

Machine learning-based classification of renal cell carcinoma and upper tract urothelial carcinoma using preoperative hematological markers

KANRAPEE NUWATKRISIN¹, CHANITA PANWOON², KIARTISAK SENCHAN³,
SAKKARN SANGKHAMANON³ and WUNCHANA SEUBWAI^{4,5}

¹Department of Surgery, Faculty of Medicine, Khon Kaen University, Khon Kaen 40002, Thailand;

²Faculty of Medicine, Vongchavalitkul University, Nakhon Ratchasima 30000, Thailand;

³Department of Pathology, Faculty of Medicine, Khon Kaen University, Khon Kaen 40002, Thailand;

⁴Department of Forensic Medicine, Faculty of Medicine, Khon Kaen University, Khon Kaen 40002, Thailand;

⁵Center for Translational Medicine, Faculty of Medicine, Khon Kaen University, Khon Kaen 40002, Thailand

Received May 15, 2026; Accepted September 2, 2026

DOI: 10.3892/br.2026.2212

Abstract. Renal tumors are the second most common type of urological cancer. These tumors consist of renal cell carcinoma (RCC; 80-85%) and upper tract urothelial carcinoma (UTUC; 5-10%). Accurate preoperative differentiation between these two entities remains challenging despite advances in imaging and endoscopic techniques, often leading to potential misdiagnoses and inappropriate treatment strategies. Therefore, the development of novel diagnostic methods to improve preoperative diagnosis remains an area of notable clinical interest. At present, the potential for using machine learning (ML) based on preoperative hematological markers as non-invasive tools for cancer diagnosis and prognosis is being investigated. However, the application of ML based on preoperative hematological markers to differentiate RCC from UTUC remains unclear. The present study aimed to develop a classification system to differentiate between RCC and UTUC using ML based on preoperative hematological markers and clinical data from 172 patients with renal cancer, including 115 cases (66.9%) of RCC and 57 cases (33.1%) of UTUC. To address class imbalance, the Synthetic Minority Oversampling Technique was applied within a leakage-free pipeline restricted to the training data. Feature selection was performed using recursive feature elimination with cross-validation. A panel of ML algorithms was screened. The six best-performing models were tuned and evaluated, with performance assessed

by accuracy, balanced accuracy, precision, recall, F1 score and the area under the receiver operating characteristic curve (AUC). The Extra Trees classifier showed the most favorable overall performance, with an accuracy of 75.0%, a balanced accuracy of 0.71 and an AUC value of 0.755 (bootstrap AUC, 0.71; 95% CI, 0.59-0.83). These preliminary findings suggest that ML models based on routinely available preoperative hematological markers may serve as a useful, low-cost adjunct to support the differentiation of RCC and UTUC.

Introduction

Renal tumors, which consist of renal cell carcinoma (RCC; 80-85%) and upper tract urothelial carcinoma (UTUC; 5-10%), represent the second most common type of urological cancer (1). Although both originate in the kidney, these malignancies develop from distinct anatomical sites and require different treatment approaches. RCC is typically managed with partial nephrectomy for small tumors (preferred treatment for tumors sized ≤ 4 cm in maximal dimension, optional treatment for tumor sized >4 to ≤ 10 cm in maximal dimension), or radical nephrectomy for larger tumors (preferred treatment for tumor sized >10 cm in maximal dimension) or more advanced disease (tumor extension beyond kidney boundary). By contrast, the gold standard for UTUC is radical nephroureterectomy with bladder cuff excision, while kidney-sparing surgery and endoscopic management may be considered for selected low-risk UTUC to minimize morbidity and preserve renal function (2-5). Current diagnostic approaches for differentiating RCC from UTUC include urine cytology, contrast-enhanced imaging of the upper urinary tract and more invasive procedures, such as ureterorenoscopy (URS) or flexible URS, with or without biopsy (6,7). Therefore, accurate preoperative diagnosis of RCC and UTUC is essential for appropriate treatment planning and improving patient outcomes.

At present, preoperative hematological markers, such as neutrophil-to-lymphocyte ratio (NLR), platelet-to-lymphocyte ratio (PLR) and white blood cell (WBC) count, are increasingly

Correspondence to: Dr Wunchana Seubwai, Department of Forensic Medicine, Faculty of Medicine, Khon Kaen University, Village 16, 123 Mittraphap Road, Nai-Muang, Muang, Khon Kaen 40002, Thailand
E-mail: wunchana@kku.ac.th

Key words: renal cell carcinoma, upper tract urothelial carcinoma, hematological markers, machine learning

recognized as important biomarkers in the diagnosis and prognosis of several cancers, such as gastric (8), breast (9) and prostate cancer (10). These markers reflect the balance between systemic inflammation and immune response, which play crucial roles in cancer development and progression. NLR, PLR and WBC count are simple and low-cost indicators that can be obtained from routine blood tests. Elevated levels of NLR and PLR have been associated with the presence of various cancers as well as with poorer clinical outcomes, such as reduced survival rates and increased risk of metastasis (11,12). Because these preoperative parameters are easily accessible and affordable, they have notable potential to support cancer diagnosis and guide clinical decision-making in patients with cancer.

Currently, machine learning (ML) techniques play an important role in healthcare, especially in cancer (13). ML can be used to improve the accuracy of cancer diagnosis (14) and to predict recurrence (15) and mortality (16). Our previous studies demonstrated that integrative bioinformatics and ML approaches can effectively identify potential biomarkers for clear cell RCC (ccRCC). Insulin-like growth factor-binding protein 3 and galectin 1 were identified as promising secreted biomarkers for ccRCC diagnosis (17). In addition, NADH dehydrogenase (ubiquinone) 1 alpha subcomplex 4-like 2, dopamine transporter 1 and fatty acid binding protein 7 were demonstrated as potential biomarkers for distinguishing ccRCC and non-ccRCC (18,19). However, the application of hematological markers, such as NLR, PLR and WBC count, in differentiating RCC from UTUC remains unclear.

