forests, and decision trees. Venn diagrams identified common DR feature variables. The prediction model's validity was assessed using the C-index, decision curve analysis (DCA), receiver operating characteristic (ROC) curves, and calibration curves. Results: Factors influencing DR were age, Diabetic Peripheral Neuropathy (DPN), Hemoglobin A1C (HbA1C) levels, High-Density Lipoprotein (HDL) cholesterol, Low-Density Lipoprotein (LDL) cholesterol, Neutrophil-to-Lymphocyte Ratio (NLR), Triglycerides (TG), Blood Urea Nitrogen (BUN), and disease duration. Univariate analysis excluded LDL as being unrelated to DR. The DR prediction model, constructed using the remaining eight variables, showed internal validation metrics with a C-index of 0.937, area under the ROC curve (AUC) of 0.773, and DCA net benefit of 11%-95%. The external validation metrics demonstrated a C-index of 0.916, AUC of 0.735, and DCA net benefit of 17%-93%. Calibration curves indicated high consistency. Conclusion: This study developed a nomogram prediction model to assess the risk of DR in patients with T2DM. The model demonstrated high precision through internal validation.

Keywords: Type 2 diabetes mellitus, diabetic retinopathy, risk factors, nomogram, predictive model, LASSO

Introduction

With the global improvement in quality of life, particularly in developing countries, the incidence of diabetes is steadily rising [1]. China, accounting for a third of the global diabetic population, has a diabetes prevalence rate of about 10% [2]. Type 2 diabetes mellitus (T2DM) is a chronic hyperglycemia disease that can exert stress on the microvasculature of multiple organ systems including the eyes [3]. Diabetic Retinopathy (DR), a complication of diabetes primarily due to metabolic dysregulation leading to abnormal ocular vasculature, is one of the leading causes of adult vision decline

and visual impairment, and it has the potential to culminate in irreversible blindness [4]. Early DR has inconspicuous symptoms, but the onset of blindness is often acute. Studies have shown that in patients with T2DM, 60% are likely to develop DR within 20 years [5]. In China, nearly 28% of T2DM patients develop DR, among which approximately 45% of DR patients' vision is threatened [6], and there are currently no effective methods to reverse vision loss caused by DR.

Persistent hyperglycemia can lead to abnormal polyol metabolism, enhance vascular inflammatory response, and induce oxidative stress.

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These factors collectively modify the biological properties and hemodynamics of the retinal microvasculature, thus leading to retinopathy [7]. The severe visual impairment caused by DR not only reduces patients' quality of life and hampers their ability to manage their disease, but also diminishes their productivity and expected lifespan. Therefore, effective therapies that can prevent or inhibit the progression of DR is of great value for both patient and society [8]. The idea of ophthalmologic screening in all diabetic patients for DR is unrealistic as many diabetes patients are treated in endocrinology, where there is often no ophthalmological examination equipment, such as wide-field retinal photography and optical coherence tomography, especially in developing countries like China [9, 10]. Still, the screening of DR should be given high priority. Existing studies have reported the risk factors for DR and the construction of risk models [11]. Although the results vary, age and duration of diabetes are the primary factors. Nowadays, increasingly researchers are putting tremendous efforts into constructing predictive models or improving existing ones [12, 13]. Among them, the construction of the nomogram models has become one of the hottest research areas. While it is acknowledged that the latest research has shown excellent prediction performance of nomograms, it's important to note that the excellence of model performance can be relative and context-dependent.

The rising prevalence of T2DM and its complications necessitates the construction and validation of predictive models tailored to different population groups. Our study, set in this context, aims to provide a tool that can help early risk identification of patients. While age and duration of diabetes are primary risk factors for DR, our study delved deeper into the potential connections between DR and other clinical indicators. By incorporating these indicators into the nomogram model, a more comprehensive understanding of DR risk factors and their interplay can be realized, and it serves as a practical tool for clinicians to predict the risk DR is provided. We believe that our study brings value to the ongoing research in this area by offering a nuanced understanding of DR risk factors and providing a practical predictive tool tailored to the needs of developing countries.

Methods and materials

Sample source

We collected data from 648 patients with T2DM who were diagnosed and underwent funduscopic examinations at Gansu Provincial Hospital of TCM between June 2020 and June 2022 for a retrospective study. The flow chart of this study is presented in **Figure 1**. This study was conducted with the approval of the medical ethics committee of Gansu Provincial Hospital of TCM.

Inclusion and exclusion criteria

Inclusion criteria: patients with confirmed diagnosis of T2DM [14]; patients who underwent funduscopic examinations, which confirmed the diagnosis of DR; patients with age between 18 and 80 years; patients with available urine and blood sample data.

Exclusion criteria: patients with tumors; patients with systolic blood pressure > 200 mmHg or diastolic blood pressure > 120 mmHg; patients with severe lipid abnormalities: total cholesterol (TC) > 10 mmol/L or triglycerides (TG) > 15 mmol/L; patients with incomplete clinical data; pregnant women.

