

Artificial Intelligence Risk Prediction Model for PICC Catheter-related Venous Thrombosis in Cancer Patients: A Systematic Review

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Abstract: *Background:* Despite the growing number of models predicting the risk of cancer-associated PICC catheter-related venous thrombosis, comprehensive evaluations of artificial intelligence (AI) and machine learning (ML) prediction models remain scarce. *Objective:* This systematic review aims to evaluate the methodological quality, predictive performance, and clinical applicability of ML models for PICC-related thrombosis in patients with cancer, with a specific focus on risk of bias and adherence to reporting guidelines. *Methods:* A systematic search was performed across PubMed, Embase, Scopus, Web of Science, the Cochrane Library, and CINAHL. The study protocol was registered with PROSPERO prior to data collection, and the review adhered to the Preferred Reporting Items for Systematic Reviews and Meta-Analyses (PRISMA) guidelines. The search sought to identify all relevant studies published from database inception to December 30, 2025. Literature screening and data extraction were performed independently by two investigators. Finally, model quality was evaluated using the PROBAST+AI framework, integrating reported model performance metrics. *Results:* A total of seven studies were included, wherein all developed models demonstrated an Area Under the Curve (AUC) exceeding 0.7. The six most frequently utilized machine learning algorithms were Random Forest (RF; 28.57%), Least Absolute Shrinkage and Selection Operator (Lasso; 17.86%), Boosting (10.71%), Support Vector Machine (SVM; 7.14%), Logistic Regression (LR; 7.14%), and Artificial Neural Network (ANN; 7.14%). Overall, the included studies exhibited a high risk of bias, although clinical applicability was deemed acceptable. *Conclusions:* Current evidence indicates that machine learning models are effective in predicting PICC-related thromboembolism in patients with cancer. However, the majority of current models are limited by suboptimal methodological quality, a lack of external validation, and restricted generalizability. Future research should prioritize external validation and focus on developing clinical decision support tools to facilitate seamless integration into clinical practice.

Keywords: Peripherally inserted central catheter-related venous thrombosis; Neoplasms; Risk prediction; Machine learning; Systematic review

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1. Introduction

Peripherally inserted central catheters (PICCs) are extensively utilized in patients with cancer to facilitate chemotherapy, significantly mitigating peripheral vascular injury and toxicity associated with vesicant or irritant agents. However, concomitant with their increasing widespread use, associated complications—particularly catheter-related thrombosis (CRT)—have garnered significant attention. Current evidence indicates that the incidence of PICC-related venous thrombosis (PICC-RVT) ranges from 1.4% to 51.4%^[1-3]. PICC-RVT is not only associated with an increased risk of pulmonary embolism but is also closely linked to catheter dysfunction, delays in chemotherapy, and prolonged hospitalization^[4]. Encouragingly, PICC-RVT can be effectively managed through early prevention strategies and precise risk stratification. The *Infusion Therapy Standards of Practice* published by the Infusion Nurses Society (INS) explicitly state that risk assessment is effective in preventing PICC-RVT^[5]. However, the efficacy of such preventive measures relies heavily on the availability of high-precision assessment tools. Currently, established assessment tools applied to patients with cancer include the Michigan Risk Score (MRS) by Chopra et al.^[6], the Seeley prediction model^[7], the Autar scale^[8], and the Caprini risk assessment model^[9]. Nevertheless, these models often fail to adequately account for the specific characteristics of the oncological population, thereby limiting their clinical applicability.

In recent years, the increasing accessibility of advanced software and high-performance computing resources has catalyzed the development of artificial intelligence (AI) and machine learning (ML) prediction models in healthcare. Leveraging advantages in data processing and pattern recognition, ML techniques have been demonstrated in numerous studies to outperform traditional statistical methods^[10,11]. Concurrently, with intensified research efforts in the field of PICC-related thrombosis, a growing number of AI-based risk prediction models for cancer-associated PICC-RVT have emerged. However, existing studies exhibit significant heterogeneity regarding the ML algorithms employed, the target oncological populations, and the predictor variables included. Furthermore, a comprehensive systematic evaluation of model quality and clinical applicability remains lacking.

