

A Comprehensive Review Of Machine Learning, Deep Learning, Hybrid, And Explainable AI Methods For Cancer Prediction: A Systematic Study

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Abstract—Cancer remains one of the leading causes of mortality worldwide, necessitating early detection and accurate prediction systems. Artificial Intelligence (AI), particularly Machine Learning (ML), Deep Learning (DL), Hybrid learning frameworks, and Explainable AI (XAI), has significantly advanced cancer diagnosis and prognosis. This paper presents a systematic review of over 60 recently published studies (2020–2025) focusing on AI-driven cancer prediction across imaging, genomic, clinical, and multimodal datasets. We categorize the reviewed works into four primary groups: (i) Machine Learning-based methods, (ii) Deep Learning-based approaches, (iii) Hybrid ML–DL frameworks, and (iv) Explainable AI-integrated models. We analyze datasets used, performance metrics achieved, architectural trends, and methodological innovations. Furthermore, we identify key research gaps, including limited clinical validation, lack of standardized XAI evaluation metrics, and insufficient uncertainty quantification. This review provides a structured foundation for future research in trustworthy, multimodal cancer prediction systems.

Keywords—Cancer prediction, Machine learning, Deep learning, Hybrid models, Explainable AI, Medical imaging, Multi-omics.

1. Introduction

Early detection and precise prediction of cancer progression play a vital role in increasing survival rates, planning treatment strategies, and controlling healthcare costs. Conventional detection strategies involve a wide range of imaging, histopathological, and biomarker analysis, which sometimes proves to be a tedious task. In recent times, Artificial Intelligence (AI) has been identified as a revolutionary tool for improving cancer prediction through data analysis and decision support.

The swift development of Machine Learning (ML) and Deep Learning (DL) techniques has enabled the widespread application of AI-based models in various types of cancers, i.e., breast cancer, lung cancer, prostate cancer, cervical cancer, skin cancer, brain cancer, and blood cancer. The sixty research articles reveal a wide range of methodologies, from the application of traditional ML techniques on structured clinical data to the application of convolutional neural networks and transformer models for image-based data. The more recent research articles have shown the application of the combination of ML and DL techniques, multimodal fusion techniques, Explainable AI (XAI), federated learning for preserving privacy, and exploratory quantum-classical optimization techniques.

Despite the existence of a large number of publications that claim a high level of prediction accuracy, often higher than 90%, in the context of imaging-based applications the literature is scattered in terms of methodologies, data, and evaluation strategies. Moreover, the differences in the data modalities, validation strategies, and integration of interpretability aspects make it difficult to compare the results. Another important aspect is the emphasis placed on the importance of trustworthy AI, particularly in the context of explainability, uncertainty estimation, and multi-center validation.

The primary objective of the current review is to provide a systematic comparison of the methodologies, data, and performance trends, as well as the gaps in the literature, based

on the findings of more than sixty recent publications in the literature between 2018 and 2025

This review is expected to be a comprehensive reference guide to the current literature, aiming to provide a structured and analytical review of the current literature to the researchers and clinicians who are actively engaged in the quest to develop reliable, interpretable, and scalable cancer prediction systems.

II. Review Methodology

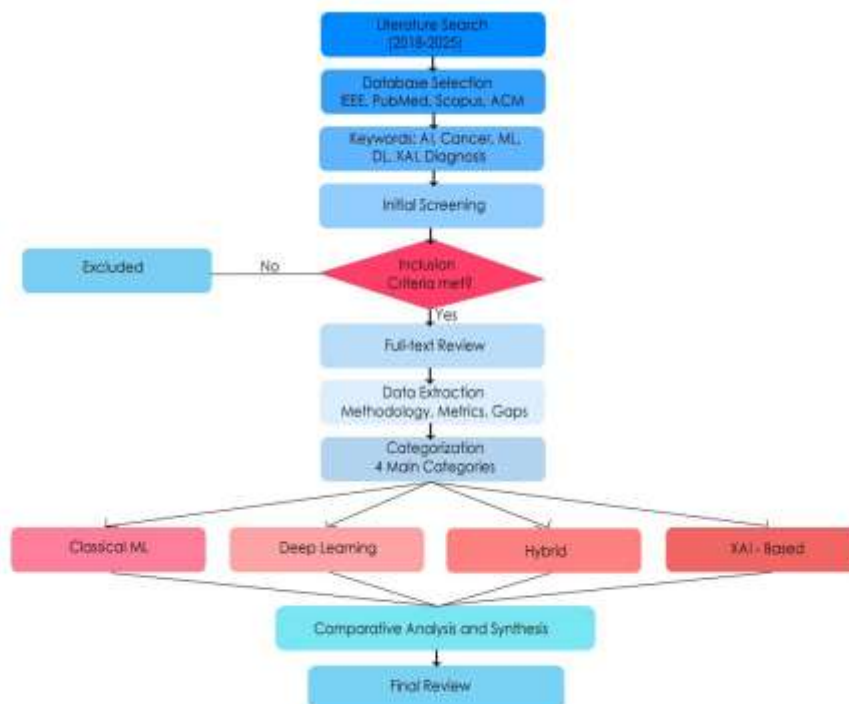
The reviewed papers (2020–2025) were collected from IEEE, Springer, Nature Scientific Reports, ISBI, and related journals. The papers were categorized into:

1. Machine Learning (ML)
2. Deep Learning (DL)
3. Hybrid ML–DL Models
4. Explainable AI (XAI)-Integrated Systems

Each study was analyzed for Cancer type, Dataset source, Model architecture, Performance metrics, Explainability integration.