Diagnostic criteria

In patients diagnosed with T2DM, funduscopic examinations were performed using both direct and indirect ophthalmoscopy. The diagnosis of DR was indicated by the presence of one or more of the following retinal changes: 1. Microaneurysms: small red dots on the retina; 2. Hard exudates: yellow lipid deposits from leaking blood vessels; 3. Cotton-wool spots: pale and fluffy areas on the retina resulting from nerve fiber layer infarctions; 4. Venous beading: changes in the caliber of retinal veins; 5. Intraretinal microvascular abnormalities; 6. Neovascularization: growth of new blood vessels on the retina or optic disc; 7. Fluorescein angiography (if required) showing areas of leakage, non-perfusion, or neovascularization; 8. Optical coherence tomography (OCT) showing retinal thickening or cystoid macular edema (if applicable) [15].

Patients without DR were confirmed through the absence of any retinal changes indicative of

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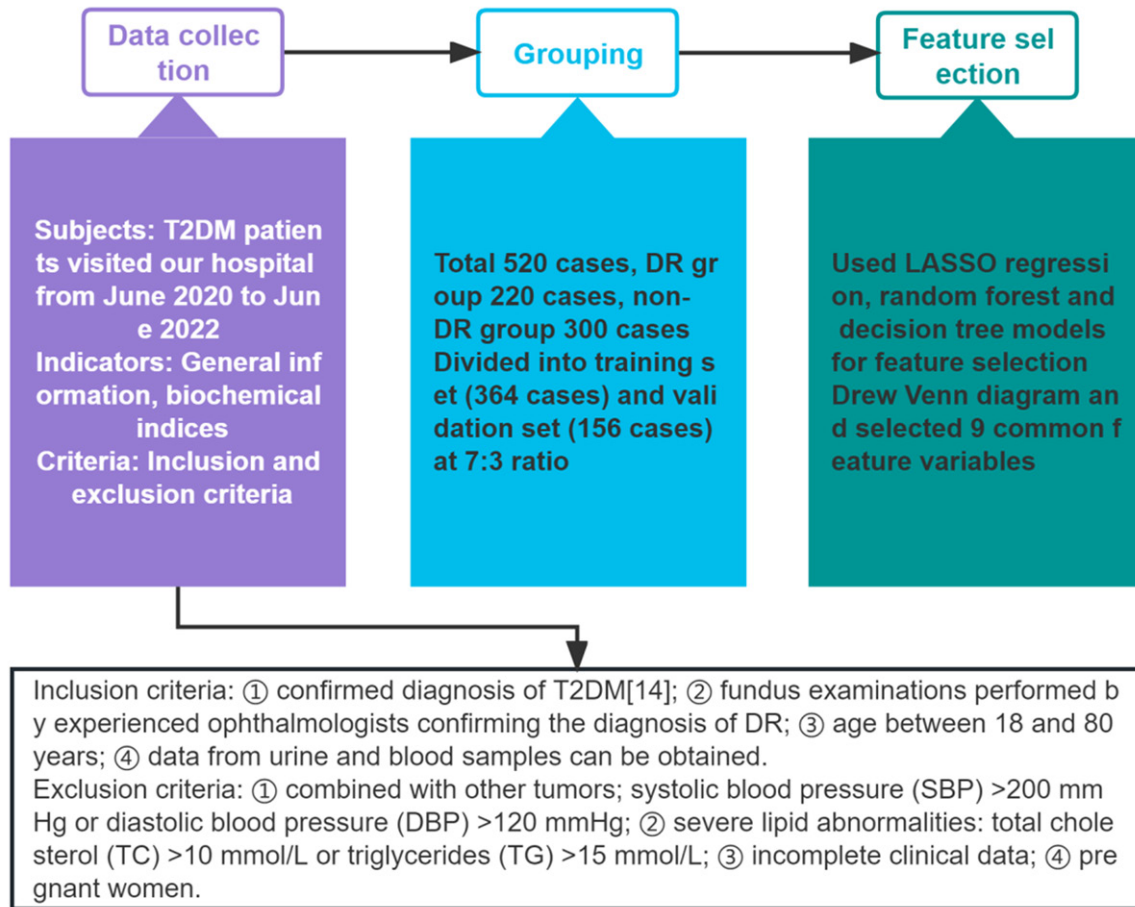


Figure 1. Study flow chart. T2DM, type 2 diabetes mellitus; DR, Diabetic Retinopathy.

DR as mentioned above, no evidence of leakage, non-perfusion, or neovascularization on fluorescein angiography (if performed), and no signs of retinal thickening or cystoid macular edema found in OCT (if applicable).

Sample selection

According to the inclusion and exclusion criteria, a total of 520 samples were collected for this study. Among them, 210 patients were diagnosed with DR, and 310 patients were not, with a morbidity rate of 40.38%. Subsequently, patients were divided into a training group (n = 364) and a validation group (n = 156) at a ratio of 7:3.