The Prediction model Risk of Bias Assessment Tool (PROBAST) provides a framework to enhance the methodological quality and transparency of prediction models^[12]. Given the ubiquitous adoption of artificial intelligence (AI), this framework has evolved into the PROBAST+AI extension. This adaptation is specifically tailored to address the unique challenges posed by machine learning models, including ensuring transparency in model development, evaluation, and generalizability.

Consequently, we conducted a systematic review to evaluate the performance of AI-based models developed for predicting PICC-RVT. This study aims to synthesize current evidence regarding their predictive performance, thereby providing an evidence-based reference for clinical model selection and the implementation of precision nursing care for patients with cancer.

2. Methods

2.1. Design

The study protocol was registered with the International Prospective Register of Systematic Reviews (PROSPERO) prior to data analysis (Registration No. CRD420251246431). This systematic review was conducted in accordance with the Preferred Reporting Items for Systematic Reviews and Meta-Analyses (PRISMA) 2020 statement^[13]. Ethical approval was not required, as this study relied exclusively on

secondary data from published literature and did not involve direct intervention with human or animal subjects.

The research question was formulated using the PIPOST framework recommended by the Joanna Briggs Institute (JBI). The specific components were defined as follows: Population (P) comprised patients with cancer undergoing PICC catheterization; Intervention (I) involved the development and validation of machine learning (ML)-based risk prediction models for PICC-RVT; Professionals (P) referred to clinical healthcare providers; Outcomes (O) focused on model performance metrics (e.g., sensitivity, specificity); Setting (S) included inpatient healthcare settings; and Type of Evidence (T) encompassed primary studies, including cohort, case-control, and cross-sectional studies^[14]. Due to the significant heterogeneity observed in model development algorithms and analytical approaches across the included studies, a quantitative meta-analysis was not performed; instead, a narrative synthesis was conducted.

2.2. Search strategies

Databases including PubMed, Embase, Scopus, Web of Science, the Cochrane Library, and CINAHL were searched. Briefly, the search strategy employed a combination of keywords and controlled vocabulary (e.g., MeSH) related to “Cancer” OR “Malignancy” AND “PICC” AND “Deep Vein Thrombosis” AND “Artificial Intelligence” OR “Machine Learning”. The literature search was executed on December 30, 2025, covering the period from database inception to the search date. The electronic search strategy was developed and verified by the first author. Subsequently, two independent investigators performed the search across the six aforementioned databases. Reference lists of relevant publications and reviews were hand-searched to identify additional eligible studies. Corresponding authors were contacted via email to request missing data where necessary.

2.3. Inclusion and exclusion criteria

The inclusion criteria were as follows:

- (1) studies focusing on the prediction of PICC-related venous thrombosis (PICC-RVT) in patients with cancer;
- (2) study designs including cohort, case-control, or cross-sectional studies;
- (3) risk prediction models developed using machine learning (ML) algorithms;
- (4) studies published in the English language.

The exclusion criteria were:

- (1) studies involving pediatric populations or animal models;
- (2) studies primarily investigating risk factors for venous thromboembolism (VTE) rather than developing prediction models;
- (3) reviews, letters, editorials, or conference abstracts;
- (4) models derived from systematic reviews or meta-analyses;
- (5) studies solely comparing existing models;
- (6) studies for which full text remained unavailable despite contacting the authors.

2.4. Study selection

Literature screening and data extraction were performed independently by two investigators (Rui Wang, LanYing Qiu). Initially, retrieved records were imported into reference management software (EndNote

X9), and duplicates were removed. Subsequently, titles and abstracts were screened to exclude irrelevant articles, followed by a full-text review to determine final eligibility based on the inclusion and exclusion criteria. Reference lists of the included studies were also scrutinized to identify any potential relevant studies. Any discrepancies were resolved through discussion and consensus involving three investigators (Xi Yang, QingLan Fu, XiaoWei Fu). A standardized data extraction form was developed in accordance with the Critical Appraisal and Data Extraction for Systematic Reviews of Prediction Modelling Studies (CHARMS) checklist ^[15]. The extracted data items included: first author, publication year, country, study design, study population, sample size, ML algorithms utilized, model validation methods, key predictors, and performance metrics (**Table 1** and **Table 2**).