Therefore, the present study aimed to develop and evaluate a ML model using preoperative hematological markers and clinical data to differentiate RCC from UTUC. A panel of ML algorithms, combined with feature selection, was used to explore the diagnostic potential of blood-derived biomarkers as a non-invasive, low-cost adjunct to current diagnostic methods, to support preoperative decision-making in clinical practice for patients with renal cancer.

Materials and methods

Samples from patients with RCC and UTUC. The current retrospective study analyzed data from the electronic medical records of patients with RCC and UTUC who visited Srinagarind Hospital, Faculty of Medicine, Khon Kaen University (Khon Kaen, Thailand) from January 2013 to December 2024. Inclusion criteria were patients with histopathologically confirmed RCC or UTUC who underwent surgical treatment at the same hospital during the study period. Exclusion criteria included patients who did not undergo surgery at the study hospital, those with missing preoperative hematological data and those with incomplete clinical data before or after treatment. The collected data included age and sex (presented in the results section), pathological diagnosis (RCC or UTUC) and hematological parameters obtained from preoperative blood tests. The parameters used in the present study, including age, NLR, PLR, platelet (PLT) count, WBC count, neutrophil percentage (NE %), lymphocyte percentage (LY %) and diagnosis, are shown in Table I.

The present study was conducted in accordance with The Declaration of Helsinki and the International Council for Harmonization Good Clinical Practice guidelines (20). All

Table I. Clinical and hematological features used for machine learning model development.

Variable	Role	Units
Age ^a	Feature	Years
NLR	Feature	N/A
PLR	Feature	N/A
WBC count	Feature	$\times 10^3/\mu\text{l}$
PLT count	Feature	$\times 10^3/\mu\text{l}$
NE %	Feature	%
LY %	Feature	%
Diagnosis ^b	Classification	N/A

^aAge of patients with RCC and UTUC; ^bclassification of RCC and UTUC diagnosis. N/A, not applicable; NLR, neutrophil-to-lymphocyte ratio; PLR, platelet-to-lymphocyte ratio; WBC, white blood cell; PLT, platelet; NE, neutrophil; LY, lymphocyte; RCC, renal cell carcinoma; UTUC, upper tract urothelial carcinoma.

patient information was confidential and presented in a format that prevents individual identification. The study protocol was approved by the Ethics Committee for Human Research of Khon Kaen University (approval no. HE671739). As this was a retrospective study using only de-identified clinical data, with no prospective data collection or patient contact, the requirement for informed consent was waived by the Ethics Committee.

Python library. All analyses were performed in Python (version 3.11.5; <https://www.python.org>). ML models were implemented using scikit-learn (version 1.4.1), class imbalance was addressed with the imbalanced-learn library (version 0.12.2) and gradient-boosted tree models were implemented with XGBoost (version 2.0.3). Data handling and numerical computations were performed using pandas (version 2.1.4), NumPy (version 1.24.3) and SciPy (version 1.11.1). Figures were generated with matplotlib (version 3.10.0) and seaborn (version 0.12.2).

Feature selection. Feature selection is a critical step in the development of ML models, as it helps reduce model complexity and improve predictive performance. In the current study, feature selection was performed using Recursive Feature Elimination with Cross-Validation (RFECV) based on a Random Forest classifier. RFECV was applied to the complete set of available features, ranking them according to the impurity-based feature importance estimated by the Random Forest model. The algorithm then iteratively removed the least important feature at each step. After each elimination, the reduced feature subset was evaluated using 10-fold stratified cross-validation, and the subset yielding the highest mean cross-validation accuracy was selected as the optimal feature set. To avoid data leakage, RFECV was fitted on the training data only.

ML model construction. A total of 23 supervised ML algorithms, including linear models (logistic regression, ridge classifier, ridge classifier with built-in cross-validation, stochastic gradient descent, perceptron and passive-aggressive), support vector

Table II. Comparison of preoperative hematological parameters between patients with RCC and UTUC.

Variable	RCC group	UTUC group	P-value		
			Shapiro-Wilk test (RCC)	Shapiro-Wilk test (UTUC)	Mann-Whitney U test
NLR	5.389±5.819	6.047±6.659	<0.001	<0.001	0.578
PLR	208.604±122.427	222.647±151.494	<0.001	<0.001	0.745
WBC count x10 ³ /μl	8.890±3.789	8.976±4.279	<0.001	<0.001	0.607
PLT count x10 ³ /μl	291.539±106.013	277.789±109.631	<0.001	<0.010	0.313
NE %	67.918±15.356	69.195±13.989	<0.050	0.212	0.693
LY %	22.019±11.718	21.204±12.003	<0.001	<0.050	0.563

Data are presented as the mean ± SD. NLR, neutrophil-to-lymphocyte ratio; PLR, platelet-to-lymphocyte ratio; WBC, white blood cell; PLT, platelet; NE, neutrophil; LY, lymphocyte; RCC, renal cell carcinoma; UTUC, upper tract urothelial carcinoma.

machines [support vector classifier (SVC), Nu-SVC and linear SVC], nearest-neighbor (k-nearest neighbors), decision trees (decision tree and extra tree), ensemble methods (random forest, extra trees, gradient boosting, AdaBoost, bagging and XGBoost), naïve Bayes (Gaussian and Bernoulli), discriminant analysis (linear and quadratic) and CalibratedClassifierCV, were used to classify RCC and UTUC based on preoperative hematological parameters. The model was constructed using a dataset comprising 115 patients with RCC and 57 patients with UTUC. To address the class imbalance between RCC and UTUC, feature standardization and the Synthetic Minority Oversampling Technique (SMOTE; sampling strategy=0.8, k_neighbors=5) were combined into a single pipeline fitted to the training data with cross-validation. These steps were fitted on the training data of each fold and were not applied to the testing data. The dataset was divided into a training set (70%) and a testing set (30%) using stratified sampling (stratified by diagnosis) with a fixed random seed (random_state=42) to preserve class proportions and ensure reproducibility. Model comparison and hyperparameter tuning were performed on the training set using grid-search with 10-fold stratified cross-validation, and the best-performing models were evaluated on the held-out test set using accuracy, balanced accuracy, precision, recall, F1 score and the area under the receiver operating characteristic curve (AUC).

