

# Applying artificial intelligence using routine clinical data for preoperative diagnosis and prognosis evaluation of gastric cancer

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**Abstract.** The present study employed artificial intelligence (AI) machine learning technology to evaluate the prognosis of gastric cancer using blood collection data, commonly used in clinical practice and subsequently performed a stratification distinct from conventional tumor-node-metastasis (TNM) classification. Experiments were conducted using four machine learning methods, namely, logistic regression (LR), random forest (RF), gradient boosting (GB) and deep neural network (DNN), to classify good or poor post-5-year prognosis based on clinicopathological data and post-5-year relapse occurrence. For each machine learning method, the importance was sorted in descending order (from the most to the least); the top features were used for clustering using the k-medoids method. The prediction accuracy and area under the curve (AUC) for 5-year survival were as follows: LR, 76.8% and 0.702; RF, 72.5% and 0.721; GB, 75.3% and 0.73; DNN, 76.9% and 0.682, respectively. The prediction accuracy and AUC for 5-year recurrence-free survival were as follows: LR, 85.5% and 0.692; RF, 79.0% and 0.721; GB, 80.5% and

0.718; DNN, 83.2% and 0.670. Clustering patients into three groups resulted in a stratification distinct from the TNM classification. In conclusion, AI machine learning using routine clinical data can help evaluate the prognosis of gastric cancer, with prognosis differing according to AI-identified clusters.

## Introduction

Gastric cancer remains a leading cause of death worldwide. According to the World Health Organization database GLOBOCAN, gastric cancer is the fourth leading cause of cancer death, accounting for 7.7% of all cancer-related deaths. In addition, gastric cancer is the fifth most common cancer, accounting for 5.6% of the total cancer cases (1). The incidence of gastric cancer varies by region, with the highest rates reported in East Asia, Eastern Europe and South America and the lowest rates in North America and parts of Africa. Furthermore, the incidence is frequently higher in males than in females (1). Although the incidence of gastric cancer is declining owing to reduced *Helicobacter pylori* infection rates, the incidence of carcinoma of the fundic region remains problematic. The prognosis of gastric cancer is stratified according to the tumor-node-metastasis (TNM) classification and multidisciplinary treatment is required. Despite advances in surgical techniques and chemotherapy, the prognosis for advanced cases remains poor. An international collaborative study (CONCRD-3) covering 71 countries and territories reported 5-year survival rates of only 20-40% (2).

Future perspectives for gastric cancer suggest that treatment strategies will move toward personalized medicine. Crucial elements in the field of personalized medicine include identifying factors that can accurately stratify patient response before the first therapeutic intervention, as well as the development of methods to determine actual treatment outcomes and prognosis. However, the human body is complex, with several nonlinear factors affecting survival. Most conventional methods for evaluating the prognosis of gastric cancer use a combination of specific biomarkers that are indicators of inflammation and nutritional status; however, their predictive accuracy is inadequate. As surrogate markers for evaluating the prognosis of gastrointestinal cancer, the advantages of

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**Abbreviations:** ALB, serum albumin; AUC, area under the curve; AI, artificial intelligence; ANN, artificial neural network; BUN, blood urea nitrogen; CA, carbohydrate antigen; CEA, carcinoembryonic antigen; DNN, deep neural network; GB, gradient boosting; KM, Kaplan-Meier; LR, logistic regression; MCHC, mean corpuscular hemoglobin concentration; MPV, mean platelet volume; NLR, neutrophil-to-lymphocyte ratio; PDW, platelet distribution width; PCT, procalcitonin; PLT, platelet; PT, prothrombin time; RBC, red blood cell count; RDW, red cell distribution width; RF, random forest; TP, total protein

**Key words:** gastric cancer, adenocarcinoma, artificial intelligence, blood sampling, blood data

TNM classification, pathological findings and grading using a combination of blood sampling data and features obtained from imaging tests (e.g., standardized uptake value by fluorodeoxyglucose-positron emission tomography) have been documented (3,4). However, although these results have been evaluated to a certain extent, they are not considered objective and versatile models owing to poor reproducibility and differences in results across institutions. This may be partly as indicators consist of a single or combination of factors, they are easy to grasp visually and it is easy to infer a causal relationship with outcomes, leading us to focus on indicators that are easy to perceive sensibly.

The essence of cancer lies in heterogeneity. To overcome the complexity of cancer and achieve personalized treatment, it is essential to utilize the advantages of AI to integrate and analyze general test information, clinical data and modality information handled in daily clinical practice in a multi-layered manner by employing AI-based machine learning technology.

To date, extracting meaningful information from large data sets with multiple input variables remains a considerable challenge; however, artificial intelligence (AI) techniques have facilitated advances in this field. Machine learning is a branch of AI technology that allows computers to ‘learn’ potential patterns from past examples. The use of machine learning approaches to predict new data by utilizing identified patterns can help detect patterns that can be difficult to recognize from complex combinations of multiple biomarkers.

The object of the present study was to utilize blood data used in real-world clinical practice and employ AI techniques to evaluate the prognosis of gastric cancer, followed by data stratification distinct from that of the traditional TNM classification.

