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Construction and interpretation of machine learning-based prognostic models for survival prediction among intestinal-type and diffuse-type gastric cancer patients

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Abstract

Background Gastric cancer is one of the most common malignant tumors worldwide, with high incidence and mortality rates, and it has a complex etiology and complex pathological features. Depending on the tumor type, gastric cancer can be classified as intestinal-type and diffuse-type gastric cancer, each with distinct pathogenic mechanisms and clinical presentations. In recent years, machine learning techniques have been widely applied in the medical field, offering new perspectives for the diagnosis, treatment, and prognosis of gastric cancer patients.

Methods This study recruited 2158 gastric cancer patients and constructed prognostic prediction models for both intestinal-type and diffuse-type gastric cancer. Clinical pathological data were collected from patients, and machine learning algorithms were used for feature selection and model construction. The performance of the models was validated with training and testing datasets. The Shapley additive explanations (SHAP) values were used to interpret the model predictions and identify the main factors that influence patient survival.

Results In the prognostic model for intestinal-type gastric cancer, the gradient boosting decision tree (GBDT) model demonstrated the best performance, with key features including pTNM, CA125, tumor size, CA199, and PALB. Similarly, in the prognostic model for diffuse-type gastric cancer, the GBDT model was utilized, with key features comprising pTNM, Borrmann type IV disease, lymphocyte (LYM), lactate dehydrogenase (LDH), potassium (K), perineural invasion (PNI), tumor size, and whole stomach location. Risk stratification analysis revealed that the prognosis of high-risk patients was significantly worse than that of low-risk patients.

Conclusion Machine learning shows great potential in predicting survival outcomes of gastric cancer patients, providing strong support for the development of personalized treatment plans.

Keywords Gastric cancer, Intestinal-type, Diffuse-type, Prognosis, Machine learning

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Introduction

Gastric cancer (GC) is one of the most common malignant tumors worldwide, with significantly higher incidence and mortality rates in Eastern countries than the global average [1, 2]. Known for its complex etiology and diverse pathological features, this cancer type is influenced by genetic, environmental, and lifestyle factors. The development of GC may be associated with various factors, including unhealthy dietary habits, smoking, and certain genetic susceptibilities [3]. According to the Lauren classification, GC can be subdivided into intestinal and diffuse types, each with unique pathogenesis and clinical manifestations [4, 5].

Intestinal-type gastric cancer is typically associated with chronic stimuli such as unhealthy diets and chronic gastritis. Its progression is relatively slow and may involve a transition from atypical hyperplasia to adenocarcinoma. This subtype of cancer is more prevalent among elderly individuals and is more closely related to environmental factors [6, 7]. In contrast, diffuse-type GC involves rapid tumor growth and high invasiveness and is characterized by tumor cells that lack structural organization, leading to extensive and rapid dissemination within the gastric wall. Diffuse-type GC is often diagnosed in younger patients and has a poorer prognosis, partly because of its frequent diagnosis at later stages [8, 9].

In recent years, machine learning (ML) techniques have increasingly been applied in the medical field, particularly in areas such as disease diagnosis, evaluation of treatment outcomes, and prognosis prediction. ML has the ability to process large volumes of complex medical data and extract patterns and trends that are helpful for diagnosis and treatment decision-making [10, 11]. In particular, in the treatment and management of GC, ML models can predict disease progression on the basis of detailed clinical and pathological data, identify potential biomarkers, and provide personalized treatment plans for patients [12].

This study utilized ML technology to develop prognostic prediction models for intestinal-type and diffuse-type GC patients. The development of these models has significant clinical implications, as they can offer tailored treatment and management recommendations for each subtype of patient, optimize treatment plans, enhance treatment specificity, and potentially improve patient survival rates and quality of life.

Patient selection

Between January 2014 and December 2017, a total of 2158 gastric cancer patients were recruited from Harbin Medical University Cancer Hospital. The inclusion criteria were as follows: (1) confirmation of gastric cancer by tissue biopsy and postoperative pathological examination; (2) pathological confirmation of intestinal-type or diffuse-type gastric cancer; (3) treatment with gastric cancer surgery; and (4) availability of complete clinical and pathological data or less than 30% clinical and pathological data missing. The exclusion criteria were as follows: (1) prior treatment with neoadjuvant radiotherapy and/or chemotherapy and (2) history of recurrent gastric cancer.

Data collection

The data included the demographic characteristics of the patients, treatment methods, laboratory indicators, and pathological histological results. Tumor staging was performed based on the eighth edition of the American Joint Committee on Cancer/Union for International Cancer Control (AJCC/UICC) TNM staging system for GC. Survival status tracking was conducted every 6 months after patient discharge.

Study endpoint

The study endpoint was the 5-year all-cause mortality rate.

Feature selection

Initially, 17 clinical variables were included. The k-nearest neighbor imputer method was used to fill in missing values for variables with a ratio of missing data less than 30%, and one-hot encoding was applied to handle multicategory variables. Key variables were selected through recursive feature elimination (RFE) via 10-fold cross-validation and Lasso joint screening.