Statistical analysis. Statistical analysis was conducted using Python libraries, including NumPy, SciPy, pandas and statsmodels (version 0.14.0), as aforementioned. The Shapiro-Wilk test was employed to evaluate the normality of data distribution. Data are presented as frequencies or mean ± SD, minimum and maximum values. For comparison of group means, independent Student's t-tests were applied to normally distributed data, while Mann-Whitney U tests were used for non-normally distributed data. $P < 0.05$ was considered to indicate a statistically significant difference.

Results

Demographic characteristics of the study population. A total of 172 patients with renal cancer were included in the present

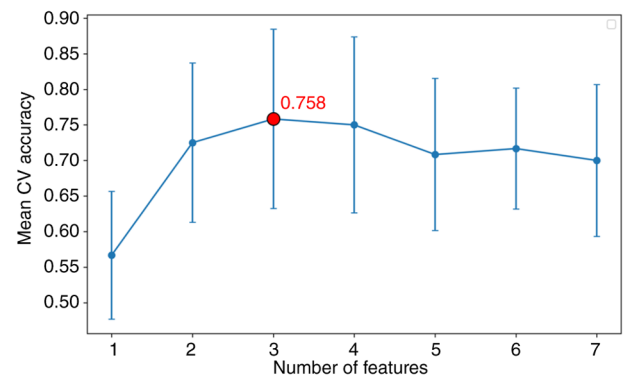


Figure 1. Recursive feature elimination with cross-validation results based on a Random Forest classifier. The x-axis shows the number of features included in the model. The y-axis shows the mean CV accuracy obtained from 10-fold stratified CV on the training set for each feature subset size. CV, cross-validation.

study. This total comprised 115 cases (66.9%) of RCC and 57 cases (33.1%) of UTUC. The study population consisted of 109 men (63.4%) and 63 women (36.6%). The mean age of all patients was 61.2 ± 12.4 years (range 20–87 years). Patients with RCC were significantly younger than patients with UTUC ($P < 0.001$). The mean age of male patients with RCC was 58.6 ± 10.8 years compared with 68.1 ± 10.0 years for male patients with UTUC. Similarly, female patients with RCC had a mean age of 56.4 ± 14.3 years, while female patients with UTUC had a mean age of 68.2 ± 9.3 years.

The mean preoperative hematological parameters for all patients were as follows: NLR of 5.61 ± 6.10 ; PLR of 213.26 ± 132.48 ; WBC count of $8,918.37$ cells/ μ l; PLT count of $286,982.56$ cells/ μ l; NE % of 68.34%; and LY % of 21.75%. Statistical analysis using the Mann-Whitney U test showed no significant differences between the RCC and UTUC groups in the hematological parameters (NLR, PLR, WBC, PLT, NE % and LY %; Table II). The feature selection process was performed using RFECV based on a Random Forest classifier. Hyperparameter tuning was performed using grid search with cross-validation. As shown in Fig. 1, three features, including age, WBC count and PLR, were determined to be the most