## Materials and methods

**Study design and patients.** The current retrospective study evaluated 1,687 patients with gastric cancer who had undergone surgical treatment at Chiba Cancer Center between January 2007 and December 2016. Table I summarizes the demographic characteristics of the patients. Among the 1,687 patients, 1,185 (70.2%) were males, while 502 (29.8%) were females and the age ranged from 29 to 92 years (median: 67 years). Considering the TNM stage, 1,171 (69.4%), 173 (10.3%), 243 (14.4%) and 100 (5.9%) patients had stage I, II, III and IV disease, respectively. The present study retrospectively examined 35 clinicopathological parameters, including age at diagnosis, preoperative biochemical data and tumor markers. This study was approved by the Chiba Cancer Center Review Board (approval no. H29-006) and was conducted in accordance with the ethical principles of the Declaration of Helsinki. All patients provided written informed consent to participate.

**Supervised machine learning classifiers.** To predict survival after 5 years based on clinicopathological data (Task 1) and relapse after 5 years (Task 2), experiments were performed using four machine learning methods, namely, logistic regression (LR), random forest (RF), gradient boosting (GB) and deep neural network (DNN).

Table I. Patient details and clinicopathological features.

Clinicopathological feature	Gastric cancer
Number	1,687
Sex, n (%)	
Male,	1,185 (70.2)
Female	502 (29.8)
Mean age, years	67
Age range, years	29-92
Depth of tumor invasion, n (%)	
T1	874 (51.8)
T2	427 (25.3)
T3	336 (20.1)
T4	50 (2.8)
Lymph node metastasis, n (%)	
Positive	449 (26.6)
Negative	1,238 (73.4)
Distant metastasis, n (%)	
Positive	92 (5.5)
Negative	1,595 (94.5)
TNM stage, n (%)	
I	1,171 (69.4)
II	173 (10.3)
III	243 (14.4)
IV	100 (5.9)
TNM tumor-node-metastasis.	

LR is a general linear model for two-class problems, where a linear combination of each feature explains the log odds of the posterior probability of each class. Therefore, it is also possible to interpret the size of regression coefficients corresponding to each feature as the importance of that feature (5). The present study used the least absolute shrinkage and selection operator-type LR, which imposed the L1 norm of regression coefficients as a constraint to obtain a sparse solution.

RF and GB are ensemble learning methods using decision tree and weak learners. RF creates multiple distinct decision trees using randomness in learning the decision trees, subsequently integrating them for classifier construction (6). GB updates decision trees sequentially and, after a specified number of updates, classifier construction is achieved by integrating all decision trees with a weighted sum (7). The DNN used in the present study was a deep learning model for tabular numerical data, which includes a layer estimating the importance of features from the data (8).

All machine learning methods were implemented using Python Version 3 (9), and LR and RF were implemented using the Scikit-learn library (10). GB was implemented using xgboost (11) and DNN was implemented using TensorFlow backend and Keras API (12). The machine learning methods used in the present study can effectively estimate the importance of features for classification. Therefore, important features for each task were selected using these four methods. However, the range of values of each feature can generally

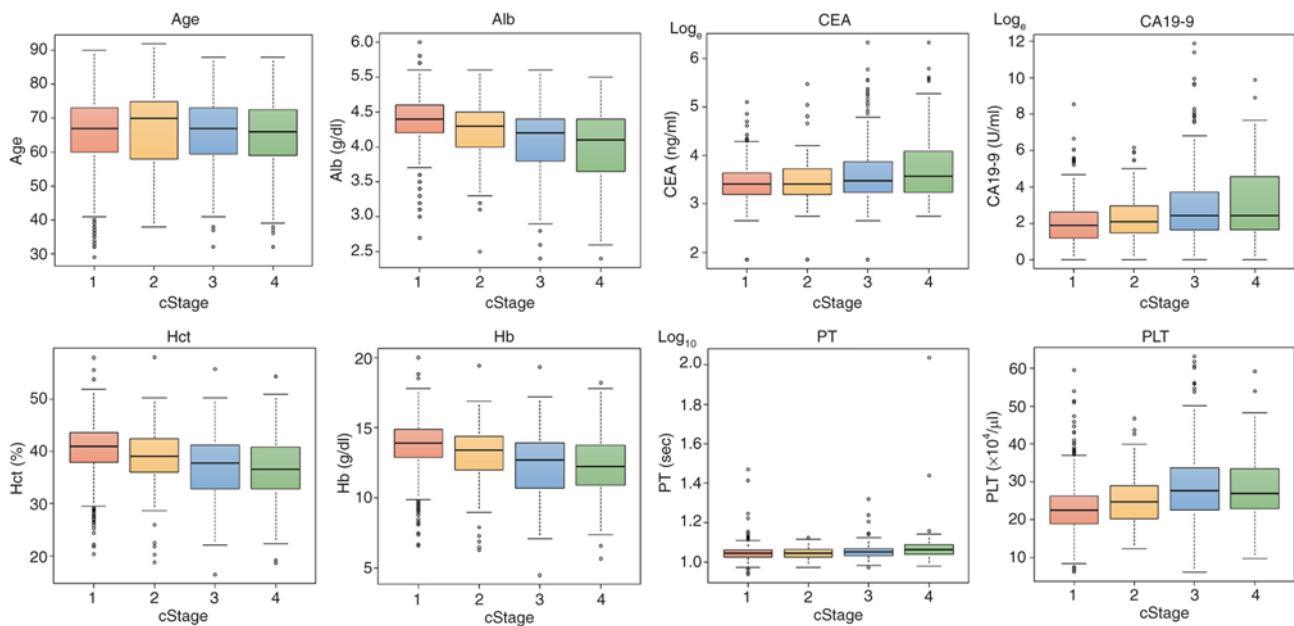


Figure 1. Box plot showing the distribution of feature values for each stage. Alb, serum albumin; CEA, carcinoembryonic antigen; CA, carbohydrate antigen; Hct, hematocrit; Hb, hemoglobin level; PT, prothrombin time; PLT, platelet.

differ considerably and thus a comparison of the estimated feature importance may not be reasonable. Therefore, data normalization was performed as preprocessing to ensure each feature would have the same scale.