Table 1. Characteristic of the included studies

Author, year	Design	Country	Participants	Database	Sample Size	RVT cases, n (%)	Measuring tools
Feifei Zhang 2024	Retrospective cohort study	China	cancer patients	Ningbo No.2 Hospital	266	3.00%	vascular Doppler ultrasound
Guiyuan Ma 2024	Prospective cohort study	China	cancer patients	Xiangya Hospital of Central South University: Qinghai University Affiliated Hospital and Hainan Provincial People's Hospital	831	4.68%	vascular Doppler ultrasound
Hankui Hu 2024	Prospective cohort study	China	cancer patients	West China Hospital of Sichuan University	452	16.10%	vascular Doppler ultrasound
Jianqin Fu 2022	Prospective cohort study	China	breast cancer patients	Fujian Medical University Union Hospital	1844	13.90%	vascular Doppler ultrasound
Shanshan Liu 2019	Prospective cohort study	China	cancer patients	the Department of Oncology of West China Hospital	348	16.30%	vascular Doppler ultrasound
Tao An 2025	Retrospective cohort study	China	breast cancer patients	National Cancer-National Clinical Research Center for the Cancer Hospital, Chinese Academy of Medical Sciences	1137	9.05%	vascular Doppler ultrasound/ color imaging
Yue Li 2025	Retrospective multi-center cohort study	China	cancer patients	27 hospitals in China	3453	15.20%	vascular Doppler ultrasound

Table 2. Information on the included prediction models

Author, year	Model development	Missing data	Continuous variable processing method	Feature selection	Validation method	Calibration method	Model performance	Features included
Feifei Zhang 2024	LASSO, SVM, GBM, RF	—	Normalization Continuous variable	multivariate LASSO logistic regression	Random split validation	—	B: 0.790	BMI, diabetic status and age

Author, year	Model development	Missing data	Continuous variable processing method	Feature selection	Validation method	Calibration method	Model performance	Features included
Guiyuan Ma 2024	LR, RF, SVM	Complete Case Analysis	Categorization	LASSO	Random split validation	H-L test	A: 0.868 B: 0.806 C: 0.708	Age, catheterisation method, catheter valve, catheter material, infection, insertion history, D-dimer concentration, operation history anaemia, diabetes and targeted drugs
Hankui Hu 2024	ML-seeley-LASSO, ML-LASSO	—	Mixed Processing	LASSO	—	—	B: 0.856	BMI, smoking, family history of DVT, NRS2002
Jianqin Fu 2022	ANN	—	Normalization Continuous variable	Stepwise logistic regression	Bootstrap	—	B: 0.742	Age, Laterality, Education status, comorbidities, CVC history, Chemotherapy status, insertion attempts, upper extremity activity
Shanshan Liu 2019	RF, Lasso-RF, Seeley-RF, Seeley-LASSO-RF	—	Normalization	LASSO	cross-validation	Kaplan-Meier curves	A: 0.935 B: 0.809	Drinking, NRS2002, Family History of DVT, Diabetes, Tip Location, Chemotherapy Cycle, Radiotherapy, Anticoagulation
Tao An 2025	RFEntr, RFGini, CatBoost, XGBoost, NeuralNet FastAI, ExtraTrees Entr, LR, Weighted Ensemble, Bayesian	Complete Case Analysis	Categorization	The Weighted Ensemble feature importance scores from Auto Gluon	Internal verification: Random split validation External verification: Independent queue	Kaplan-Meier curves	A: 0.888 B: 0.688	Hemoglobin, APTT, total cholesterol, catheterization approach