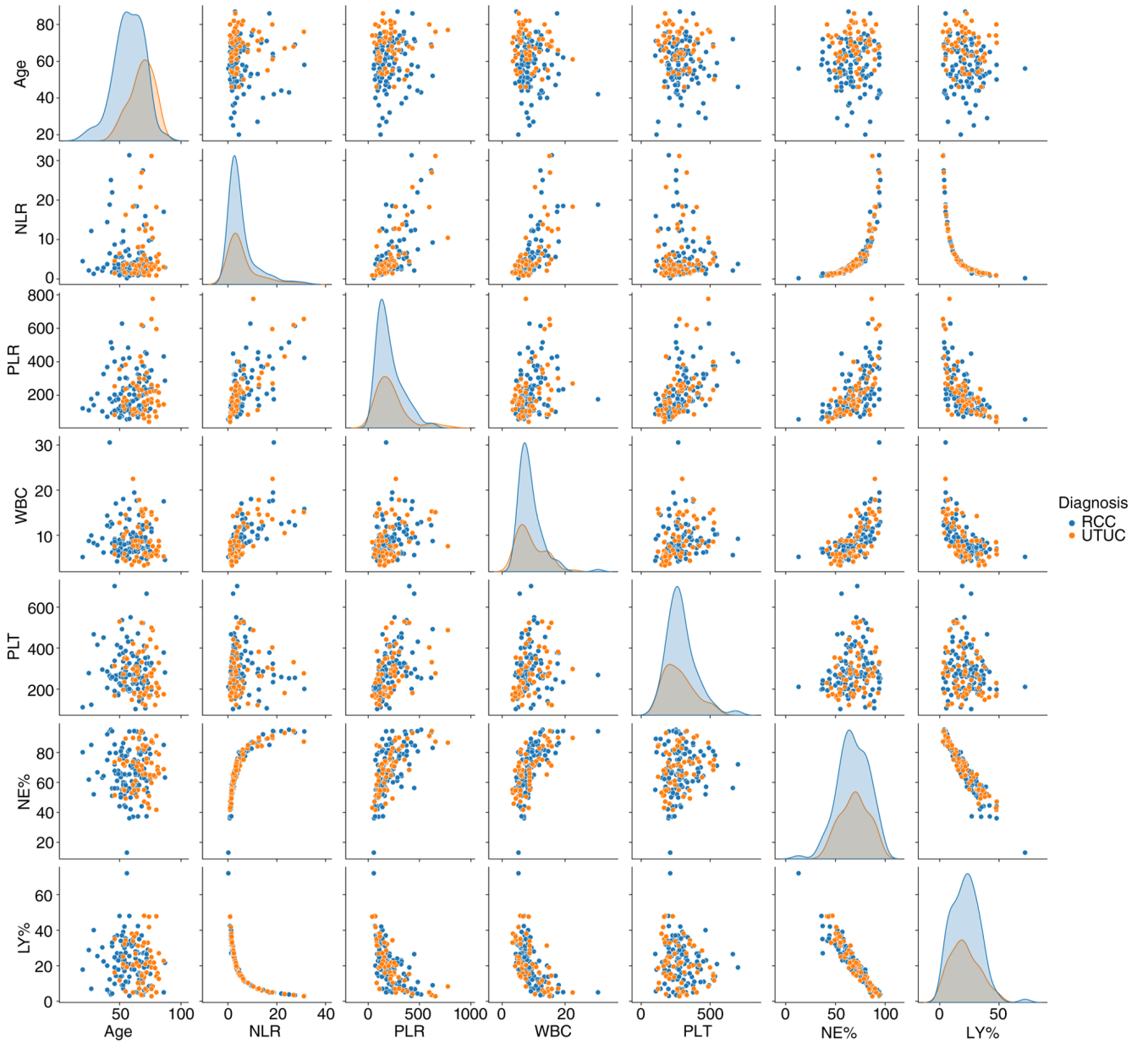


Figure 2. Pair plot of all features. The diagonal shows the distribution of individual features, while the scatter plots in the off-diagonal display show pairwise relationships between variables, color-coded by diagnosis (RCC in blue, UTUC in orange). NLR, neutrophil-to-lymphocyte ratio; PLR, platelet-to-lymphocyte ratio; WBC, white blood cell; PLT, platelet; NE, neutrophil; LY, lymphocyte; RCC, renal cell carcinoma; UTUC, upper tract urothelial carcinoma.

important features for an effective model. This optimal feature set from RFECV achieved a test-set accuracy of 73.08%, with a precision of 0.76 for RCC and 0.64 for UTUC, a recall of 0.89 for RCC and 0.41 for UTUC, and F1 scores of 0.82 for RCC and 0.50 for UTUC.

To further explore the distribution and relationships between the selected features, a pair plot of all features (age, NLR, PLR, WBC count, PLT count, NE % and LY %) categorized by diagnosis (RCC vs. UTUC) was generated (Fig. 2). Among these features, RFECV retained age, PLR and WBC count as the optimal subset for classification. Age showed the clearest separation between groups, with the density plots indicating that patients with UTUC were typically older than patients with RCC. Inflammatory markers showed only modest, non-significant differences between groups (Table II). In the density plots, patients with UTUC tended to have higher

PLR values and NE % than patients with RCC, even though a few individual patients with RCC had the highest values shown in the scatter plots, likely because the RCC group was larger. For WBC count, the distributions of the two groups largely overlapped, with comparable dispersion, although a small number of patients with RCC had the highest values. Similarly, the density curves for PLT count were similar in shape and range for both groups, indicating substantial overlap between RCC and UTUC.

Classification model for differential diagnosis of RCC and UTUC. To address the class imbalance between RCC and UTUC, SMOTE was applied to the training data within a cross-validation pipeline to prevent data leakage. A total of 23 supervised ML algorithms were screened to develop classification models to differentiate RCC from UTUC. The