**Clustering and visualization using 10 significant features.** The importance of each machine learning method was ranked in descending order and the top  $m$  features were employed to perform clustering using the k-medoids method. Unlike the k-means method, the k-medoids method utilizes the center of gravity as the representative point of each cluster and uses medoids as the representative point of the cluster. The medoids are calculated as follows:  $\operatorname{argmin}_{x \in X_i} \sum_{y \in (X_i - x)} d(x, y)$ , where  $X_i = \{x\}$  are clusters and  $d(x, y)$  is the dissimilarity between data  $x$  and  $y$ . Additionally, the k-medoids method performs clustering by minimizing the sum of distances between the medoid and data points. Unlike the k-means method, which evaluates loss using the square of the distance, the k-medoids method evaluates loss using the absolute value of the distance. Thus, the k-medoids method is less affected by outliers. Clustering is performed in a high-dimensional space and, as such, it is not possible to directly evaluate the results. Therefore, t-distributed stochastic neighbor embedding (t-SNE) was used to project data onto a two-dimensional space and visually evaluate results qualitatively.

## Results

**Gastric cancer prognosis based on multiple preoperative blood markers.** The 5-year survival rate of patients with gastric cancer was predicted using multiple supervised machine learning methods (Task 1; Table II). The predictive accuracy and area under the curve (AUC) were 76.8% and 0.702 for LR, 72.5% and 0.721 for RF, 75.3% and 0.73 for GB and 76.9% and 0.682 for DNN, respectively. Similarly, multiple supervised machine learning methods were employed to predict the 5-year recurrence-free survival rate of patients with gastric cancer (Task 2;

Table II). The prediction accuracy and AUC were 85.5% and 0.692 for LR, 79.0% and 0.721 for RF, 80.5% and 0.718 for GB and 83.2% and 0.670 for DNN, respectively. These supervised machine learning analyses were reasonably accurate in evaluating prognosis and recurrence using clinical data.

Next, important features were extracted for analyzing prognosis (Table II). The top 10 features were selected for each of the four AIs. Based on the results, selected features differed for each AI method. However, for 5-year overall survival, age and serum levels of tumor markers, including albumin (ALB), carcinoembryonic antigen (CEA), carbohydrate antigen (CA)19-9, hematocrit (Hct), hemoglobin level (Hb), prothrombin time (PT) and platelet (PLT) count, were selected for most AIs. Fig. 1 presents the box-and-whisker plots for each feature by progression level and Fig. 2A presents the box-and-whisker diagrams divided by 5-year survival for Task 1 of each feature. In addition, Fig. 2B shows Kaplan-Meier (KM) curves divided into two groups by the median value of each feature.

Next, important features were extracted for the recurrence analysis. The top 10 features were selected for each of the four AIs. The results revealed differences in features selected for each AI (Table II). However, for the 5-year recurrence-free survival, the tumor markers CEA and CA19-9, as well as ALB, total protein (TP), Hb, mean corpuscular hemoglobin concentration (MCHC), PT and procalcitonin level (PCT) were similarly selected in several AIs. Fig. S1A presents the box-and-whisker diagrams for each selected feature by progression. Fig. S1B shows the box-and-whisker plots of 5-year recurrence-free survival for Task 2 of each feature. Fig. S1C presents the KM curves divided into two groups by the median of each feature.

**Clustering analysis of prognosis using the machine learning approach.** Next, clustering analysis was performed to identify specific patient subgroups with various prognoses based on the same 35 preoperative blood markers and age. Clustering was performed using the top 10 features extracted for each

Table II. Predicting 5-year gastric cancer survival using multiple supervised machine learning methods and Significant Features Ranking.

## A, Predicting 5-year gastric cancer survival

AI	Logistic regression	Random forest	Gradient boosting	Deep neural network
Task 1				
Accuracy, %	76.8	72.5	75.3	76.9
AUC	0.702	0.721	0.73	0.682
Task 2				
Accuracy, %	85.5	79	80.5	83.2
AUC	0.692	0.721	0.718	0.67

## B, Significant Features Ranking

AI	Logistic regression	Random forest	Gradient boosting	Deep neural network
Task 1				
1	ALB	Hct	ALB	ALB
2	PLT	ALB	Hgb	CEA
3	PCT	Hgb	Hct	P.T
4	Hgb	CA19-9	CEA	CA19-9
5	P.T	CEA	CA19-9	Cl
6	Cl	RBC	Cl	BUN
7	CA19-9	RDW	age	age
8	MPV	age	RBC	Hgb
9	CEA	Ly	ALT	LDH
10	PDW	MCH	RDW	PDW
Task 2				
1	PCT	ALB	ALB	MCHC
2	MCHC	MCHC	Hgb	P.T
3	PLT	CEA	MCHC	TP
4	NEU	Hgb	CEA	RDW
5	RDW	Hct	P.T	AST
6	TP	CA19-9	TP	CRNN
7	Hgb	PT	Hct	MPV
8	Ly	TP	CA19-9	WBC
9	MCV	RBC	AST	ALP
10	ALB	PCT	age	BUN

Task 1, 5-year survival rate of patients with gastric cancer; Task 2, 5-year recurrence-free survival rate of patients with gastric cancer; ALB, serum albumin; ALT, alanine transaminase; AST, aspartate aminotransferase; AUC, area under the curve; BUN, blood urea nitrogen; CA, carbohydrate antigen; CEA, carcinoembryonic antigen; Hb, hemoglobin level; Hct, hematocrit; LDH, lactate dehydrogenase; MCHC, mean corpuscular hemoglobin concentration; MPV, mean platelet volume; NEU, neutrophil; PCT, procalcitonin; PDW, platelet distribution width; PLT, platelet count; PT, prothrombin time; RBC, red blood cell count, RDW, red cell distribution width; TP, total protein.