Clinical data collection

All of the patients were admitted between June 2020 and June 2022. The general data and biochemical data were collected through electronic medical records and outpatient review records. General data included gender, age, Diabetic Peripheral Neuropathy (DPN), hyper-

tension, systolic blood pressure, diastolic blood pressure, and disease course. For biochemical data, an automatic blood analyzer (Sysmex, poch-100i) was used to test patient blood routine indicators including White Blood Cell (WBC) count, Eosinophil count (EOS), Neutrophil count (NE), Lymphocyte count (LY), and the Neutrophil to Lymphocyte Ratio (NLR). An automatic biochemical analyzer (Beckman Coulter, AU5800) was used to test TC, Aspartate Aminotransferase (AST), High-Density Lipoprotein (HDL), Low-Density Lipoprotein (LDL), Alanine Aminotransferase (ALT), Glycated Serum Protein (GSP), Glucose (GLC), Hemoglobin A1c (HbA1C), Apolipoprotein A1 (ApoA1), Apolipoprotein B (ApoB), TG, and Blood Urea Nitrogen (BUN).

Feature selection process

Decision trees, LASSO, and Random Forests were used for feature selection from the training dataset, and a Venn diagram was used to determine the final feature variables. These feature variables were validated for comparability in both training and validation datasets,

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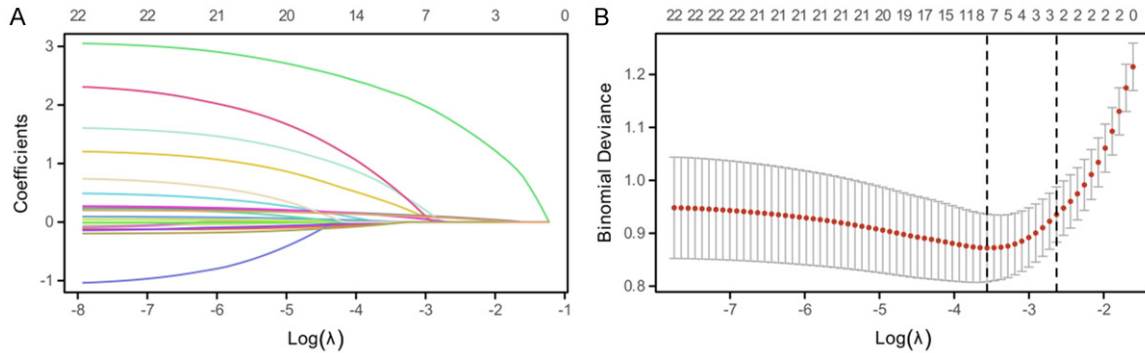


Figure 2. Lasso Regression for the screening of feature variables. A. Selection of genes with non-zero coefficients for model construction. B. Log lambda values of genes corresponding to the point with minimal cross-validation error.

and a DR risk prediction nomogram was constructed based on these features.

Model evaluation and validation

Several statistical methods were employed to evaluate the performance and validity of the constructed risk prediction model. 1. C-index: This index reflects the proportion of consistent case pairs between the predicted and actual results. It indicates the consistency of the predicted results with the actual observations. A higher C-index suggests better model performance. 2. Calibration curve: This curve represents the fit line between the predicted risk and actual risk. The closer the predicted values are to the actual values, the higher the model accuracy. 3. Area Under the Receiver Operating Characteristic (ROC) Curve (AUC): AUC indicates the ability of the model to distinguish between positive and negative outcomes. The larger the AUC value, the higher the accuracy of the model. 4. Decision Curve Analysis (DCA): Although not a conventional validation method, DCA assumes significance as a vital tool for evaluating the clinical utility of a model. It assesses the net benefits of using the model in decision-making, thereby helping high-risk patients to receive necessary interventions and low-risk patients to avoid unnecessary treatments. This ensures that the model meets practical clinical decision needs.

Statistical analysis

Initial data processing was performed using SPSS26.0. This included tasks such as data cleaning (e.g., deletion of missing or irrelevant data), data imputation (filling in missing values using appropriate statistical methods), and random grouping for subsequent analyses.

Decision tree and random forest analyses were conducted through the SPSSAU platform. The decision tree was constructed to identify the primary splits in the data, while the random forest model was used to assess the importance of each variable and improve prediction accuracy. Advanced statistical analyses were performed using R software. The “glmnet” package was employed to construct the LASSO regression model, which aids in feature selection by shrinking some regression coefficients to zero. The “rms” package was used to plot the nomogram, a graphical representation of the prediction model. The “rmda” package was utilized for DCA plotting, and the “rocr” package for ROC curve plotting. Both are essential for assessing the model’s predictive performance. The “rms” package was also used to plot the calibration curve, which assesses the agreement between predicted and observed outcomes, and to calculate the C-index, a measure of the model’s discriminative ability. In addition, normally distributed measured data were described by mean \pm standard deviation (mean \pm SD) and compared by t-test. Intergroup comparisons were performed using independent samples t-test. The χ^2 test was used to compare the counting data, expressed by percentage (%). All statistical tests were two-sided, and a *P*-value less than 0.05 was considered statistically significant.