Model development

Multiple ML models were used to predict the 5-year all-cause mortality rate of GC patients in this study. Intestinal-type and diffuse-type gastric cancer patients were randomly divided into training and testing sets at a 7:3 ratio. Models were built on the training set and evaluated on the testing set via various performance metrics. The ML model with the best performance was selected after comprehensive evaluation.

Model interpretation and feature importance

The SHAP values were used to interpret the predictive models, and feature importance was ranked to identify the main predictors affecting the survival of gastric cancer patients.

Statistical analysis

All the statistical calculations were performed via Python 3.9 and R language 4.2.1. Machine learning model performance was assessed via metrics such as the area under

the receiver operating characteristic curve (AUC), sensitivity, specificity, and F1 score. Intergroup differences were analyzed via the Pearson chi-square test or Fisher's exact test. The Youden index was used to determine the optimal threshold for dividing patients into low-risk and high-risk groups. The Kaplan–Meier method was used to plot survival curves, and log-rank tests were used to compare survival curves between groups. A p value less than 0.05 was considered statistically significant.

Results

Patient characteristics

This study tracked the 5-year survival status of 2158 gastric cancer patients, of which 66.5% (1435 patients) had intestinal-type gastric cancer and 33.5% (723 patients) had diffuse-type gastric cancer. Among these patients, males accounted for 72% (1553 patients), and females accounted for 28% (605 patients). The largest proportion were Stage III gastric cancer patients representing 46.6% (1005 patients). The main primary site of gastric cancer was the gastric antrum (1413 patients, 65.5%), followed by the gastric body (437 patients, 20.3%). At the end of the study period, a total of 796 patients (36.8%) had died. Compared with intestinal-type gastric cancer, diffuse-type gastric cancer was associated with later pTNM staging, PNI, and positive lymphovascular invasion (LVI), among other clinicopathological features (Table 1). Kaplan-Meier curve analysis revealed that the survival of diffuse-type gastric cancer patients was significantly worse than that of intestinal-type gastric cancer patients (Figure S1).

Data preprocessing and feature selection

The k-nearest neighbor imputer method was applied to impute missing values for variables with a missing rate of less than 30%, and one-hot encoding was used to handle nonordinal multicategory variables. Through 10-fold cross-validation via the RFE–RF feature selection method, 5 features were selected for intestinal-type gastric cancer, and 11 features were selected for diffuse-type gastric cancer. Using Lasso, 11 features were selected for intestinal-type gastric cancer, and 9 features were selected for diffuse-type gastric cancer. By taking the intersection of features selected by RFE-RF and Lasso, 5 key features were ultimately determined for intestinal-type gastric cancer: pTNM, CA125, tumor size, CA199, and serum prealbumin (PALB); additionally, 8 key features were determined for diffuse-type gastric cancer: pTNM, Borrmann IV, lymphocytes (LYM), lactate dehydrogenase (LDH), potassium (K), PNI, tumor size, and location-whole (Fig. 1).

Development and validation of machine learning models

Prognostic model for intestinal-type gastric cancer

Patients were randomly allocated to training (1004 cases) or testing (431 cases) sets at a 7:3 ratio. The feature distribution between the training and testing sets was random and uniform (Table S1).

ML models, including logistic regression (LR), support vector machine (SVM), random forest (RF), gradient boosting decision tree (GBDT), decision tree (DT), k nearest neighbors (KNN), and XGBoost (XGB), were constructed from the 5 selected variables in the training set and validated in the testing set. After a comprehensive comparison of multiple model evaluation metrics in the training and testing sets, GBDT exhibited the best performance. The training set presented an AUC of 0.862, a sensitivity of 0.852, a specificity of 0.805, an accuracy of 0.801, a precision of 0.816, a recall of 0.714, and an F1 score of 0.735. In the testing set, the corresponding metrics were 0.822, 0.804, 0.724, 0.749, 0.721, 0.662, and 0.674, respectively (Fig. 2A and C).

Prognostic model for diffuse-type gastric cancer

Patients were randomly allocated to training (506 patients) or testing (217 patients) sets at a 7:3 ratio. The feature distribution between the training and testing sets was random and uniform (Table S2).

Machine learning models, including the LR, SVM, RF, GBDT, DT, KNN, and XGB models, were constructed from the selected 8 variables in the training set and validated in the testing set. After a comprehensive comparison of multiple model evaluation metrics in the training and testing sets, the GBDT model exhibited the best performance. In the training set, it demonstrated an AUC of 0.902, a sensitivity of 0.812, a specificity of 0.820, an accuracy of 0.802, a precision of 0.802, a recall of 0.804, and an F1 score of 0.802. In the testing set, the corresponding metrics were 0.878, 0.851, 0.776, 0.811, 0.810, 0.810, and 0.810, respectively (Fig. 2B and D).