Author, year	Model development	Missing data	Continuous variable processing method	Feature selection	Validation method	Calibration method	Model performance	Features included
Yue Li 2025	network-based algorithms, RSF, MP-LogitR, MP-AdaBoost, ThresReg	Complete Case Analysis	Feature Scaling	Shap	five-fold cross-validation, Random split validation	Brier	A: 0.950 B: 0.950	Albumin, Pre-filled tube sealing fluid, APTT, Main diagnosis of admission, Targeted drugs, PICC catheter opening, Platinum drugs, Tube placement method

A, development model; B, internal validation of model; C, external validation of model; SVM, Support Vector Machine; GBM, Gradient Boosting Machine; LR, Logistic Regression; RF, Random Forest; ANN, Artificial Neural Network; RSF, Random Survival Forest; H-L test, HosmerLemeshow

2.5. Data extraction and quality assessment

The risk of bias and clinical applicability of the included studies were assessed independently by two investigators using the PROBAST+AI tool ^[12]. Each domain was graded as “low risk,” “high risk,” or “unclear.” An overall judgment of “low risk” was made only if all domains were rated as low risk. Conversely, if at least one domain was adjudicated as “high risk,” the overall assessment was classified as “high risk.” Finally, if one or more domains were rated as “unclear” in the absence of any “high risk” domains, the overall assessment was deemed “unclear.”

The risk of bias was assessed across four domains—participants, predictors, outcome, and analysis—comprising a total of 20 signaling questions. Each signaling question was answered as “Yes,” “Probably Yes,” “Probably No,” “No,” or “No Information.” Specifically, “Yes” and “Probably Yes” indicate a low risk of bias, whereas “No” and “Probably No” imply a high risk. “No Information” was selected when the original study failed to report sufficient data. Regarding domain-level judgment, a domain was deemed “low risk” only if all signaling questions were answered as “Yes” or “Probably Yes.” Conversely, if any signaling question was answered as “No” or “Probably No,” the domain was categorized as “high risk.” A domain was labeled as “unclear risk” if one or more questions were answered as “No Information” in the absence of any “No” or “Probably No” responses. Two investigators (LanYing Qiu, QingLan Fu) independently conducted the assessment and data extraction. Any discrepancies were resolved through consensus involving a third investigator (Rui Wang).

3. Results

3.1. Study selection

The initial database search yielded a total of 1,299 records. After removing 495 duplicates, the remaining records were screened by title and abstract. Subsequently, 38 full-text articles were assessed for eligibility. Ultimately, seven studies met the inclusion criteria and were included in this systematic review ^[16-22]. The detailed study selection process is illustrated in **Figure 1**.