Results

Lasso feature selection

Using the LASSO algorithm and performing 10-fold cross-validation, we selected the lambda.1se parameter as 0.028664 (Figure 2A, 2B). This resulted in a total of 12 relevant variables: age, ApoA1, DPN, HbA1C, HDL,

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Table 1. The random forest feature variable screening for weight value

Nape	Weight value
DPN	0.189
Age	0.13
BUN (mmol/L)	0.104
HbA1C (%)	0.054
AST (mmol/L)	0.048
NE (10 ⁹ /L)	0.04
HDL (mmol/L)	0.039
Disease course (year)	0.037
ALT (mmol/L)	0.036
EOS (10 ⁹ /L)	0.034
GSP (%)	0.033
ApoA1 (g/L)	0.032
LDL (mmol/L)	0.028
NLR	0.027
GLC (mmol/L)	0.027
LY (10 ⁹ /L)	0.026
TC (mmol/L)	0.026
WBC (10 ⁹ /L)	0.025
ApoB (g/L)	0.024
TG (mmol/L)	0.024
Hypertension	0.014

Note: DPN, Diabetic Peripheral Neuropathy; WBC, White Blood Cell Count; EOS, Eosinophil Fraction; NE, Neutrophil Count; LY, Lymphocyte Count; NLR, Neutrophil to Lymphocyte Ratio; TC, Total Cholesterol; AST, Aspartate Aminotransferase; HDL, High-Density Lipoprotein; LDL, Low-Density Lipoprotein; ALT, Alanine Aminotransferase; GSP, Glycated Serum Protein; GLC, Glucose; HbA1C, Hemoglobin A1c; ApoA1, Apolipoprotein A1; ApoB, Apolipoprotein B; TG, Triglycerides; BUN, Blood Urea Nitrogen.

hypertension, LDL, NE (10⁹/L), NLR, TG, BUN, and duration of disease.

Random forest feature selection

Random forest model was used on the training dataset to determine the weights between the relevant variables and the model, as well as rank the important variables (**Table 1**). Variables with weights less than 0.01 were eliminated, and we finally obtained 21 relevant variables: DPN, age, BUN, HbA1C, AST, NE, HDL, duration of disease, ALT, EOS, GSP, ApoA1, LDL, NLR, GLC, LY, TC, WBC, ApoB, TG, and hypertension.

Decision tree feature selection

We used the decision tree model on the training dataset to determine the weight relationships between the relevant variables and the

Table 2. Decision tree feature variable screening weight value

Nape	Weight value
DPN	0.348
Age	0.152
BUN (mmol/L)	0.099
GSP (%)	0.082
EOS (10 ⁹ /L)	0.052
GLC (mmol/L)	0.049
HbA1C (%)	0.04
HDL (mmol/L)	0.039
ALT (mmol/L)	0.039
Disease course (year)	0.022
ApoB (g/L)	0.021
LDL (mmol/L)	0.016
NLR	0.015
AST (mmol/L)	0.011
TG (mmol/L)	0.011

Note: DPN, Diabetic Peripheral Neuropathy; EOS, Eosinophil Fraction; NLR, Neutrophil to Lymphocyte Ratio; AST, Aspartate Aminotransferase; HDL, High-Density Lipoprotein; LDL, Low-Density Lipoprotein; ALT, Alanine Aminotransferase; GSP, Glycated Serum Protein; GLC, Glucose; HbA1C, Hemoglobin A1c; ApoB, Apolipoprotein B; TG, Triglycerides; BUN, Blood Urea Nitrogen.

model, and rank the variables by importance (**Table 2**). Variables with weights less than 0.01 were eliminated, and we finally obtained 15 relevant variables: DPN, age, BUN, GSP, EOS, GLC, HbA1C, HDL, ALT, duration of disease, ApoB, LDL, NLR, AST, and TG.

Common feature selection

Using a Venn diagram, we further screened the feature variables selected by the above three methods. As a result, we found 9 common feature variables: age, DPN, HbA1C, HDL, LDL, NLR, TG, BUN, and duration of disease (**Figure 3**).