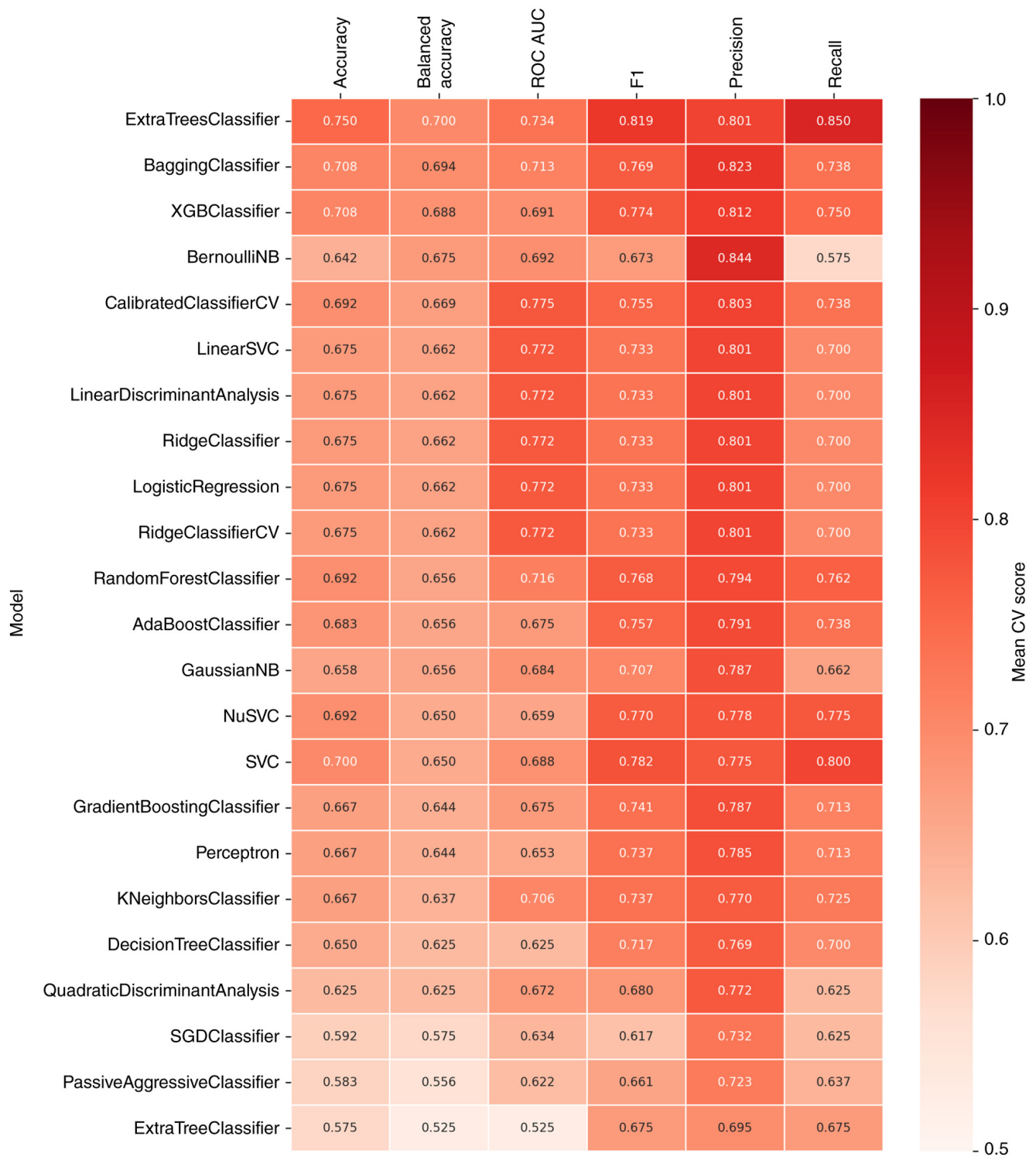


Figure 3. Performance comparison of machine learning classifiers for differentiating renal cell carcinoma from upper tract urothelial carcinoma. Each row represents a classifier and each column a performance metric, including accuracy, balanced accuracy, ROC AUC, F1 score, precision and recall. Values represent the mean scores obtained from stratified 10-fold cross-validation on the training set. Cell colors are scaled according to the mean cross-validation score. ROC AUC, receiver operating characteristic area under the curve; CV, cross-validation; SVC, support vector classifier; NB, naïve Bayes; XGB, extreme gradient boosting; SGD, stochastic gradient descent.

performance of all 23 candidate models was first screened using accuracy, balanced accuracy, precision, recall, F1 score and AUC values from 10-fold cross-validation on the training set (Fig. 3); the top six models were then tuned and evaluated on the held-out test set (Table III and Fig. 4). Among the algorithms evaluated, the Extra Trees classifier showed the

most favorable overall performance on the test set, with an accuracy of 75.0%, a balanced accuracy of 0.71 and an AUC value of 0.755. The confusion matrix for the Extra Trees model (Fig. 4A) showed that of the 35 patients with RCC in the test set, 29 were correctly classified as RCC, and of the 17 patients with UTUC, 10 were correctly classified as UTUC. Several

Table III. Performance comparison of top six supervised machine learning algorithms for differentiating between RCC and UTUC using preoperative hematological and clinical data.

Model	Accuracy, %	Balanced accuracy, %	AUC	Precision		Recall		F1 score	
				RCC	UTUC	RCC	UTUC	RCC	UTUC
ETC	75.00	70.8	0.755	0.806	0.625	0.829	0.588	0.817	0.606
BC	63.46	65.3	0.717	0.808	0.462	0.600	0.706	0.689	0.558
XGB	63.46	63.8	0.713	0.786	0.458	0.629	0.647	0.698	0.537
BNB	61.54	66.9	0.619	0.857	0.452	0.514	0.824	0.643	0.583
CCCV	65.38	68.2	0.711	0.840	0.481	0.600	0.765	0.700	0.591
LSVC	65.38	69.7	0.718	0.870	0.483	0.571	0.824	0.690	0.609

ETC, ExtraTreesClassifier; BC, BaggingClassifier; XGB, extreme gradient boosting classifier; BNB, Bernoulli naïve Bayes; CCCV, calibrated classifier cross-validation; LSVC, linear support vector classifier; RCC, renal cell carcinoma; UTUC, upper tract urothelial carcinoma; AUC, area under the receiver operating characteristic curve.

other models achieved broadly comparable discrimination, with AUC values clustered 0.71-0.72 (Fig. 4B), whereas the remaining algorithms performed less consistently. To assess the robustness of these estimates, the Extra Trees model was further evaluated using out-of-bag bootstrap resampling (1,000 iterations). The bootstrap results were consistent with the test performance, with a mean accuracy of 0.73 (95% CI, 0.64-0.82), a balanced accuracy of 0.66 (95% CI, 0.56-0.76) and an AUC value of 0.71 (95% CI, 0.59-0.83).

Discussion

The development of a non-invasive and low-cost tool for differentiating RCC from UTUC has notable clinical implications because RCC and UTUC require distinct treatment approaches. RCC is typically managed with partial or radical nephrectomy, whereas UTUC requires radical nephroureterectomy with bladder cuff excision (5,21). In unresectable or metastatic cases, UTUC may be managed with palliative chemotherapy and radiotherapy. By contrast, RCC is relatively resistant to conventional chemotherapy and radiotherapy. Systemic treatments, such as targeted therapy or immunotherapy, are therefore often considered for RCC treatment (6,7). Misdiagnosis may lead to inappropriate treatment and, consequently, poorer outcomes for these patients. However, to the best of our knowledge, no preoperative blood-based biomarker panel has been widely accepted for distinguishing RCC from UTUC in clinical practice.

Both RCC and UTUC are associated with alterations in systemic inflammatory markers with different underlying mechanisms. In RCC, an elevated NLR is considered to result from dysregulation of the hypoxia-inducible factor pathway. This dysregulation leads to increased production of pro-inflammatory cytokines, such as IL-6, IL-8, TNF- α and granulocyte-macrophage colony-stimulating factor, that promote neutrophilia and may suppress lymphocyte counts and function (22). An elevated NLR has been associated with advanced tumor stages, higher nuclear grades and poorer survival outcomes in patients with RCC (23-25). Similarly, an elevated PLR has emerged as an important prognostic factor in

RCC. Multiple studies have consistently shown that higher PLR is associated with decreased overall survival, cancer-specific survival and progression-free survival (26,27). In UTUC, alterations in NLR, PLR and WBC count are influenced by tumor-associated inflammation, changes in the immune micro-environment (T-cell-depleted tumor immune contexture and altered programmed death-ligand 1 expression) and genomic alterations (fibroblast growth factor receptor 3 mutations, TP53 mutations and DNA mismatch repair deficiency/microsatellite instability) (28,29). The distinct mechanisms underlying alterations in hematological parameters in RCC and UTUC suggest that these markers may be useful for differentiating between the two tumor types.

However, the present study revealed no statistically significant differences in individual hematological parameters between patients with RCC and UTUC. This finding suggests that single hematological parameters alone may be insufficient to differentiate RCC from UTUC. More advanced analytical approaches, such as ML, may therefore be required to identify the complex, multivariable patterns across these markers that could improve diagnostic accuracy.