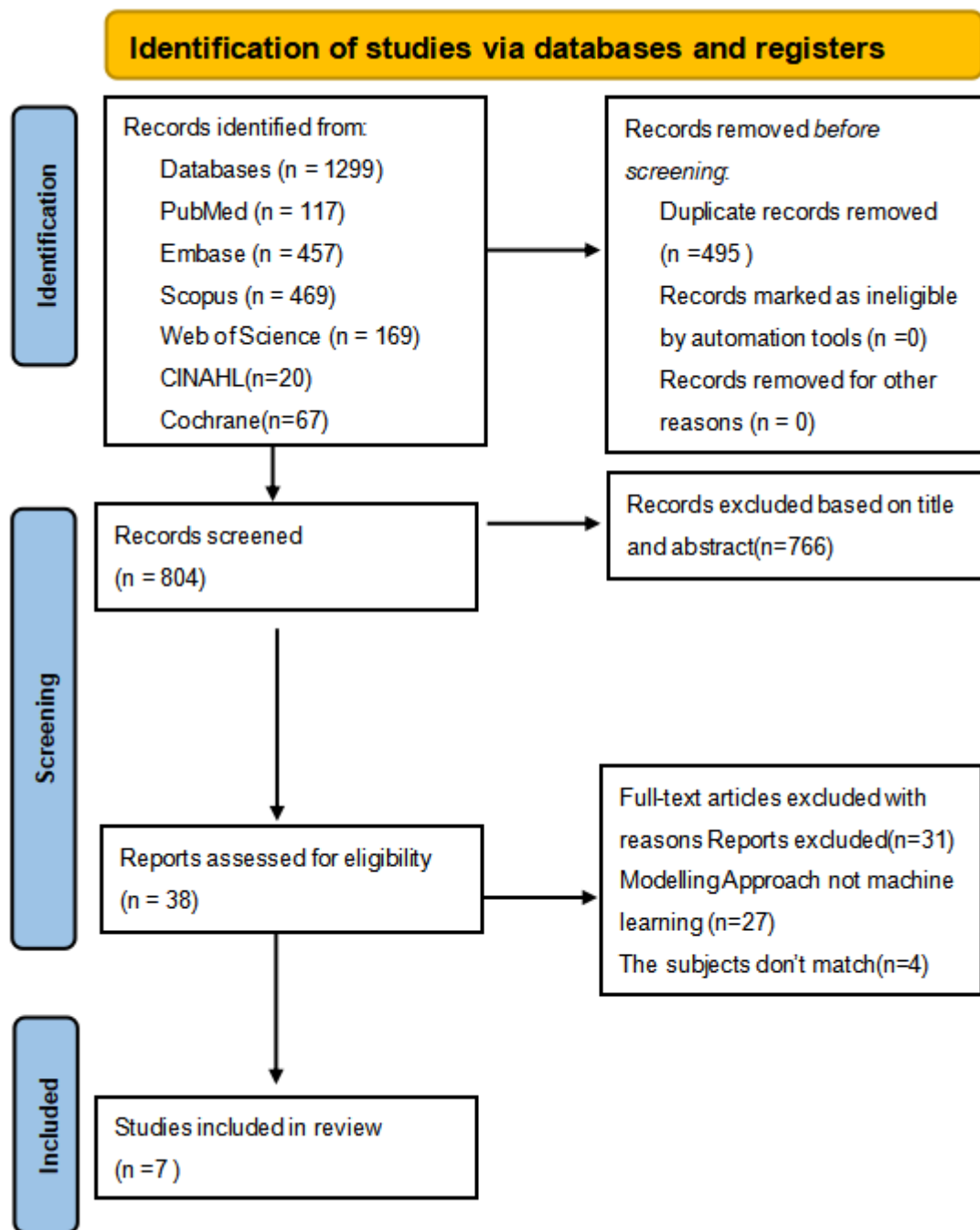


Figure 1. PRISMA diagram.

3.2. Study characteristics

Table 1 summarizes the study designs and participant characteristics of the included studies. The systematic review comprised five single-center studies ^[16-19, 21], and two multicenter studies ^[20, 22]. Geographically, all seven studies originated from China. In terms of study design, three were retrospective ^[16, 21, 22], while four were prospective ^[17-20]. Sample sizes ranged from 266 to 3,453 participants. Studies utilizing machine learning approaches to predict cancer-associated PICC-RVT have emerged since 2019. Regarding outcome

assessment, the majority of studies employed vascular Doppler ultrasound to confirm thrombosis. Notably, one study broadened its inclusion criteria to encompass all venous access devices, involving Central Venous Catheters (CVCs) and Implantable Venous Access Ports (IVAPs) in addition to PICCs^[20]. Another study assessed outcomes extending beyond PICC-RVT to include other PICC-related complications^[21].

Table 2 summarizes the characteristics of the prediction models within the included studies. Generally, the studies employed multiple machine learning algorithms to develop risk prediction models, aiming to identify the optimal model for subsequent validation. The six most frequently utilized algorithms were Random Forest (RF; 28.57%), Lasso (17.86%), Boosting (10.71%), Support Vector Machine (SVM; 7.14%), Logistic Regression (LR; 7.14%), and Artificial Neural Network (ANN; 7.14%).

The primary predictor variables integrated into the final machine learning models encompassed participant demographics, comorbidities, catheter- and treatment-related factors, laboratory indices, and medication usage. Age emerged as the most frequently identified demographic characteristic, followed by Body Mass Index (BMI). Regarding comorbidities, diabetes mellitus was the most prevalent predictor, followed by a family history of Deep Vein Thrombosis (DVT). A detailed overview of these predictor variables is presented in **Table 2**.