Univariate analysis of the 9 feature variables

Initially, values were assigned to the nine variables, and subsequently, the measurement data were grouped based on the descending ROC cut-off value (**Table 3**). This was followed by conducting a univariate analysis. The results showed statistical differences in 8 feature variables (age, DPN, NLR, HDL, duration of disease, HbA1C, TG, and BUN) between DR and non-DR groups (**Table 4**, $P < 0.05$), but no statistical difference in LDL between the two groups ($P >$

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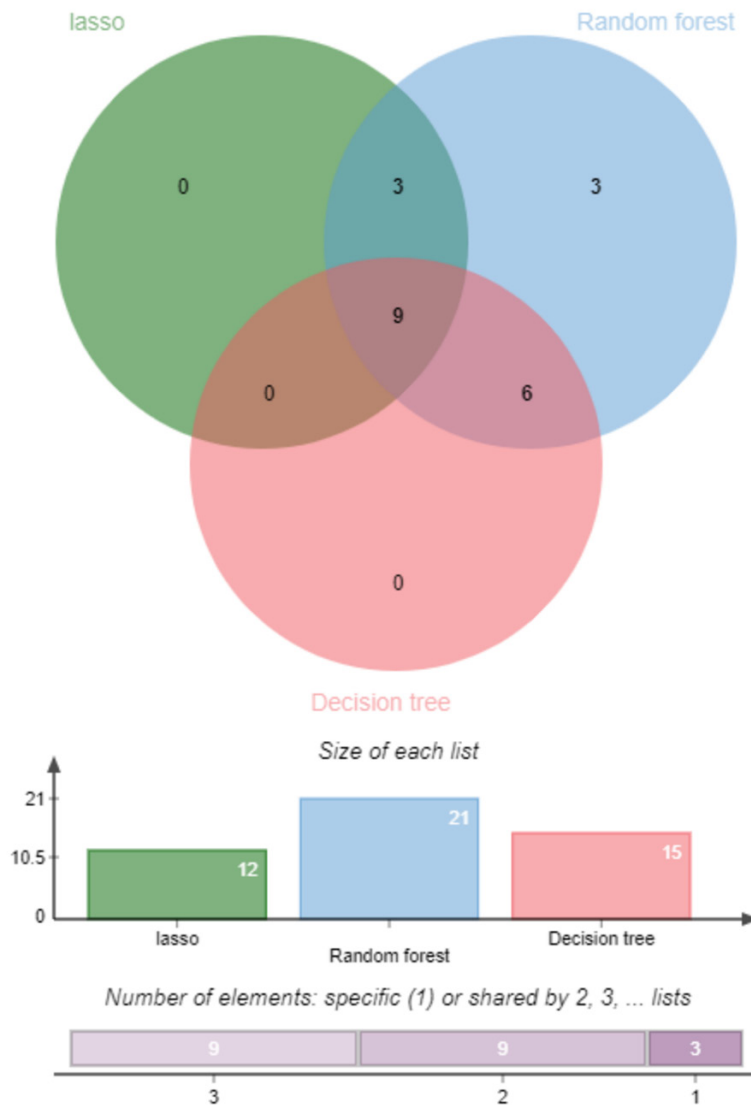


Figure 3. Wayn diagram for the screening of feature variables.

Table 3. Assignment table

Factor	Assignment
Age	≥ 50 year = 1, < 50 year = 0
DPN	Yes = 1, No = 0
NLR	≥ 2.357 = 1, < 2.357 = 0
HDL (mmol/L)	≥ 0.945 = 1, < 0.945 = 0
LDL (mmol/L)	≥ 2.395 = 1, < 2.395 = 0
Disease course (year)	≥ 9.89 = 1, < 9.89 = 0
HbA1C (%)	≥ 8.835 = 1, < 8.835 = 0
TG (mmol/L)	≥ 2.515 = 1, < 2.515 = 0
BUN (mmol/L)	≥ 46.436 = 1, < 46.436 = 0
DR	Yes = 1, No = 0

Note: DPN, Diabetic Peripheral Neuropathy; NLR, Neutrophil to Lymphocyte Ratio; HDL, High-Density Lipoprotein; LDL, Low-Density Lipoprotein; HbA1C, Hemoglobin A1c; TG, Triglycerides; BUN, Blood Urea Nitrogen; DR, Diabetic Retinopathy.

0.05). We also compared the differences in these 8 feature variables between the validation and training datasets, and found no statistical differences, demonstrating comparability ($P > 0.05$, **Table 5**).

Construction of the DR nomogram

We used the LASSO, random forest, and decision tree machine learning algorithms to select feature variables, and 8 common features were identified through the Wayn diagram (**Figure 3**). These variables were then used to construct the nomogram, which was set up based on the coefficients obtained from the multivariate logistic regression analysis. In logistic regression, the coefficients of each variable determine its weight in the nomogram, ensuring that the nomogram accurately reflects the relative importance of each variable in predicting outcomes (**Figure 4**). In the visualization of the risk prediction nomogram, the “Points” represent the scores corresponding to the variables. Different variable values correspond to different “Points” values.

The summation of the scores corresponding to each variable yields the “TotalPoints”, from which the corresponding DR risk for each patient can be ascertained from the “Risk of DR” below. This model can facilitate individualized prediction of DR in clinical practice.