The integration of routine preoperative hematological markers with ML algorithms for cancer diagnosis and prognosis has been reported in several types of cancer, such as oral squamous cell carcinoma (30), colorectal cancer (31) and cervical cancer (32). However, to the best of our knowledge, no previous study has used preoperative hematological markers together with ML to distinguish RCC from UTUC. In the present study, ML models based on preoperative hematological markers and clinical data were used to differentiate between RCC and UTUC. After feature selection, age and the hematological markers PLR and WBC count were retained as the most informative predictors. The Extra Trees model demonstrated the best overall performance, with an accuracy of 75.0% and an AUC value of 0.755. This level of performance does not exceed that of established imaging techniques. Contrast-enhanced CT has been reported to achieve a sensitivity of 85-95% and a specificity of 75-85% for RCC detection (33,34), while offering 80-90% sensitivity and 70-80% specificity for UTUC. Rather than replacing

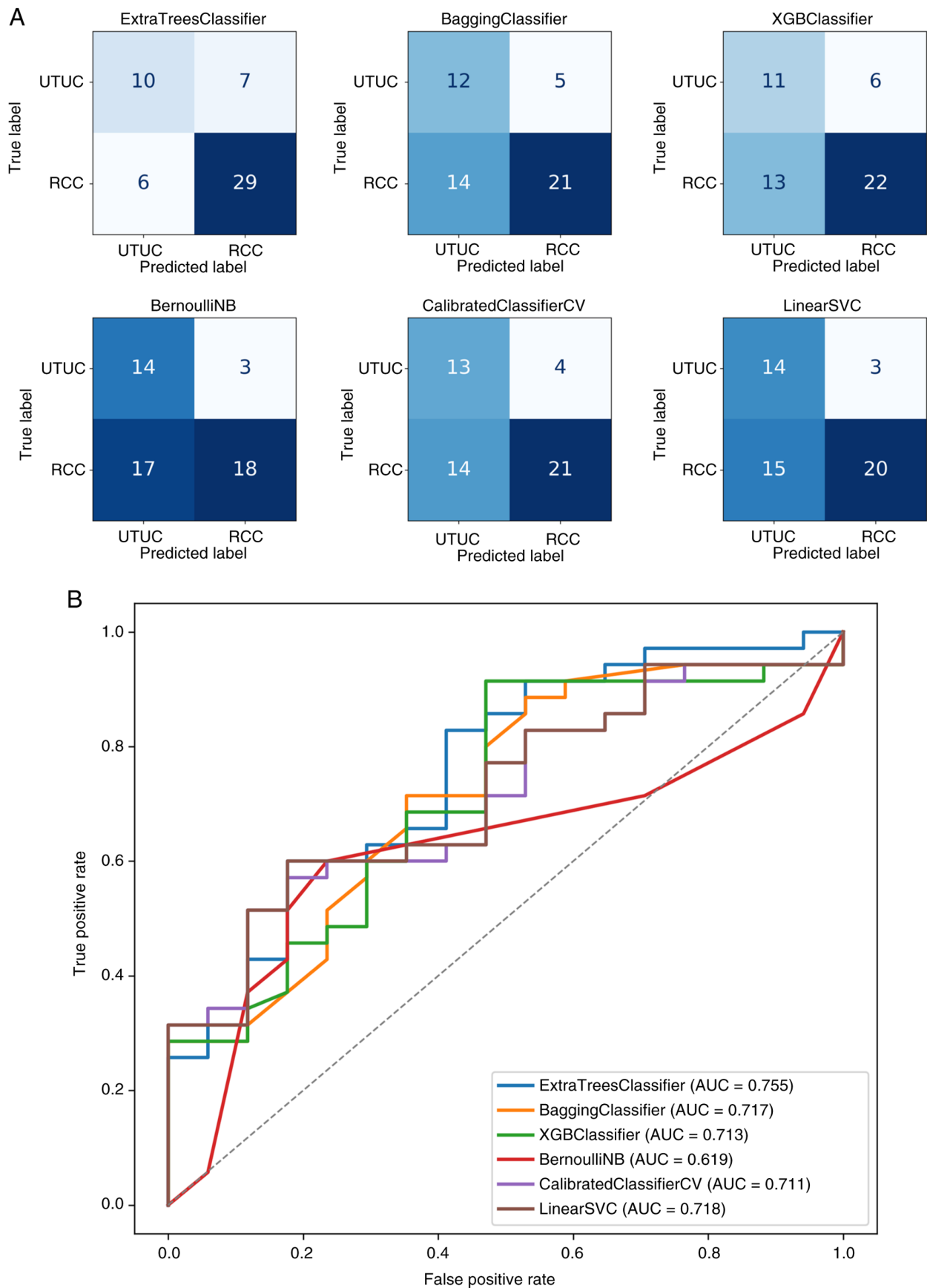


Figure 4. Performance of six supervised machine learning models for the differential diagnosis of RCC and UTUC. (A) Confusion matrices for the top six supervised ML algorithms, including ExtraTreesClassifier, BaggingClassifier, XGBClassifier, BernoulliNB, CalibratedClassifierCV and LinearSVC. Rows represent the actual diagnosis, and columns represent the predicted diagnosis. (B) ROC curves and AUC scores of six ML algorithms for the differential diagnosis of RCC and UTUC based on clinical and preoperative hematological data. ROC, receiver operating characteristic; AUC, area under the ROC curve; ML, machine learning; RCC, renal cell carcinoma; UTUC, upper tract urothelial carcinoma; CV, cross-validation; SVC, support vector classifier; NB, naïve Bayes; XGB, extreme gradient boosting.

gold-standard diagnostic methods, a ML model based on routinely available blood parameters may serve as a simple, non-invasive and low-cost tool. A ML model could provide additional information to support preoperative assessment and complement conventional diagnostic workflows.