AI. The k-medoids method was used to visualize clustering results in 10-dimensional space, which were transformed into two dimensions using t-SNE (Fig. 3). In the visualization, each cluster was represented by a color, each stage was represented by a plot size and the prognosis was represented by a symbol to indicate differences among data.

A total of 10 factors were used for clustering in each of the four AIs as follows: i) in LR: ALB, PLT count, PCT, Hb, PT, Cl, CA19-9, mean platelet volume (MPV), CEA and platelet

distribution width (PDW); ii) in RF: Hct, ALB, Hb, CA19-9, CEA, red blood cell count (RBC), red cell distribution width (RDW), age, Ly and MCHC; iii) in GB: ALB, Hb, Hct, CEA, CA19-9, Cl, age, RBC, alanine transaminase level and RDW; and iv) in DNN: ALB, CEA, PT, CA19-9, Cl, blood urea nitrogen level (BUN), age, Hgb, lactate dehydrogenase level and PDW. Clustering was performed in three groups. The KM curve was plotted for the three clusters and the results of all AI clustering revealed significant differences in prognosis

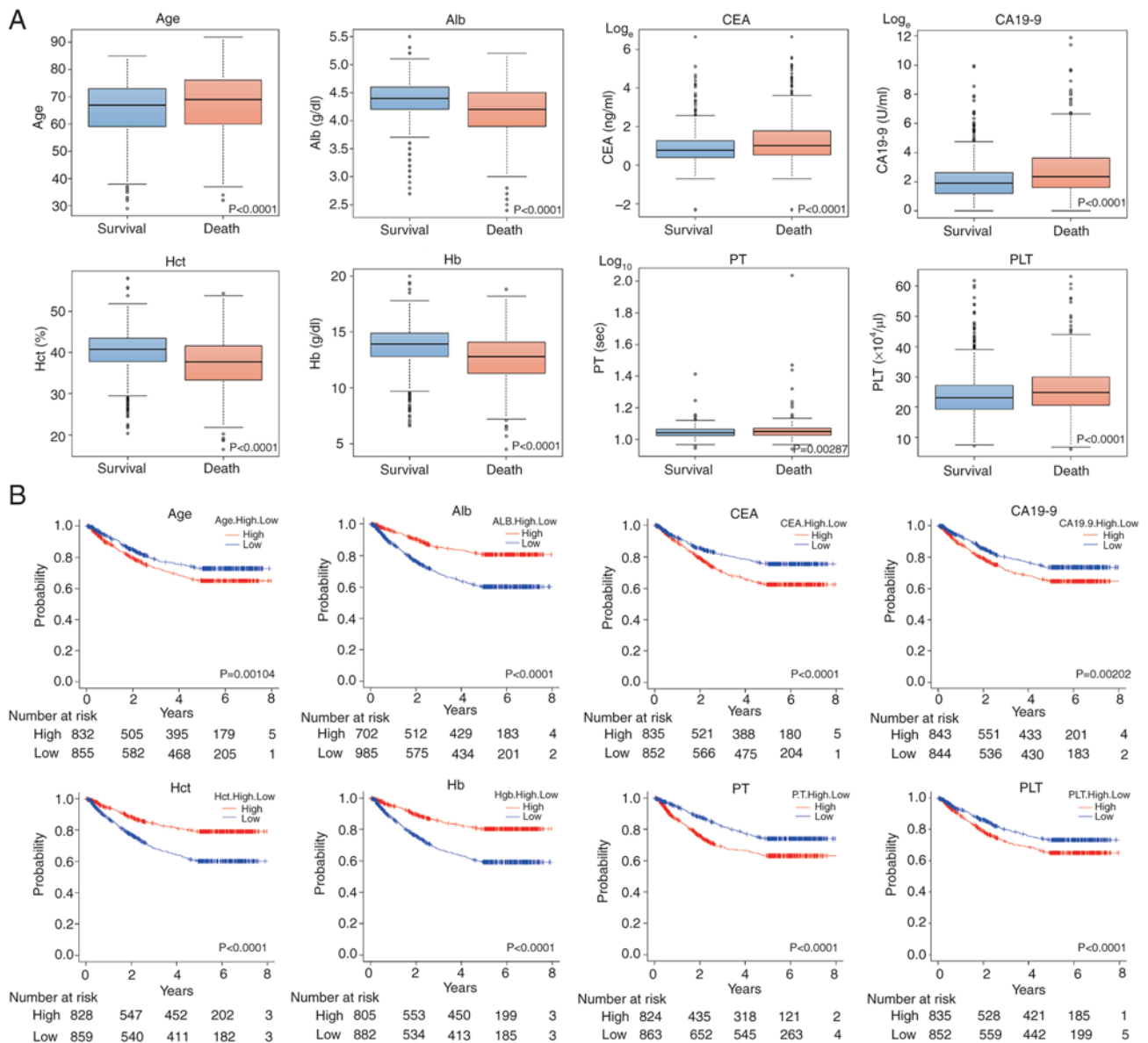


Figure 2. Stratification by multiple preoperative blood markers in patients with gastric cancer. (A) Distribution of selected features, divided into two groups according to whether or not patients survived for 5 years, shown as box plots. The distribution of selected features is shown in a box-and-whisker diagram for patients who did and did not survive for 5 years. (B) Survival analysis according to the median value of selected significant features. Alb, serum albumin; CEA, carcinoembryonic antigen; CA, carbohydrate antigen; Hct, hematocrit; Hb, hemoglobin level; PT, prothrombin time; PLT, platelet.

(Fig. 4A). The KM curves for each stage of progression (cStage I, cStage II+III and cStage IV) showed that all AIs in stage I clustered in different prognostic groups. In stage II+III, GB data were divided into three clusters with different prognoses (Fig. 4B). For GB, considering stage I, Cluster number 2 (green) included more mortalities than Cluster numbers 1 and 3 (Fig. 5).

Comparable results were obtained for recurrence-free survival. Recurrence-free survival was similarly validated using 10 factors in each of the four AI methods; i) in LR: PCT, MCHC, PLT count, neutrophil (NEU), RDW, TP, Hb, Ly, mean corpuscular volume and ALB; ii) in RF: ALB, MCHC, CEA, Hb, Hct, CA19-9, PT, TP, RBC and PCT; iii) in GB: ALB, Hb, MCHC, CEA, PT, TP, Hct, CA19-9, aspartate aminotransferase and age; and iv) in DNN: MCHC, PT, TP, RDW, aspartate aminotransferase level, CRNN, MPV, white

blood cell count, alkaline phosphatase level and BUN. Data were divided into three clusters. The KM curve was plotted in three clusters to verify the prognosis; the clustering results of RF and GB showed that clustering was performed in three groups with significantly different prognoses. In the RF and GB clustering, the KM curve for each stage of progression (cStage I, cStage II+III and cStage IV) revealed that the prognoses of patients with stage I differed from those of patients with stage II+III and stage IV. In RF clustering, the prognoses differed for patients with stage II+III (Fig. S2).

## Discussion

The present study evaluated the prognosis of patients with gastric cancer by analyzing routine clinical data using machine learning of multiple AI types. The advantages of machine