Risk prediction and model validation

We validated the risk prediction model using four methods, AUC of ROC curve, C-index, DCA, and calibration curve. The effectiveness of the risk prediction model was obtained: (1) The internal validation AUC was 0.773, and the external validation AUC was 0.735, with no difference in AUC between internal and external AUC (Delong test, $P > 0.05$), indicating that the

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Table 4. Univariate analysis

Factor	DR group (n = 144)	Non-DR group (n = 220)	χ^2 value	P value
Age			131.039	< 0.0001
≥ 50	125	56		
< 50	19	164		
DPN			65.447	< 0.0001
Yes	120	89		
No	24	131		
NLR			4.717	0.029
≥ 2.357	44	92		
< 2.357	100	128		
HDL (mmol/L)			9.531	0.002
≥ 0.945	106	127		
< 0.945	38	93		
LDL (mmol/L)			1.648	0.199
≥ 2.395	84	143		
< 2.395	60	77		
Disease course (year)			10.271	0.001
≥ 9.89	72	73		
< 9.89	72	147		
HbA1C (%)			13.655	< 0.001
≥ 8.835	80	79		
< 8.835	64	141		
TG (mmol/L)			6.157	0.013
≥ 2.515	64	127		
< 2.515	80	93		
BUN (mmol/L)			50.932	< 0.0001
≥ 46.436	113	89		
< 46.436	31	131		

Note: DPN, Diabetic Peripheral Neuropathy; NLR, Neutrophil to Lymphocyte Ratio; HDL, High-Density Lipoprotein; LDL, Low-Density Lipoprotein; HbA1C, Hemoglobin A1c; TG, Triglycerides; BUN, Blood Urea Nitrogen; DR, Diabetic Retinopathy.

prediction model has good discriminative ability (**Figure 5A, 5B**). (2) The calibration curves of internal and external validations indicated that the predicted probability of DR aligns well with the actual situation, demonstrating the accuracy of the prediction model (**Figure 5C, 5D**). (3) The C-index of internal and external validation was 0.937 (0.913-0.961) and 0.916 (0.874-0.959), respectively, indicating good consistency between the actual and predicted probabilities of DR. (4) The DCA of internal and external validations demonstrated a good clinical net benefit of the prediction model at different threshold probabilities (internal: 11%~95%; external: 17%~93%), confirming its practicality (**Figure 5E, 5F**).

Discussion

The development of DR is associated with several factors, including oxidative stress triggered

by high blood sugar, accumulation of advanced glycation end-products, increased reactive oxygen species, abnormal activation of protein kinase C, and aberrant activation of the renin-angiotensin system [16]. These factors can also result in the concurrent of DR and diabetic nephropathy. However, despite the similar pathogenesis, pathological changes and influencing factors vary between the two [17]. Clinically, due to the lack of simplified DR screening methods, DR and diabetic nephropathy exhibit asynchrony in clinical manifestation [18]. Therefore, actively exploring risk factors for DR and intervening accordingly bears significant clinical relevance for early diagnosis and treatment of diabetic microvascular complications and even for the prevention of these complications.

Machine learning is multidisciplinary field that draws upon statistics and various academic

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Table 5. Comparison of 9 characteristic variables between patients in the training group and the validation group

Factor	Training groups (n = 364)	Validation groups (n = 156)	χ^2 value	P value
Age			2.029	1.543
≥ 50	181	94		
< 50	183	62		
DPN			2.029	0.154
Yes	209	79		
No	155	77		
NLR			0.056	0.812
≥ 2.357	136	60		
< 2.357	228	96		
HDL (mmol/L)			0.066	0.795
≥ 0.945	233	98		
< 0.945	131	58		
Disease course (year)			1.793	0.180
≥ 9.89	145	72		
< 9.89	219	84		
HbA1C (%)			1.757	0.184
≥ 8.835	159	78		
< 8.835	205	78		
TG (mmol/L)			1.744	0.186
≥ 2.515	191	72		
< 2.515	173	84		
BUN (mmol/L)			0.005	0.938
≥ 46.436	202	86		
< 46.436	162	70		

Note: DPN, Diabetic Peripheral Neuropathy; NLR, Neutrophil to Lymphocyte Ratio; HDL, High-Density Lipoprotein; HbA1C, Hemoglobin A1c; TG, Triglycerides; BUN, Blood Urea Nitrogen; DR, Diabetic Retinopathy.

disciplines. It leverages computer technology to process big data and is a subset of artificial intelligence. By using machine learning algorithms, we can filter out required feature variables from large amounts of data, thereby effectively improving learning efficiency [19]. At present, machine learning has been widely applied in the medical field, especially in radiomics and pathological image segmentation, but further research is needed for risk prediction of clinical diseases [20, 21]. Thus, in this study, we used decision tree, LASSO, and random forest machine learning algorithms to screen risk factors for DR and constructed a risk prediction model [22, 23]. Furthermore, we performed internal and external validations of this model to verify its accuracy, reliability, applicability, and clinical application value, providing reliable data support for the prevention, treatment, and prognosis of DR.