Certain limitations should be acknowledged. The present study was retrospective and conducted at a single center with a relatively small sample size. The findings require external validation on larger, multicenter datasets to confirm the model's robustness. Moreover, the models were trained on a class-imbalanced dataset in which UTUC cases were underrepresented. In addition, a further limitation concerns SMOTE. In the training set of 120 patients (80 patients with RCC, 40 patients with UTUC), a sampling strategy of 0.80 generated 24 synthetic UTUC samples. Because SMOTE interpolates between neighboring minority cases, the resulting values may not preserve the interdependence of hematological variables. This may not fully reflect real biological relationships among variables and may affect model generalizability. For these reasons, the present work should be regarded as a proof-of-concept study rather than a clinically applicable diagnostic classifier. Further evaluation using data from multicenter studies will be needed to assess clinical utility before implementation. In addition, combining these blood-based markers with imaging or other clinical features may further improve model performance in future work.

In the present proof-of-concept study, ML models based on preoperative hematological markers and clinical data were developed to differentiate RCC from UTUC. Among the algorithms evaluated, the Extra Trees model showed the most favorable performance with an accuracy of 75.0%, a balanced accuracy of 0.71 and an AUC value of 0.755. These preliminary findings suggest that ML approaches using readily available blood parameters may serve as supportive information to complement conventional imaging and histopathological evaluation in differentiating RCC from UTUC. However, multicenter studies with larger and more balanced cohorts, together with external validation, are needed before the clinical applicability of the proposed ML models can be established.

Acknowledgements

Not applicable.

Funding

The present study was supported by a grant from the Fundamental Fund of Khon Kaen University, under the National Science, Research and Innovation Fund, Thailand (grant no. 161843).

Availability of data and materials

The data generated in the present study may be requested from the corresponding author.

Authors' contributions

KN participated in conceptualization, data curation, reviewing and editing the manuscript and study supervision.

CP was involved in acquisition of data and data curation. KS was involved in methodology, data curation, data analysis, interpretation of data and writing the original draft. SS participated in conceptualization, methodology, writing the original draft, study supervision and funding acquisition. WS was involved in conceptualization, methodology, data curation, data analysis, interpretation of data, writing the original draft, reviewing and editing the manuscript and study supervision. KN and KS confirm the authenticity of all the raw data. All authors read and approved the final manuscript.

Ethics approval and consent to participate

The present study was approved by the Ethics Committee for Human Research of Khon Kaen University (approval no. HE671739). The requirement for informed consent was waived by the Ethics Committee due to the retrospective nature of the study.

Patient consent for publication

Not applicable.

Competing interests

The authors declare that they have no competing interests.

Use of artificial intelligence tools

During the preparation of this work, artificial intelligence tools (ChatGPT; OpenAI) were used to improve the readability and language of the manuscript, and subsequently, the authors revised and edited the content produced by the artificial intelligence tools as necessary, taking full responsibility for the ultimate content of the present manuscript.

References

1. Siegel RL, Miller KD, Wagle NS and Jemal A: Cancer statistics, 2023. *CA Cancer J Clin* 73: 17-48, 2023.
2. Qi N, Chen Y, Gong K and Li H: Concurrent renal cell carcinoma and urothelial carcinoma: Long-term follow-up study of 27 cases. *World J Surg Oncol* 16: 16, 2018.
3. Upfill-Brown A, Lenis AT, Faiena I, Salmasi AH, Johnson DC, Pooli A, Drakaki A, Gollapudi K, Blumberg J, Pantuck AJ and Chamie K: Treatment utilization and overall survival in patients receiving radical nephroureterectomy versus endoscopic management for upper tract urothelial carcinoma: Evaluation of updated treatment guidelines. *World J Urol* 37: 1157-1164, 2019.
4. Roupêt M, Babjuk M, Burger M, Capoun O, Cohen D, Compérat EM, Cowan NC, Dominguez-Escrig JL, Gontero P, Hugh Mostafid A, *et al*: European association of urology guidelines on upper urinary tract urothelial carcinoma: 2020 update. *Eur Urol* 79: 62-79, 2021.
5. Doehn C, Grunwald V, Steiner T, Follmann M, Rexer H and Krege S: The diagnosis, treatment, and follow-up of renal cell carcinoma. *Dtsch Arztebl Int* 113: 590-596, 2016.
6. Bex A, Ghanem YA, Albiges L, Bonn S, Campi R, Capitanio U, Dabestani S, Hora M, Klatte T, Kuusk T, *et al*: European association of urology guidelines on renal cell carcinoma: The 2025 update. *Eur Urol* 87: 683-696, 2025.
7. Masson-Lecomte A, Birtle A, Pradere B, Capoun O, Compérat E, Domínguez-Escrig JL, Liedberg F, Makaroff L, Mariappan P, Moschini M, *et al*: European association of urology guidelines on upper urinary tract urothelial carcinoma: Summary of the 2025 update. *Eur Urol* 87: 697-716, 2025.