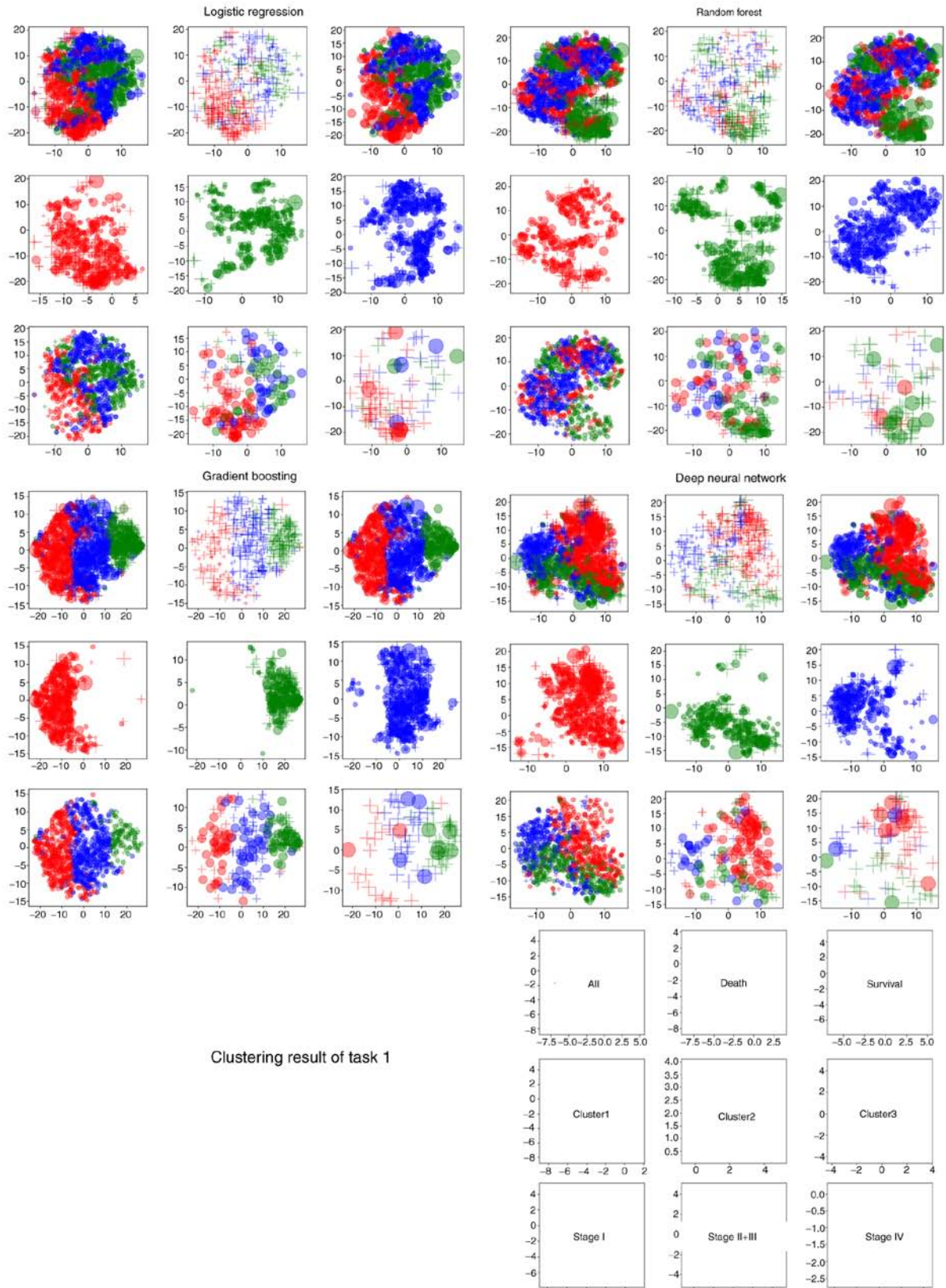


Figure 3. Clustering results of Task 1. Plotted on the grouping plane into three groups; Cluster 1 (red), Cluster 2 (green) and Cluster 3 (blue). Stages are represented by plot sizes: Stage I is small, stage II + III is moderate and stage IV is largest. For the prognosis, O indicates survivors and + indicates non-survivors. Results are presented with four classifiers.

learning is that it can simultaneously process large datasets containing several factors and predict new data by recognizing hidden patterns (13,14). TNM staging is the most widely used