In this study, we collected T2DM patients who had already undergone fundoscopic examination and divided them into DR and non-DR groups. We compared the relevant data between the two groups, screened out significant risk factors, and built a DR prediction model based on them. Our research found that age, DPN, NLR, HDL, disease duration, HbA1C, TG, and BUN were risk factors affecting the occurrence of DR in diabetic patients. Compared to older patients, it was found that patients of younger age and shorter disease duration had a higher risk of DR, suggesting that younger age might be a protective factor for DR. Yin et al. [24] also found that age was a risk factor for DR in T2DM patients, and the older the age, the greater the likelihood of disease worsening, and the higher the risk of DR, which is consistent with our research results. Our study also found that high expression of

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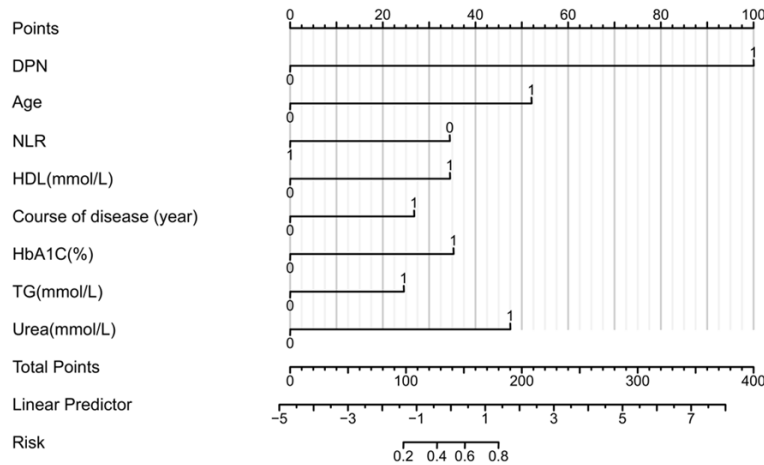


Figure 4. DR Risk prediction nomogram. Note: DPN, diabetic peripheral neuropathy; NLR, Lymphocyte to neutrophil ratio to value; HDL, High-Density Lipoprotein; LDL, Low-Density Lipoprotein; HbA1C, Hemoglobin A1c; TG, Triglycerides; Urea, Blood Urea Nitrogen; DR, diabetic retinopathy.

NLR was a protective factor for DR. This might be related to the systemic inflammatory response and immune system response in diabetic patients. NLR is an indicator reflecting the body's inflammatory and immune status. Existing research has shown [25] that inflammatory and immune responses play a key role in the pathogenesis of diabetes. High blood sugar can lead to an enhanced systemic inflammatory response, which may lead to an increase in the number of neutrophils, while affecting the function of lymphocytes, which may cause a relative decrease in lymphocyte count, resulting in an increase of NLR in diabetic patients [26]. However, the occurrence of DR is related to the inflammatory response and angiogenesis. In the process of DR, some inflammatory mediators and growth factors, such as vascular endothelial growth factor, might promote angiogenesis and pathological changes [27]. This process is possibly related to the response of lymphocytes, potentially causing a relative increase in lymphocytes, thereby reducing NLR.

DPN is a type of diabetic microvascular complication, and its development and progression involve several interrelated pathophysiological mechanisms [28]. Foremost of these is the sustained hyperglycemic state caused by poor long-term blood sugar control, which triggers a series of biochemical reactions, such as non-enzymatic glycosylation, activation of the sorbitol pathway, oxidative stress, inflammatory response, and endothelial dysfunction [29]. A

multicenter study by Peng et al. [30] revealed that the occurrence of DPN was related to retinopathy in diabetic patients, which is consistent with our research results. In addition, the cross-sectional study by Wang et al. [31] also found that DPN was a risk factor for the occurrence of DR. Currently, HbA1c, which can reflect blood glucose levels over the past 6-8 weeks, is widely used as a screening indicator for T2DM in clinical practice and is considered the "gold standard" for diagnosing T2DM. Our research found that abnormally elevated levels of HbA1c are also a

risk factor for DR, which is consistent with the research results of Su et al. [32]. In addition, studies have shown that an increase in HbA1c mediates damage to vascular endothelial cells and triggers adhesion of leukocytes to the surface of vascular endothelial cells, thereby promoting thrombosis. At the same time, oxidative stress products and/or inflammation states induced by high glucose levels, through their effects on the vascular wall and the vascular matrix, intensify the harm to the vascular endothelium and tissues. They collaboratively contribute to the pathogenesis and progression of DR. Therefore, patients with elevated HbA1c levels have a significantly higher risk of developing DR. In addition, our results also showed that elevated HDL, TG, and BUN were also risk factors for DR, which is consistent with previous research results [33-35].