Visualization of feature importance and interpretation for personalized prediction

SHAP values were used to rank the importance of variables by their means, revealing the features most relevant to patient survival risk. By optimizing the model, risk factors affecting prognosis were ranked by importance, where higher feature values (in red) indicated an increased risk of patient death. Case examples were then used to illustrate the interpretability of the model. The arrows indicate the direction of influence of each variable on the prediction outcome, with red and blue arrows

Table 1 Patients' demographics and clinical characteristics

	Overall	Intestinal type	Diffuse type	*P* value
Variables	2158	1435	723	
Sex (%)				
Male	1553 (72.0)	1111 (77.4)	442 (61.1)	< 0.001
Female	605 (28.0)	324 (22.6)	281 (38.9)	
Age (mean (SD))	58.72 (9.90)	60.06 (9.41)	56.07 (10.31)	< 0.001
BMI (mean (SD))	22.70 (3.20)	22.84 (3.21)	22.43 (3.15)	0.004
pTNM (%)				
I	427 (19.8)	338 (23.6)	89 (12.3)	< 0.001
II	646 (29.9)	461 (32.1)	185 (25.6)	
III	1005 (46.6)	594 (41.4)	411 (56.8)	
IV	80 (3.7)	42 (2.9)	38 (5.3)	
Borrmann (%)				
0	298 (13.8)	234 (16.3)	64 (8.9)	< 0.001
I	76 (3.5)	58 (4.0)	18 (2.5)	
II	423 (19.6)	322 (22.4)	101 (14.0)	
III	1194 (55.3)	775 (54.0)	419 (58.0)	
IV	167 (7.7)	46 (3.2)	121 (16.7)	
LVI (%)				
Negative	1037 (48.1)	722 (50.3)	315 (43.6)	0.004
Positive	1121 (51.9)	713 (49.7)	408 (56.4)	
PNI (%)				
Negative	666 (30.9)	520 (36.2)	146 (20.2)	< 0.001
Positive	1492 (69.1)	915 (63.8)	577 (79.8)	
HER2 (%)				
0	1203 (55.7)	664 (46.3)	539 (74.6)	< 0.001
1+	572 (26.5)	428 (29.8)	144 (19.9)	
2+	251 (11.6)	219 (15.3)	32 (4.4)	
3+	132 (6.1)	124 (8.6)	8 (1.1)	
Chemotherapy (%)				
No	1114 (51.6)	774 (53.9)	340 (47.0)	0.003
Yes	1044 (48.4)	661 (46.1)	383 (53.0)	
Location (%)				
Low	1413 (65.5)	985 (68.6)	428 (59.2)	< 0.001
Middle	437 (20.3)	269 (18.7)	168 (23.2)	
Upper	197 (9.1)	140 (9.8)	57 (7.9)	
Whole	111 (5.1)	41 (2.9)	70 (9.7)	
Tumor size (mean (SD))	47.85 (25.12)	46.03 (23.60)	51.48 (27.54)	< 0.001
LYM (mean (SD))	1.99 (0.68)	2.02 (0.70)	1.94 (0.62)	0.012
LDH (mean (SD))	160.19 (38.68)	160.40 (41.69)	159.78 (31.88)	0.723
PALB (mean (SD))	250.18 (72.14)	249.66 (74.76)	251.20 (66.68)	0.64
K (mean (SD))	4.26 (0.42)	4.28 (0.43)	4.22 (0.40)	0.001
CA199 (mean (SD))	43.98 (130.67)	44.82 (133.83)	42.30 (124.24)	0.673
CA125 (mean (SD))	13.15 (14.18)	13.24 (15.11)	12.99 (12.14)	0.703

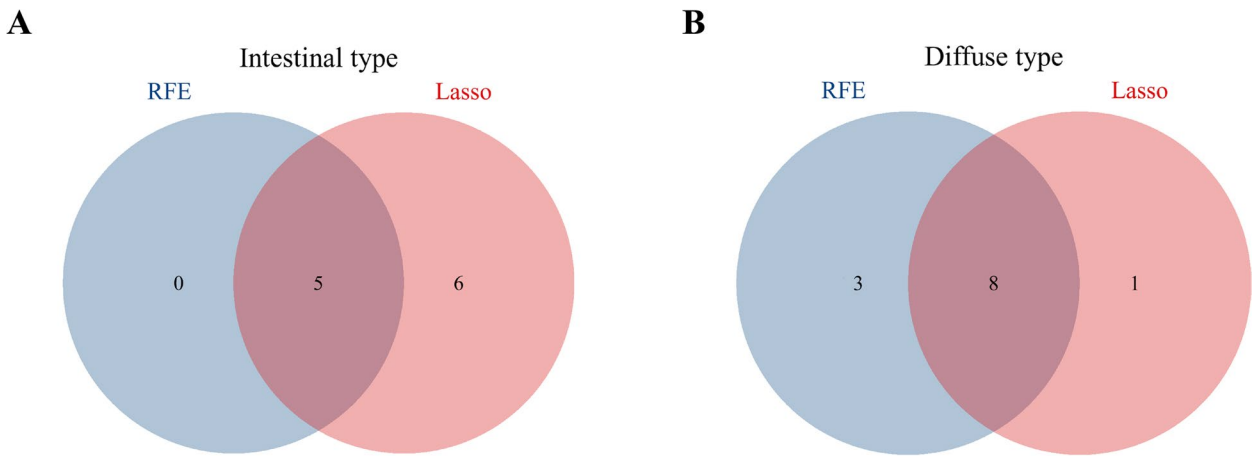

Fig. 1 Selection of key clinical pathological features for prognostic models of intestinal-type and diffuse-type gastric cancer