8. Nguyen MLT, Pham C, Le QV, Nham PLT, Tran DH, Le TS, Hoang VT, Can VM, Nguyen LT and Bui KC: The diagnostic and prognostic value of neutrophil-to-lymphocyte ratio and platelet-to-lymphocyte ratio on gastric cancer patients. *Medicine (Baltimore)* 102: e34357, 2023.
9. Yang DL, Wang HY, Aisimutula D, Zhao J, Zhu QM, Li J, Li HF and Gao XL: Diagnostic role of the neutrophil-to-lymphocyte ratio and the platelet-to-lymphocyte ratio in breast cancer: A systematic review and meta-analysis. *Oncol Lett* 29: 41, 2024.
10. Huszno J, Kolosza Z, Mrochem-Kwarciak J, Telka E, Jochymek B and Miszczuk L: Role of neutrophil-lymphocyte ratio, platelet-lymphocyte ratio, lymphocyte-monocyte ratio and platelets in prognosis of patients with prostate cancer. *Oncol Lett* 24: 305, 2022.
11. Gao Y, Wang WJ, Zhi Q, Shen M, Jiang M, Bian X, Gong FR, Zhou C, Lian L, Wu MY, *et al*: Neutrophil/lymphocyte ratio is a more sensitive systemic inflammatory response biomarker than platelet/lymphocyte ratio in the prognosis evaluation of unresectable pancreatic cancer. *Oncotarget* 8: 88835-88844, 2017.
12. Jia W, Yuan L, Ni H, Xu B and Zhao P: Prognostic value of platelet-to-lymphocyte ratio, neutrophil-to-lymphocyte ratio, and lymphocyte-to-white blood cell ratio in colorectal cancer patients who received neoadjuvant chemotherapy. *Technol Cancer Res Treat* 20: 15330338211034291, 2021.
13. Kourou K, Exarchos KP, Papaloukas C, Sakaloglou P, Exarchos T and Fotiadis DI: Applied machine learning in cancer research: A systematic review for patient diagnosis, classification and prognosis. *Comput Struct Biotechnol J* 19: 5546-5555, 2021.
14. Zhu SL, Dong J, Zhang C, Huang YB and Pan W: Application of machine learning in the diagnosis of gastric cancer based on noninvasive characteristics. *PLoS One* 15: e0244869, 2020.
15. Zhou L, Hong H, Chu F, Chen X and Wang C: Predicting the recurrence of ovarian cancer based on machine learning. *Cancer Manag Res* 16: 1375-1387, 2024.
16. Li X, Zhou Z, Zhang X, Cheng X, Xing C and Wu Y: Predicting 3-year all-cause mortality in rectal cancer patients based on body composition and machine learning. *Front Nutr* 12: 1473952, 2025.
17. Seubwai W, Sangkhamanon S and Zhang X: Identification of IGFBP3 and LGALS1 as potential secreted biomarkers for clear cell renal cell carcinoma based on bioinformatics analysis and machine learning. *Adv Clin Exp Med* 34: 1649-1659, 2025.
18. Panwoon C, Seubwai W, Thanee M and Sangkhamanon S: Identification of novel biomarkers to distinguish clear cell and non-clear cell renal cell carcinoma using bioinformatics and machine learning. *PLoS One* 19: e0305252, 2024.
19. Panwoon C, Seubwai W, Thanee M and Sangkhamanon S: FABP7: A potential diagnostic and prognostic biomarker for clear cell renal cell carcinoma. *In Vivo* 38: 2912-2920, 2024.
20. World Medical Association: World medical association declaration of Helsinki: Ethical principles for medical research involving human participants. *JAMA* 333: 71-74, 2025.
21. Leow JJ, Liu Z, Tan TW, Lee YM, Yeo EK and Chong YL: Optimal management of upper tract urothelial carcinoma: Current perspectives. *Onco Targets Ther* 13: 1-15, 2020.
22. Thompson AAR, Binham J, Plant T, Whyte MKB and Walmsley SR: Hypoxia, the HIF pathway and neutrophilic inflammatory responses. *Biol Chem* 394: 471-477, 2013.
23. Widz D, Mitura P, Buraczynski P, Plaza P, Bar M, Cabanek M, Nowak G, Ostrowska A and Bar K: Preoperative neutrophil-lymphocyte ratio as a predictor of overall survival in patients with localized renal cell carcinoma. *Urol J* 17: 30-35, 2020.
24. Hu K, Lou L, Ye J and Zhang S: Prognostic role of the neutrophil-lymphocyte ratio in renal cell carcinoma: A meta-analysis. *BMJ Open* 5: e006404, 2015.
25. Pedersen MM, Donskov F, Pedersen L, Zhang ZF and Norgaard M: Elevated neutrophil-lymphocyte ratio combined with hyponatremia indicate poor prognosis in renal cell carcinoma. *Acta Oncol* 59: 13-19, 2020.
26. Zhou X and Luo G: A meta-analysis of the platelet-lymphocyte ratio: A notable prognostic factor in renal cell carcinoma. *Int J Biol Markers* 37: 123-133, 2022.
27. Wang X, Su S and Guo Y: The clinical use of the platelet to lymphocyte ratio and lymphocyte to monocyte ratio as prognostic factors in renal cell carcinoma: A systematic review and meta-analysis. *Oncotarget* 8: 84506-84514, 2017.
28. Inman B and Tay KJ: Inflammation: A significant contributor to upper-tract urothelial carcinoma prognosis? *Eur Urol Focus* 1: 64-65, 2015.
29. Evmorfopoulos K, Mitrakas L, Karathanasis A, Zachos I, Tzortzis V and Vlachostergios PJ: Upper tract urothelial carcinoma: A rare malignancy with distinct immuno-genomic features in the era of precision-based therapies. *Biomedicines* 11: 1775, 2023.
30. Wu X, Yao Y, Dai Y, Diao P, Zhang Y, Zhang P, Li S, Jiang H and Cheng J: Identification of diagnostic and prognostic signatures derived from preoperative blood parameters for oral squamous cell carcinoma. *Ann Transl Med* 9: 1220, 2021.
31. Xu R, Chi H, Zhang Q, Li X and Hong Z: Enhancing the diagnostic accuracy of colorectal cancer through the integration of serum tumor markers and hematological indicators with machine learning algorithms. *Clin Transl Oncol* 27: 299-308, 2025.
32. Zhao H, Wang Y, Sun Y, Wang Y, Shi B, Liu J and Zhang S: Hematological indicator-based machine learning models for preoperative prediction of lymph node metastasis in cervical cancer. *Front Oncol* 14: 1400109, 2024.
33. Shen J and Zou Y: Diagnostic value of contrast-enhanced CT in clear cell renal cell carcinoma: A systematic review and meta-analysis. *BMC Urol* 24: 189, 2024.
34. Akram F, Mazhar A, Javed H, Fayyaz M, Khan A and Ahmad K: Diagnostic accuracy of contrast enhanced Ct for detection of renal cell carcinoma taking histopathology as gold standard. *J Ayub Med Coll Abbottabad* 35: 84-87, 2023.



Copyright © 2026 Nuwatkrisin et al. This work is licensed under a Creative Commons Attribution-NonCommercial-NoDerivatives 4.0 International (CC BY-NC-ND 4.0) License.