In recent years, there has been a focus on developing predictive models for DR in patients with T2DM. For instance, Wang et al. [36] developed a DR risk nomogram for a Chinese population with T2DM. Their model, based on data from 213 patients, identified 8 prediction variables and achieved a C-index of 0.848. Pan et al. [37], utilizing machine learning techniques, created a DR risk prediction model based on a larger sample size of 2,385 T2DM patients. The AUC of their model was 0.703. In comparison to these studies, our study employed three machine learning algorithms (LASSO, random forest, and decision tree) and identified 8 key

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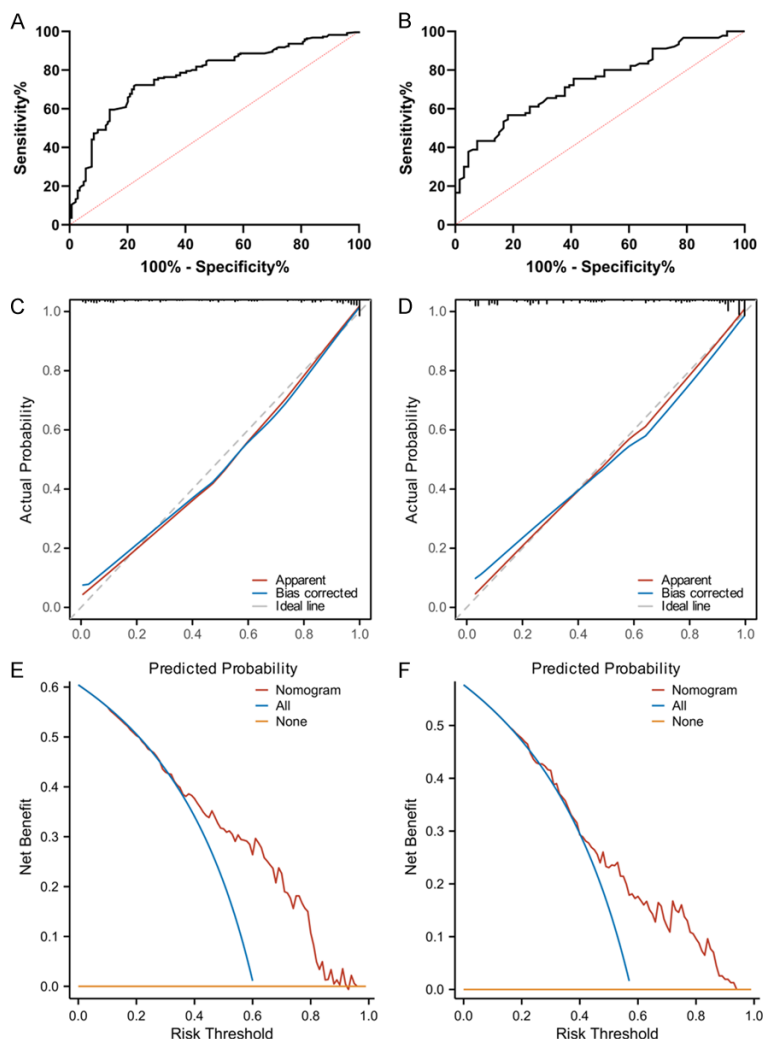


Figure 5. Risk forecast and model verification. A. ROC curve analysis of the model effectiveness in the training group. B. ROC curve analysis of the model effectiveness in the validation groups. C. Calibration curve of the model in the training group. D. Calibration curve of the model in the validation group. E. DCA curve of the model in the training group. F. DCA curve of the model in the validation group. Note: DR, diabetic retinopathy; ROC, subject working curve; DCA, decision curve analysis.

characteristic variables. We successfully constructed a DR risk prediction nomogram, which demonstrated an AUC of 0.773 for internal validation and 0.735 for external validation, indicating a high accuracy and discriminative power of our model. Additionally, our model performed well in terms of C-index, calibration curve, and DCA, further showcasing its significance in clinical practice. This research offers a comprehensive understanding of risk factors for DR and their interactions, as well as provides clinicians with a practical tool. It is important to note that various models exist for predicting the risk of

DR in patients with T2DM, and each model offers its own unique perspective. Our study contributes to the expanding knowledge in this field by providing a detailed understanding of DR risk factors and practical predictive tools that are tailored to specific patient populations and settings.

However, there are certain limitations to this study. First, as a single-center study, whether our results can be generalized requires validation with more data. Secondly, this study only used data from the same medical center for validation and did not carry out validation with data from other medical centers. Therefore, in subsequent research, it is necessary to validate with data from other medical centers to reduce selection bias, calibrate the prediction model, and optimize this model, so as to provide a more advantageous reference for clinical determination of the risk of DR in T2DM patients.

In conclusion, this study developed an innovative, intuitive, objective, and accurate Nomogram prediction model that can predict the risk of retinopathy in patients with

T2DM, and proved through internal validation that it has high precision.

Disclosure of conflict of interest

None.

Address correspondence to: Qinhu Wang, Department of Endocrinology, The Third People's Hospital of Gansu Province, No. 763 Duanjiatan Road, Chengguan District, Lanzhou 730020, Gansu, China. Tel: +86-0931-8497337; E-mail: 86531311@qq.com

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