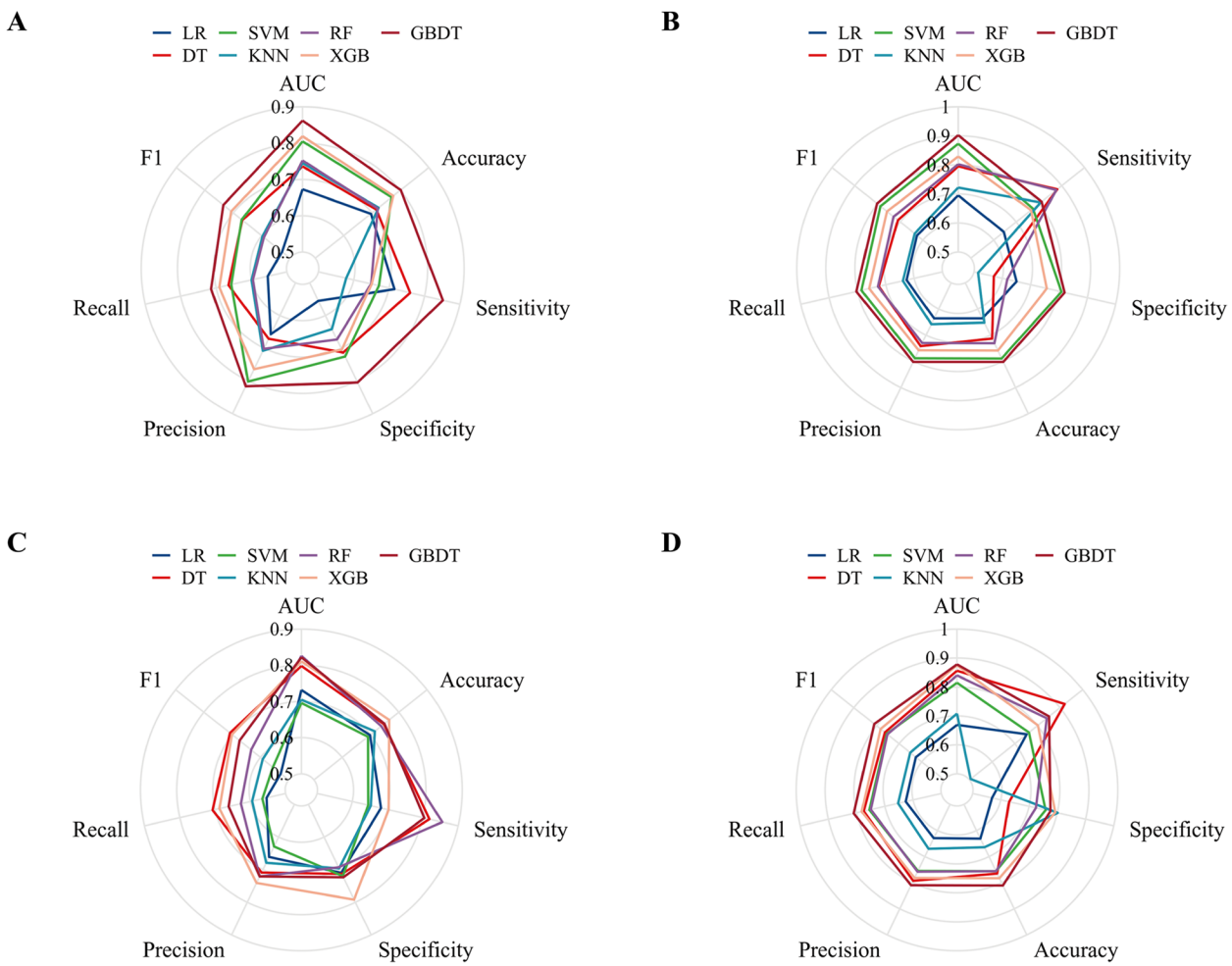

Fig. 2 Comparison of the predictive performance of different machine learning models for the prognosis of intestinal-type and diffuse-type gastric cancer. (**A**) Intestinal-type gastric cancer - training set; (**B**) Diffuse-type gastric cancer - training set; (**C**) Intestinal-type gastric cancer - test set; (**D**) Diffuse-type gastric cancer - test set

representing increased and decreased risk of death, respectively.

Interpretation of the prognostic model for intestinal-type gastric cancer

pTNM stage was the feature most relevant to survival risk in patients with intestinal-type gastric cancer. A later pTNM stage, higher CA125 level, larger tumor size, higher CA199, and lower PALB indicate poorer outcomes. Two patient cases were presented to illustrate the interpretability of the model: one with stage I and higher PALB suggesting long-term survival and another with stage IV and higher CA199 resulting in death within 5 years. SHAP values and prediction scores, reflecting lower SHAP values (-2.24) and prediction scores (0.096103) for surviving patients and higher SHAP values (0.99) and prediction scores (0.729057) for deceased patients, were calculated by integrating the effects of all variables (Fig. 3).