3.3. Models' validation

All included studies implemented internal validation procedures^[16,19,20], while three studies additionally performed independent external validation. The reported Area Under the Curve (AUC) or C-statistics ranged from 0.688 to 0.984. Regarding calibration, reporting was limited; only a single study^[20] assessed goodness-of-fit using the Hosmer-Lemeshow (H-L) test.

3.4. Bias risk and suitability assessment

3.4.1. Bias risk

The results of the risk of bias assessment are summarized in **Figure 2**. All included studies were adjudicated as having a high risk of bias, primarily stemming from deficiencies within the “Analysis” and “Participants” domains. Specifically, two studies^[20,21] exhibited a high risk in the participants domain; this was attributed to sampling strategies that distorted the original distribution of predictors within the target population, and inappropriate exclusion criteria that compromised dataset representativeness. Regarding the “Analysis” domain, all studies were rated as high risk. This was predominantly driven by insufficient sample sizes leading to potential overfitting, the dichotomization of continuous predictors, and the application of the Synthetic Minority Over-sampling Technique (SMOTE) to address class imbalance without subsequent model recalibration. Conversely, the risk of bias was deemed low across all studies within the “Predictors” and “Outcome” domains.

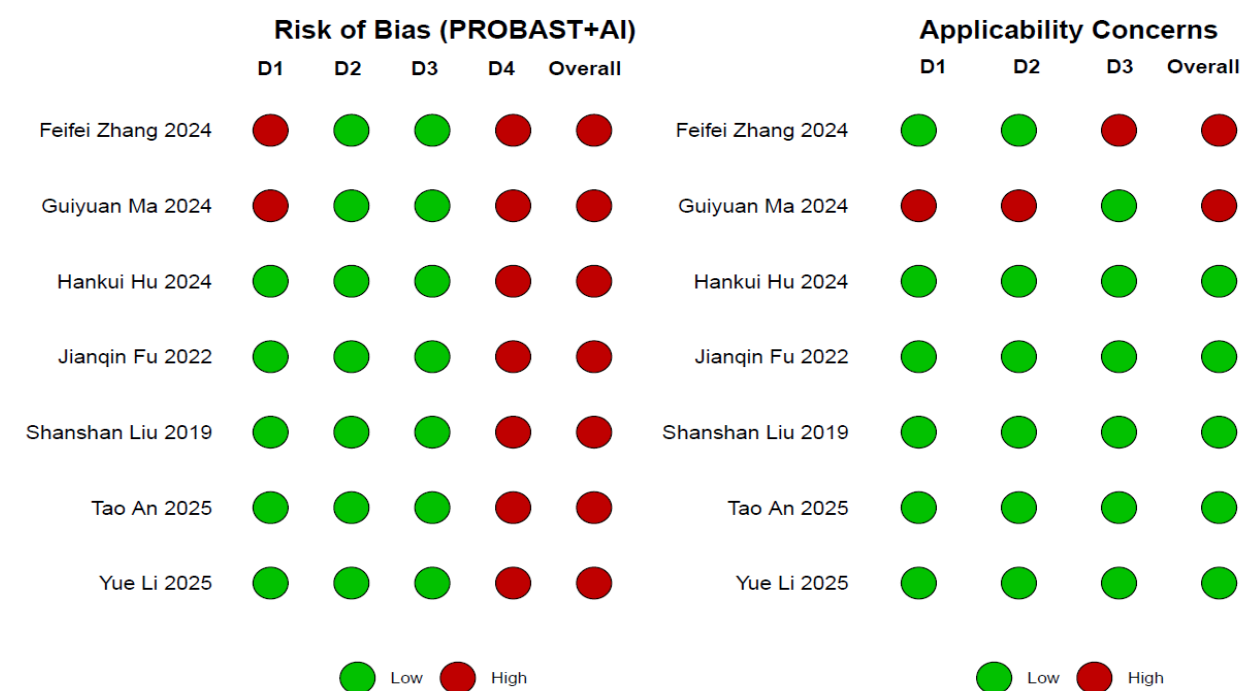


Figure 2. Risk of bias and applicability concerns of the included studies.