system for staging gastric cancer and determining the treatment and prognosis (15). However, the prognosis varies even among patients exhibiting the same disease stage. Prediction

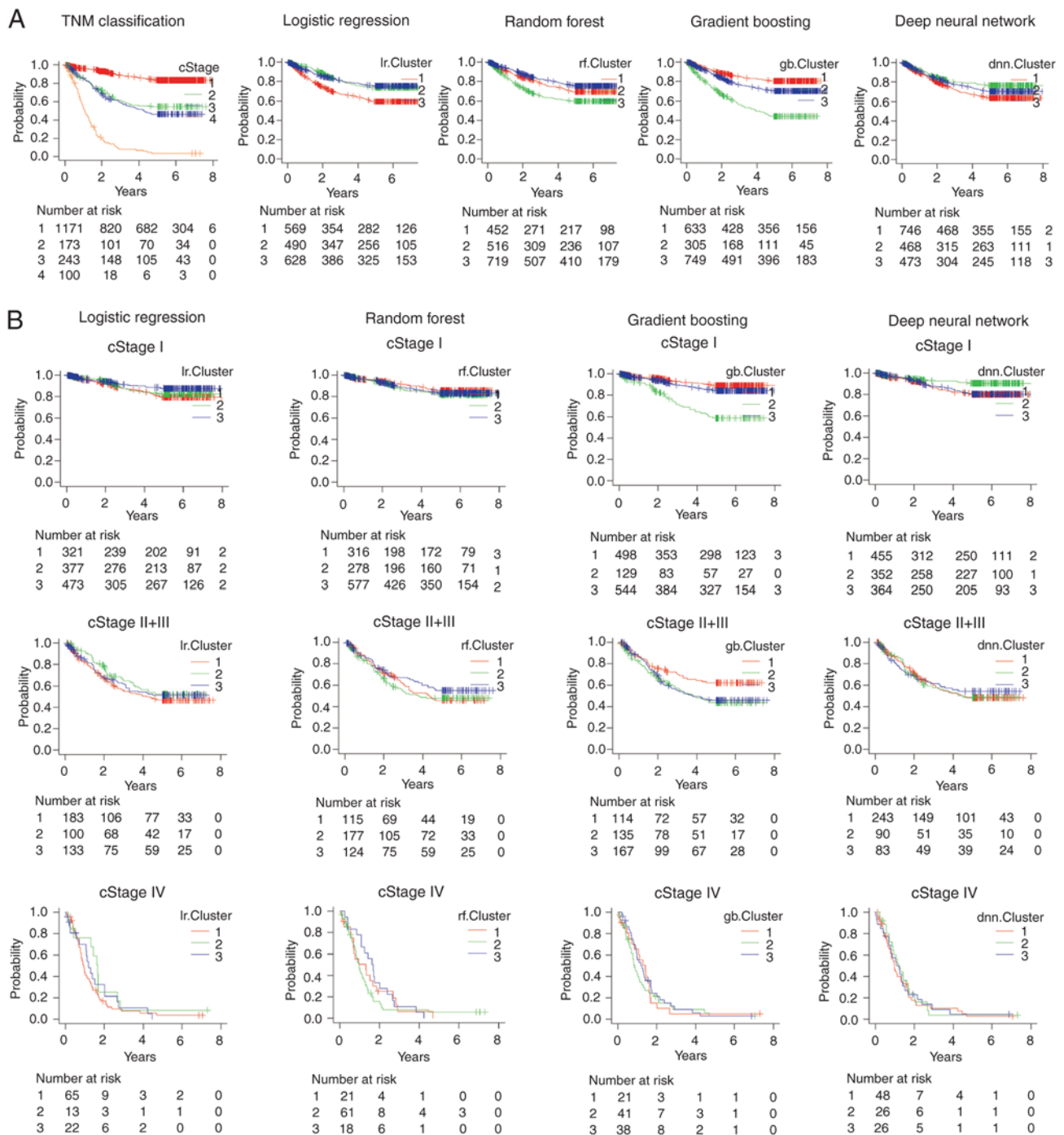


Figure 4. Kaplan-Meier curves plotted for the three clusters. (A) Survival analysis results in clustering by TNM classification and each AI classifier. (B) Survival analysis results in clustering by AI classifier for each stage. AI, artificial intelligence; TNM, tumor-node-metastasis.