Interpretation of the prognostic model for diffuse-type gastric cancer

pTNM stage and whether Borrmann type IV disease is present were the two features most relevant to survival risk in patients with diffuse-type gastric cancer. Later, pTNM stage, Borrmann type IV disease, lower LYM, higher LDH, lower K, positive PNI, larger tumor size, and whole stomach involvement were associated with poorer outcomes. Two patient cases are presented to illustrate the interpretability of the model: one with stage I and higher LYM, suggesting long-term survival, and another with stage IV and lower LYM, resulting in death within 5 years. SHAP values and prediction scores, reflecting lower SHAP values (-2.1) and prediction scores (0.109062) for surviving patients and higher SHAP values (1.68) and prediction scores (0.843024) for deceased patients, were calculated by integrating the effects of all the variables (Fig. 4).

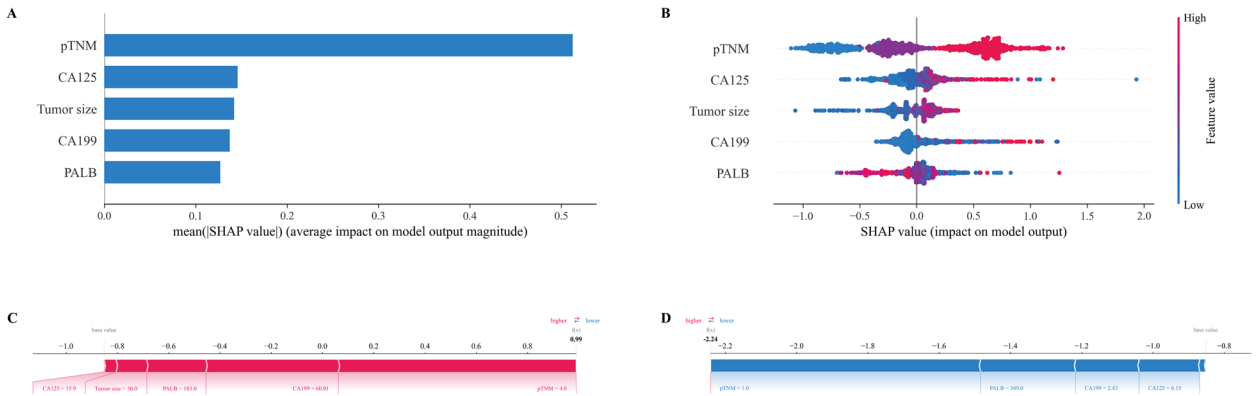

Fig. 3 Global and local explanations of the prognostic model for intestinal-type gastric cancer

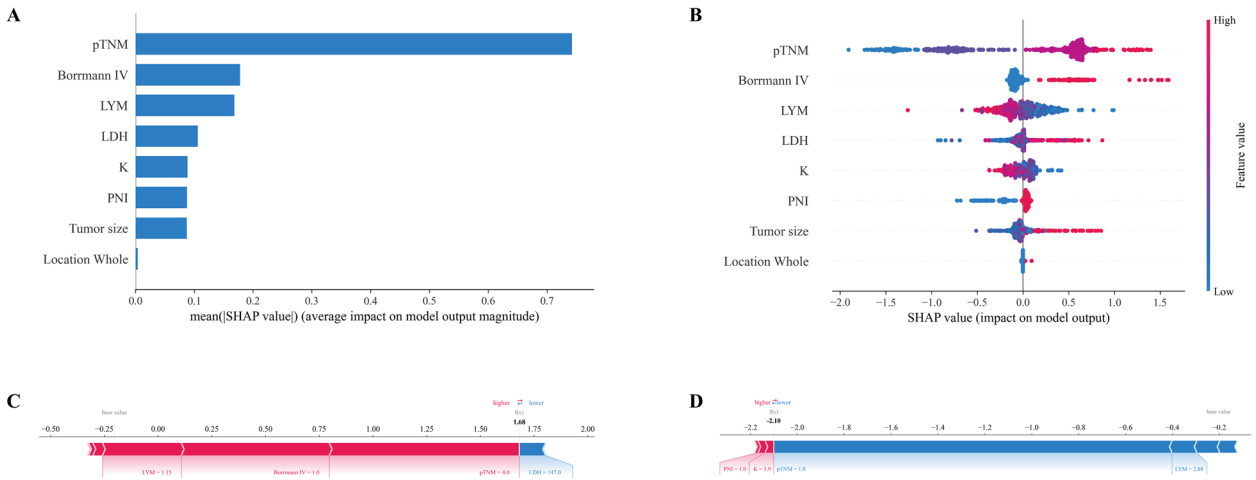

Fig. 4 Global and local explanations of the prognostic model for diffuse-type gastric cancer