3.4.2. Suitability assessment

The results of the clinical applicability assessment are summarized in **Figure 2**. Specifically, two studies ^[20,21] were rated as having great concern regarding applicability. This was attributed to the use of composite outcome measures and the inclusion of broad Central Venous Access Devices (CVADs) rather than exclusively PICCs, respectively. The remaining studies demonstrated low concern regarding applicability.

Our findings indicate that compared to existing clinical risk scales, machine learning models generally exhibit superior predictive performance, characterized by higher sensitivity and specificity in screening for PICC-RVT in patients with cancer, suggesting their potential to guide prophylactic strategies. However, several limitations persist within the current literature, including the absence of external validation, inadequate handling of missing data, and insufficient sample sizes.

4. Discussion

This systematic review synthesized evidence from seven studies retrieved from English-language databases, focusing on machine learning models developed to predict PICC-RVT in patients with cancer. We comprehensively summarized the characteristics and predictive performance of these models, while concurrently assessing their risk of bias and clinical applicability. The majority of the included models demonstrated low concern regarding applicability and excellent discriminative performance. However, notable methodological shortcomings were identified, resulting in a high risk of bias, particularly within the statistical “analysis” domain.

Regarding data sources, the majority of included studies relied on single-center designs, with only two studies ^[20,22] utilizing multicenter data. Specifically, Ma et al. ^[20] conducted external validation using

multicenter data, while Li et al. ^[22] leveraged retrospective data from multiple institutions, employing a random partitioning strategy for performance validation. The remaining studies were dependent on single-center datasets derived from hospital admission registries. Given the inherent variability in data registration protocols across institutions, such heterogeneity poses a potential threat to the generalizability of these models. Consequently, large-scale multicenter studies utilizing standardized data collection protocols are warranted. Notably, it was observed that Ma et al. ^[20] employed a 1:2 case-control sampling strategy to construct their training set. This implies that the training dataset did not reflect the natural prevalence of the disease within the target population. While such sampling strategies are often adopted for efficiency, they necessitate subsequent correction, such as recalibration or weighting adjustments based on the sampling fraction, to ensure accurate probability estimates.

In terms of predictor selection, compared to traditional modeling approaches, machine learning (ML) facilitates the incorporation of a more diverse array of variables, including tumor-specific and genomic characteristics. Furthermore, given the multifactorial etiology of catheter-related thrombosis, the predictors identified vary significantly across different cancer types, and the predictive weight assigned to identical features differs among models. This observed heterogeneity suggests that future PICC-RVT prediction models may need to account for the specificity inherent to different cancer types. Consequently, future research should prioritize robust feature selection and aim to elucidate the complex interplay between tumor-specific predictors and PICC-RVT risk.

In terms of statistical analysis, developing prediction models based on machine learning algorithms typically necessitates substantial sample sizes to mitigate the risk of overfitting. We observed that although Liu et al. ^[17] and Zhang et al. ^[21] employed shrinkage methods to reduce the number of included features, such techniques cannot compensate for an insufficient sample size. Even applying conventional rules of thumb, the Events Per Variable (EPV) in these studies remained below 10. Training machine learning models with such limited sample sizes poses a substantial risk of overfitting and model instability ^[23,24]. Furthermore, An et al. and Fu et al. utilized the Synthetic Minority Over-sampling Technique (SMOTE) to address class imbalance ^[16,19]. However, in the context of risk prediction, this approach may cause more harm than good. Evidence suggests that without subsequent recalibration, such methods for handling class imbalance are often detrimental to model performance ^[25,26].