of high-risk patients after radical surgery is crucial for post-operative follow-up, selecting adjuvant therapy and planning new treatment strategies. Inflammatory biomarkers, such as neutrophil count, PLT count and lymphocyte count (16,17); preoperative ALB and transthyretin levels; and the tumor marker CA19-9, have been employed to evaluate the prognosis of patients with gastric cancer (18-20). In addition, the function of prognostic indices, including the Controlling Nutritional Status score (21,22), which is calculated from ALB, total lymphocyte count and serum total cholesterol levels; the Glasgow prognostic score, a combination of inflammation and nutritional status indices; the neutrophil-to-lymphocyte

ratio (NLR); and the Prognostic Nutritional Index, have been reported (23-25).

However, the prognostic ability of specific biomarkers, or their combination, remains poor, which can be explained by the complexity of the human body, with numerous nonlinear factors affecting survival. Furthermore, with the advent of various molecular-targeted drugs and the prognostic association between immune cells and gastric cancer (26), treatment options will continue to diversify. In recent years, AI has been used to evaluate the prognosis of gastric cancer, including survival and risk of recurrence, by combining multiple factors (Table SI). There are four studies that have employed the

Table III. Multivariate analysis showed that clustering results were independent prognostic factors.

Multivariate analysis	Hazard ratio	Lower 95% CI	Upper 95% CI	P-value
Logistic regression	0.8767	0.7798	0.9856	$2.76 \times 10^{-3}$
cStage I-IV	2.338	2.14	2.555	<0.001
Random forest	0.9905	0.8732	1.124	$8.82 \times 10^{-1}$
cStage I-IV	2.383	2.182	2.602	<0.001
Gradient boosting	1.144	1.021	1.281	$2.09 \times 10^{-2}$
cStage I-IV	2.374	2.176	2.59	<0.001
Deep neural network	0.9999	0.8893	1.124	$9.99 \times 10^{-1}$
cStage I-IV	2.385	2.185	2.604	<0.001

CI, confidence interval; cStage, stage of progression.

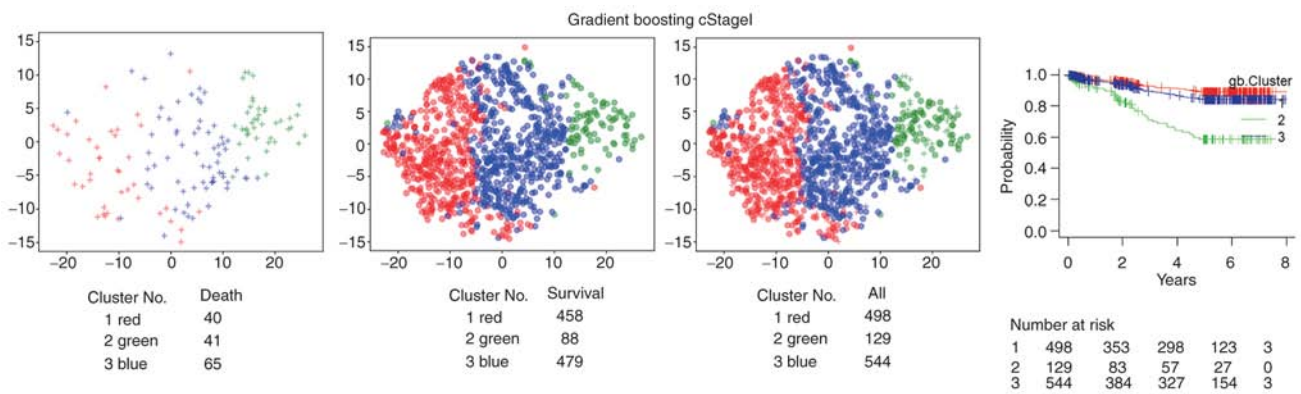


Figure 5. Clustering results and survival analysis limited to stage I cases analyzed with gb. gb, gradient boosting.

artificial neural network (ANN) in their prediction model. Que *et al* (27) predicted the 3-year overall survival using a preoperative ANN and the tool showed 75.2% accuracy, 86.5% sensitivity and 43.8% specificity. Kangi *et al* (28), Oh *et al* (29) and Li *et al* (30) predicted the 5-year overall survival and the AUC values were 0.935, 0.81 and 0.84, respectively. Afrash *et al* (31) predicted the 5-year survival for gastric cancer using multiple AIs, with Hist GB exhibiting the best predictive ability (accuracy, 88.37%; sensitivity, 89.72%; specificity, 86.24%; and AUC, 0.88). Based on the findings of these reports, prognosis can be evaluated to a certain level. However, these studies selected tumor diameter and TNM factors as critical factors and so their models may fail to represent a new alternative stratification to the TNM classification.