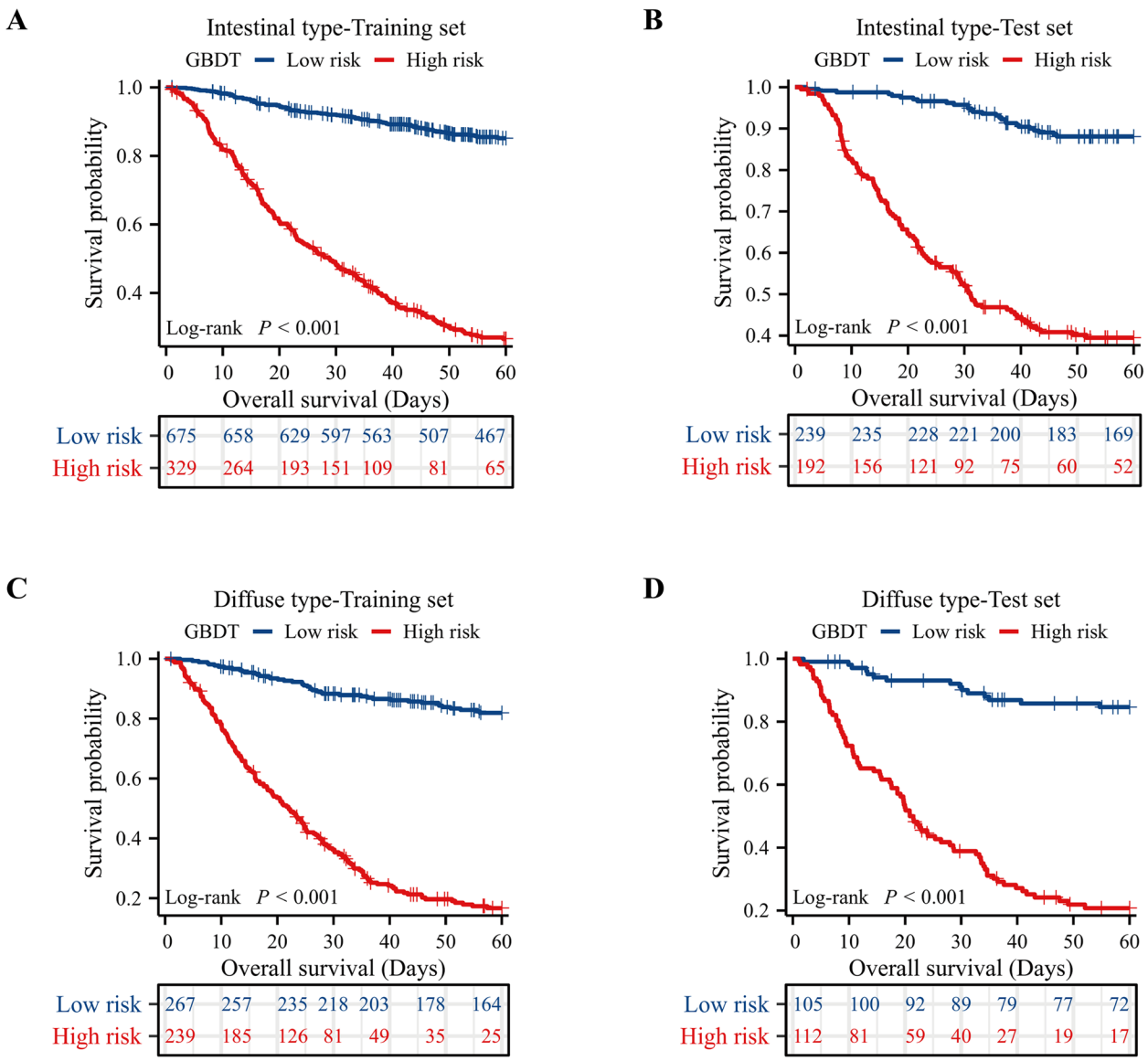

Fig. 5 Kaplan-Meier curves for high and low ML risk subjects in patients with intestinal-type and diffuse-type gastric cancer

Risk stratification

Using ROC curves, optimal cutoff values for the training and testing sets of intestinal-type and diffuse-type gastric cancer patients were determined separately, and patients were divided into high-risk and low-risk groups. Survival analysis revealed that the prognosis of high-risk patients was significantly worse than that of low-risk patients ($P < 0.001$) (Fig. 5).

Discussion

In this study, we successfully constructed a framework for predicting the prognosis of intestinal and diffuse gastric cancer patients by applying machine learning techniques, particularly the gradient boosting decision tree (GBDT) model [13–15]. These two subtypes of gastric cancer exhibit significant differences in clinical presentation and pathological features, which are crucial for determining treatment strategies and prognosis assessment. Our research highlights the potential of machine learning in accurately predicting survival outcomes in gastric cancer patients, particularly in the development of personalized medical and precision treatment strategies.

The GBDT model was chosen due to its ability to handle complex datasets, effectively identifying and combining multiple decision trees to capture nonlinear relationships and complex interactions among variables.

In this study, the GBDT model demonstrated excellent performance on both the training and testing datasets, validating its feasibility and effectiveness in real-world clinical applications.

Of particular interest are the key biomarkers identified by the model, which are crucial for predicting the survival outcomes of patients with intestinal and diffuse gastric cancer. In intestinal gastric cancer, key prognostic indicators include the pTNM stage, CA125, tumor size, CA199, and PALB. In our study, the pTNM stage, as the primary classification criterion for tumors, directly reflects the status of lymph node involvement and distant metastasis, serving as an important basis for prognosis assessment. CA125 and CA199, as tumor markers, are typically associated with increased tumor burden and can serve as indicators of disease progression. Moreover, low levels of PALB, reflecting systemic nutrition and inflammatory status, are closely related to poor prognosis, possibly because of malnutrition and the impact of chronic illness on overall health and disease resistance [16–18].