4.1. Comparative performance: AI-based versus traditional prediction models

Our comparative analysis of traditional scoring systems versus machine learning (ML)-based models for predicting PICC-RVT yielded several key insights:

- (1) Performance Disparity: ML-based prediction models consistently demonstrated superior discrimination compared to traditional methods.
- (2) Clinical Trade-offs: ML models exhibited significant performance variability across different institutions, suggesting that simpler, more parsimonious models may offer greater robustness. Research indicates that despite the superior accuracy of ML models, clinicians often prioritize interpretability, favoring established risk stratification tools ^[27]. For instance, Deng et al. ^[28] reported that despite the availability of precise ML predictions, 78% of clinicians preferred using the Caprini risk classification, highlighting the barrier posed by the “black box” nature of complex algorithms.
- (3) Implementation Challenges: Studies note that ML models often require time-intensive data preprocessing

[29]. This underscores the critical necessity of developing integrated PICC-RVT informatics systems to streamline data management and enhance thrombosis control measures in clinical practice. Collectively, these findings suggest that while AI-based models offer quantifiable performance advantages, their successful clinical translation requires addressing stringent prerequisites. These include demonstrating clear evidence of clinical impact, developing specialized intelligent systems to improve efficiency, and ensuring model interpretability to facilitate user acceptance.

4.2. The nascent stage of machine learning models for predicting PICC-RVT risk in patients with cancer

This systematic review identified a diverse array of over 20 machine learning algorithms employed to predict PICC-related thrombosis in patients with cancer, with the literature predominantly concentrated within the last five years. While research in this specific domain emerged relatively recently, it is experiencing rapid expansion, characterized by the active exploration of various algorithms for clinical application. Regarding predictive performance, all included models yielded an Area Under the Curve (AUC) exceeding 0.7, demonstrating generally acceptable discriminative ability. However, the total volume of literature remains limited. Furthermore, the studies exhibited a high risk of bias, particularly regarding data analysis, and frequently lacked rigorous external validation in their study designs. Consequently, the landscape of risk prediction modeling for PICC-RVT in patients with cancer remains in a developmental phase.

4.3. Limitations and future research directions

Several critical limitations exist regarding the evaluation and development of machine learning models for predicting PICC-related thromboembolism. First, while the PROBAST+AI tool facilitated a rigorous quality assessment, it does not offer a quantitative evaluation of predictive performance. Given that a quantitative meta-analysis was deemed unreliable due to substantial heterogeneity in model development, analysis, and validation, we relied on this qualitative assessment framework to characterize these methodological variations. The absence of established “gold standards” for ML development in this domain (e.g., protocols for handling missing data) [30] further exacerbates this methodological ambiguity. Additionally, variability in patient populations across studies—and even between hospitals within the same region—contributes to heterogeneity, potentially leading to substantial fluctuations in model performance [31,32]. Notably, the majority of included studies originated from China, which may restrict the generalizability of findings to Western populations. Consequently, recalibration or local validation is essential prior to applying these models in diverse settings. Therefore, this review does not endorse a single specific model as the optimal tool for predicting PICC-RVT in patients with cancer. Furthermore, all studies shared AI-specific limitations, specifically the lack of assessment regarding algorithmic fairness and the absence of analyses concerning deployment feasibility. While this field demonstrates promise for future clinical application, current evidence does not support replacing established risk assessment tools with AI-based methods. Substantial methodological improvements and extensive clinical validation are required prior to routine implementation.

Consequently, future research is advised to leverage machine learning technologies to develop and rigorously validate robust risk prediction models for PICC-RVT. Emphasizing the mitigation of bias is essential to facilitate the effective translation of these models into clinical practice, ultimately enhancing patient safety and quality of life.

5. Conclusion

This systematic review included seven studies and comprehensively evaluated the characteristics of AI-based risk prediction models for PICC-RVT in patients with cancer across four dimensions: participants, predictors, outcome, and analysis. Our findings indicate a generally high risk of bias across the included literature, despite the clinical applicability of the models being deemed acceptable. The majority of models lacked multicenter validation, thereby compromising their stability and generalizability. Furthermore, research utilizing unstructured data remains underexplored, and few prediction models have been effectively implemented in clinical settings to date. Future research should integrate multimodal data using rigorous machine learning methodologies to elucidate the complex interactions among risk factors across different tumor types. Such efforts are essential to facilitate the clinical translation of these models, ultimately enhancing the efficacy of prophylactic strategies for PICC-RVT.

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