The novelty of the present study was that it evaluated prognosis using only blood test data, excluding clinicopathological features such as tumor depth and lymph node metastasis, which are typically employed in the conventional TNM classification. The findings revealed that AI techniques could predict the 5-year overall survival and recurrence-free survival with a certain degree of accuracy even when only clinical data from blood sampling and age and not pathological factors, were analyzed. In the present study, 10 significant features were selected for prediction by AI. Based on the selected features, patients were stratified into three groups by clustering them with each of the four AIs. Regarding the 5-year overall survival, the four AIs, i.e., LR, RF, GB and DNN, presented substantially

distinct prognoses. Based on multivariate analysis, clustering results were an independent prognostic factor (Table III). In addition, the prognosis differed in the three groups subjected to clustering, even when evaluated by stage. For GB, in stage I, Cluster number 2 (green) included more mortalities than Cluster numbers 1 and 3 (Fig. 5). For stage II + III, Cluster number 1 (red) included fewer mortalities. These findings suggested that the clustering results of the current study were stratified in a different manner when compared with the TNM classification staging. Among patients with stage I disease in Cluster number 2 (green), 41/129 patients succumbed. This was a noteworthy result, well below the traditional TNM stage I survival rate; the 5-year survival rates for patients with gastric cancer treated with surgery alone are 95.1% for stage IA and 88.9% for stage IB (32).

The prognosis of patients with cancer cannot be evaluated in a unified manner owing to the complex interplay of factors such as age, nutritional status and inflammatory response, as well as the degree of tumor progression in the TNM classification. The selection criteria for the four machine learning methods included LR, RF, GB and DNN, which were all chosen due to their capacity to quantify the importance of specific minutiae. Regarding the importance ranking, all methods stem from the learning of data that 'increasing the importance of these selected minutiae will increase the classification accuracy of the data as a whole'. Although the selection process may be unclear, it can be assumed that the AI has determined that the data possesses this characteristic. The 10 features selected in the current study



included not only the tumor markers CEA and CA19-9 but also ALB, TP, age and lymphocyte count, which reflect nutritional status. In addition, these items have been previously reported as factors associated with prognosis in gastric cancer (16-25). The preoperative NLR is an independent prognostic factor in gastric cancer (33). Lin *et al* (16) have also reported that the lymphocyte-to-monocyte ratio and Hb levels are independent prognostic factors. Conversely, some features, such as CI, which have rarely been reported before the application of AI methods, were extracted, with CI found to affect prognosis (Fig. S3).

Notably, different feature values were also extracted for each of the four AIs; these need to be validated using multiple AIs rather than in a single AI and can be undertaken in the future.

All selected features, including nutritional status, reflect the general condition of patients. However, AI can simultaneously analyze all input variables, including these critical features and unselected items, to evaluate prognosis that reflects the general condition of patients. In addition, given that the combination of these items is judged comprehensively and stratified by clustering, there is no need to arbitrarily set cutoff values and evaluate risk, unlike conventional judgments based on a single evaluation item. In the present study, the analysis was conducted using items that excluded information regarding existing TNM classification. The stratification results showed that the prognoses were divided, indicating that AI-based machine learning algorithms afford a powerful tool that can provide important information for prognostic evaluation. It is assumed that stratification was performed based on the general characteristics of patients, such as age and nutrition, using a distinct approach from the TNM classification, which is related to oncological data. Additional analysis of the poor prognosis group may allow further consideration of treatment strategies, such as the indication for chemotherapy.

The present study has some limitations. It is difficult to verify the process through which the AI prediction results led to the observed conclusion. The AI methods used in the current study could calculate and rank the features that were mechanisms contributing to the predictions of the model. In the present study, the top 10 features were used for clustering, which is highly interpretable and could be white-boxed. However, some issues could not be explained, such as criteria for which variables alter predictions and by how much. In addition, the current study did not distinguish the timing of chemotherapy (preoperatively compared with postoperatively). Additional information should be added in future analyses. Furthermore, the study was a single-center study and needs to be validated with data from other hospitals. Despite these limitations, the multilayered AI analysis identified important prognostic factors reflecting the condition of patients. Further analysis of the background factors of stratified groups, with additional cases and clinical information, will improve the usefulness of the tool for clinical practice.

In conclusion, AI machine learning using routine clinical data can help evaluate the prognosis of gastric cancer and the prognosis differs according to the clusters identified by the type of AI. Analyzing the background of gastric cancer patients with poor prognosis, despite early-stage disease, can be used to determine the need for additional treatment. Further accumulation of cases will facilitate a more accurate prognosis evaluation.

Ultimately, a comprehensive assessment of tumors, including TNM, would be desirable.

The objective of the present study was to determine whether a new index for measuring tumor malignancy could be constructed using only AI with blood test data, excluding TNM. It is considered that the results of the current study are no better than TNM but could have been stratified differently as in stage I clustered by GB.

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## Availability of data and materials

The datasets used and/or analyzed during the current study are available from the corresponding author on reasonable request.

## Authors' contributions

NK and IH conceived the study. NK and IH confirm the authenticity of all the raw data. YM, HY, YI and TU developed the statistical analysis plan and conducted statistical analyses. IH, YI and TU contributed to the interpretation of the results. NK drafted the original manuscript. IH, YI and TU supervised the conduct of this study. All authors reviewed the manuscript draft and revised it critically on intellectual content. All authors read and approved the final manuscript.

## Ethics approval and consent to participate

The present study was approved by the Chiba Cancer Center Review Board (approval no. H29-006) and was conducted in accordance with the ethical principles of the Declaration of Helsinki. All patients provided written informed consent to participate.

## Patient consent for publication

Not applicable.

## Competing interests

The authors declare that they have no competing interests.

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