In contrast, diffuse gastric cancer has a poorer prognosis because of its rapid disease progression and high invasiveness. The lack of structural organization in this subtype of tumor cells leads to rapid and extensive spread within the gastric wall, often resulting in a diagnosis at an advanced stage. The key prognostic factors for diffuse gastric cancer include advanced pTNM stage, Borrmann type IV disease (indicating high tumor invasiveness), low lymphocyte count (LYM), high lactate dehydrogenase (LDH) levels, peripheral nerve infiltration (PNI), large tumor size and whole stomach location. Elevated LDH levels typically reflect the high metabolic status of tumor cells, whereas the presence of peripheral nerve infiltration (PNI) indicates greater tumor invasiveness, both of which are associated with poor treatment response and survival rates [19–21].

The application of SHAP values provides us with an important tool for explaining the predictions of the model, allowing us to demonstrate the specific contributions of each variable to prognosis prediction. This transparency is crucial for the acceptance and trust of machine learning models in clinical applications [22, 23].

However, our study has several limitations. First, the research is based on data from a single center, which may introduce some sample selection bias. Future studies should validate the model's generalizability through collaboration with multicenter data. Second, despite the partial alleviation of the "black box" nature of machine learning models via SHAP values, further research and development are needed for complete transparency and explanation of the models. Finally, studies have shown inconsistent results, indicating a more pronounced risk among individuals who consume large quantities of alcohol and individuals with specific types of gastric cancer, including the diffuse type [24]. These diverse findings highlight the need for more targeted research, particularly in elucidating how and to what extent alcohol affects different types of gastric cancer. We plan to collaborate with other research institutions in future studies to collect and analyze such data, enhancing the breadth and depth of the research.

While this study successfully predicted the survival outcomes of gastric cancer patients via machine learning models, we recognize the potential importance of identifying trends in recurrence sites for further personalized treatment. Detailed information about recurrence sites is crucial for clinical decision-making, as it helps in formulating more precise treatment plans. However, owing to the limitations of the current dataset, we were unable to conduct this analysis in this study. Future research could expand the scope of data collection to include detailed information on recurrence sites and incorporate it into machine learning models to identify and analyze recurrence trends. This would not only enhance the predictive power of the models but also provide stronger support for personalized treatment. Additionally, as the volume and quality of data improve, we will have the opportunity to build more complex models to explore potential correlations between recurrence sites and other clinical variables. These research directions will not only contribute to a deeper understanding of the mechanisms underlying gastric cancer recurrence but also promote the development of data-driven personalized treatment strategies.

Conclusion

Machine learning has demonstrated great potential in predicting the survival prognosis of gastric cancer patients. By constructing predictive models, we found that the survival outcomes of intestinal and diffuse gastric cancer patients are influenced by various factors, including pTNM stage, tumor size, and specific biomarkers. These models provide clinicians with more accurate prediction tools, aiding in the formulation of personalized treatment plans and improving treatment effectiveness and patient survival rates.

Supplementary Information

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Supplementary Material 1.

Supplementary Material 2.

Supplementary Material 3.

Authors' contributions
K.J. and L.S. provided the idea for the article and completed the writing of the main manuscripts; Y.F., L.W., H.G., H.L., J.X., S.X., B.X., E.L. and Y.Z.were involved in data collection; C.L. and M.L were involved in statistical analysis. All authors contributed to the article and approved the submitted version.

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Availability of data and materials
No datasets were generated or analysed during the current study.

Declarations

Ethics approval and consent to participate
This study was approved by the Ethics Committee of Harbin Medical University Cancer Hospital and Heilongjiang Provincial Hospital, and the research process was in accordance with the 1964 Helsinki Declaration.
All patients included in this study have signed written informed consent.

Competing interests
The authors declare no competing interests.

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References

1. Kim SG, Eom BW, Yoon H, Kim YW, Ryu KW. Prognostic value of preoperative systemic inflammatory parameters in advanced gastric cancer. J Clin Med. 2022;11:11.
2. Fu M, Zhang X, Shen F, Ma J, Li Z. Prognostic value of peripheral blood neutrophil/lymphocyte ratio, platelet/lymphocyte ratio, pan-immune-inflammation value and systemic immune-inflammation index for the efficacy of immunotherapy in patients with advanced gastric cancer. Immunotherapy. 2024;16(8):551–63.
3. Thrift AP, Wenker TN, El-Serag HB. Global burden of gastric cancer: epidemiological trends, risk factors, screening and prevention. Nat Rev Clin Oncol. 2023;20:338–49.
4. Singh S, Bhat MY, Sathe G, Gopal C, Sharma J, Madugundu AK, Joshi NS, Pandey A. Proteomic signatures of diffuse and intestinal subtypes of gastric cancer. Cancers (Basel). 2021;13:5930.
5. Oue N, Sentani K, Sakamoto N, Uraoka N, Yasui W. Molecular carcinogenesis of gastric cancer: Lauren classification, mucin phenotype expression, and cancer stem cells. Int J Clin Oncol. 2019;24:771–8.
6. Fang X, Wei J, He X, An P, Wang H, Jiang L, Shao D, Liang H, Li Y, Wang F, Min J. Landscape of dietary factors associated with risk of gastric cancer: a systematic review and dose-response meta-analysis of prospective cohort studies. Eur J Cancer. 2015;51:2820–32.
7. Ishikura N, Ito H, Oze I, Koyanagi YN, Kasugai Y, Taniyama Y, Kawakatsu Y, Tanaka T, Ito S, Tajika M, et al. Risk prediction for gastric cancer using GWAS-identifie polymorphisms, Helicobacter pylori infection and lifestyle-related risk factors in a Japanese Population. Cancers (Basel). 2021;13:5525.
8. Yamaguchi H, Nagamura Y, Miyazaki M. Receptor tyrosine kinases amplified in diffuse-type gastric carcinoma: potential targeted therapies and novel downstream effectors. Cancers (Basel). 2022;14:14.
9. Schauer M, Peiper M, Theisen J, Knoefel W. Prognostic factors in patients with diffuse type gastric cancer (linitis plastica) after operative treatment. Eur J Med Res. 2011;16:29–33.
10. Tran KA, Kondrashova O, Bradley A, Williams ED, Pearson JV, Waddell N. Deep learning in cancer diagnosis, prognosis and treatment selection. Genome Med. 2021;13:152.
11. Ahsan MM, Luna SA, Siddique Z. Machine-learning-based disease diagnosis: a comprehensive review. Healthc (Basel). 2022;10:10.
12. Klang E, Sourosh A, Nadkarni GN, Sharif K, Lahat A. Deep learning and gastric cancer: systematic review of AI-Assisted Endoscopy. Diagnostics (Basel). 2023;13:13.
13. Akabane S, Miyake K, Iwagami M, Tanabe K, Takagi T. Machine learning-based prediction of postoperative mortality in emergency colorectal surgery: a retrospective, multicenter cohort study using Tokushukai medical database. Heliyon. 2023;9: e19695.
14. Zhang C, Wang J, Yang Y, Dai B, Xu Z, Zhu F, Yu H. Machine learning for predicting the risk stratification of 1–5 cm gastric gastrointestinal stromal tumors based on CT. BMC Med Imaging. 2023;23:90.
15. Zhou CM, Xue Q, Wang Y, Tong J, Ji M, Yang JJ. Machine learning to predict the cancer-specific mortality of patients with primary non-metastatic invasive breast cancer. Surg Today. 2021;51:756–63.
16. Feng F, Tian Y, Xu G, Liu Z, Liu S, Zheng G, Guo M, Lian X, Fan D, Zhang H. Diagnostic and prognostic value of CEA, CA19-9, AFP and CA125 for early gastric cancer. BMC Cancer. 2017;17:737.
17. Sun Z, Zhang N. Clinical evaluation of CEA, CA19-9, CA72-4 and CA125 in gastric cancer patients with neoadjuvant chemotherapy. World J Surg Oncol. 2014;12: 397.
18. Li Z, Wang Y, Ying X, Shan F, Wu Z, Zhang L, Li S, Jia Y, Ren H, Ji J. Different prognostic implication of ypTNM stage and pTNM stage for gastric cancer: a propensity score-matched analysis. BMC Cancer. 2019;19:80.
19. Chen J, Zou X. Prognostic significance of lactate dehydrogenase and its impact on the outcomes of gastric cancer: a systematic review and meta-analysis. Front Oncol. 2023;13: 1247444.
20. Song XH, Zhang WH, Kai L, Chen XL, Zhao LY, Chen XZ, Kun Y, Zhou ZG, Hu JK. Prognostic impact of Borrmann classification on advanced gastric cancer: a retrospective cohort from a single institution in western China. World J Surg Oncol. 2020;18:204.
21. Jia H, Li R, Liu Y, Zhan T, Li Y, Zhang J. Preoperative prediction of Perineural Invasion and Prognosis in Gastric Cancer based on machine learning through a Radiomics-Clinicopathological Nomogram. Cancers (Basel). 2024;16:614.
22. Cordova C, Muñoz R, Olivares R, Minonzio JG, Lozano C, Gonzalez P, Marchant I, González-Arriagada W, Olivero P. HER2 classification in breast cancer cells: a new explainable machine learning application for immunohistochemistry. Oncol Lett. 2023;25:44.
23. Li R, Shinde A, Liu A, Glaser S, Lyou Y, Yuh B, Wong J, Amini A. Machine learning-based interpretation and visualization of nonlinear interactions in prostate cancer survival. JCO Clin Cancer Inf. 2020;4:637–46.
24. Rota M, Pelucchi C, Bertuccio P, Matsuo K, Zhang ZF, Ito H, Hu J, Johnson KC, Palli D, Ferraroni M, et al. Alcohol consumption and gastric cancer risk-A pooled analysis within the StoP project consortium. Int J Cancer. 2017;141:1950–62.

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