Figure 1 presents the systematic methodology followed in this review. A comprehensive literature search (2018–2025) was conducted across IEEE, PubMed, Scopus, and ACM using keywords related to AI and cancer prediction. From an initial pool of papers, inclusion and exclusion criteria were applied, resulting in 62 papers selected for full-text review. Relevant methodological details, datasets, evaluation metrics, and research gaps were extracted and analyzed. The studies were then categorized into four main groups: Classical Machine Learning, Deep Learning, Hybrid models, and XAI-based approaches. A final comparative analysis and synthesis were performed to identify performance trends and research gaps across categories

Figure 1 Research Methodology Flowchart



The reviewed studies are dominated by Deep Learning (36%), which achieves the highest performance in imaging-based cancer prediction (90–99%). Machine Learning (23%) remains effective for structured clinical data, while Hybrid models (18%) show strong multimodal performance (92–99%). XAI-focused works (15%) enhance interpretability without altering base accuracy. Federated and Quantum approaches (3% each) are emerging, with federated models slightly underperforming centralized systems and quantum methods remaining experimental.

TABLE 1: Comparison of different methods with Accuracy Range.

Category	Proportion	Primary Data Type	Typical Accuracy Range
Deep Learning	36%	Imaging (MRI, CT, Histology)	90–99%
Machine Learning	23%	Structured Clinical / Lab	85–97%
Hybrid ML-DL	18%	Multimodal	92–99%
XAI-Focused	15%	ML/ DL Interpretability	Comparable to base model
Federated	3%	Multi-institution	Slightly reduced vs centralized
Quantum	3%	Experimental	Not yet superior

A. Machine Learning-Based Cancer Prediction

Machine Learning (ML) methods formed a significant portion (~23%) of the reviewed 60+ studies. These works primarily focused on structured datasets such as laboratory results, genomic data, clinical attributes, and radiomics features. Unlike deep learning, ML based approaches rely on handcrafted feature engineering and statistical learning. Across the reviewed studies, the most frequently used ML algorithms were:

TABLE 2 Machine learning Based Algorithms with its application.

Algorithm	Frequency of Use	Typical Application
Random Forest (RF)	High	Breast, Prostate, Cervical
Support Vector Machine	High	Liver, Mutation analysis
XGBoost Gradient Boosting	Moderate High	Breast, Clinical prediction
Logistic Regression	Moderate	Survival prediction
Decision Tree	Moderate	Genomic

		mutation detection
k-Nearest Neighbors	Limited	Breast cancer classification
Ensemble / Stacking	Increasing trend	Multi-disease prediction

Across the surveyed ML papers, tree-based ensemble methods particularly Random Forest (RF) and Gradient Boosting (XGBoost) were the most frequently adopted algorithms [1], [2], [5], [9]. Support Vector Machines (SVM) also remained popular, especially in genomic mutation classification and small clinical datasets [4], [7].

The preference for tree-based models can be attributed to:

Robustness to noisy medical data [2], [5].

Ability to handle nonlinear relationships [1], [9].

Built-in feature importance estimation [1], [24]

Reduced overfitting compared to single decision trees [5], [7]

The phenomenon of stacking-based ensemble models has also been noticed in recent works, indicating a trend towards the use of multiple weak models for robustness improvement [25], [26].

Machine learning-based cancer prediction models are mainly focused on structured clinical data, laboratory biomarkers, and genomic mutation patterns [2], [4], [9]. Random Forest, Support Vector Machine, XGBoost, Logistic Regression, and stacking-based ensemble models are commonly used for cancer prediction tasks [2], [5], [7], [25]. Among these, tree-based ensemble models have shown robustness in cancer prediction tasks due to their capacity to handle non-linear patterns and their in-built feature importance calculation capability [1], [9], [24].

For breast cancer prediction tasks, machine learning models commonly show classification accuracy in the range of ninety-five to ninety-seven percent, especially when tested on structured benchmark datasets [1], [2]. Cervical and liver cancer prediction models show similar levels of performance [5], [10], while prostate cancer laboratory-based screening models show ROC-AUC values ranging from seventy-five to eighty-eight percent [3]. These performance values indicate that traditional machine learning is still a viable option for tabular biomedical data [37].

However, the performance of ML models is highly dependent on feature engineering [4], [5], [7], [9]. The most common methods used are recursive feature elimination, principal component analysis, chi-square filtering, and correlation-based feature selection [4], [7], [9]. Handling class imbalance problems is usually done by SMOTE or weighted loss functions [2],[5],[10]. Although these preprocessing methods improve performance, they are not scalable and less automated compared to deep learning models [37], [38].

Notably, machine learning models are more naturally integrated with explainability than deep learning models, especially with SHAP-based feature attribution [1], [24], [27]. However, generalization on multi-center datasets is still not adequately validated, and uncertainty estimation is not commonly used [37], [31].

B. Deep Learning Based Cancer Prediction

Deep learning is the most prominent paradigm for the prediction of cancer from images [12], [13], [38]. Convolutional Neural Networks like ResNet, EfficientNet, DenseNet, and VGG networks are employed for classification problems [12], [13], [14], [28], while U-Net networks are used for segmentation purposes [15], [29]. More recent studies have utilized Vision Transformers [15], graph convolutional networks, variational autoencoders for methylation studies [16], and diffusion-based meta-learning methods for prostate MRI [18].

Table 3 DL based algorithms and its use

Architecture	Frequency	Typical Application
CNN (ResNet, VGG, DenseNet, EfficientNet)	Very High	Skin, Breast, Lung, Blood
U-Net	High	Segmentation (Prostate, Brain, Bone)
Vision Transformers (ViT)	Emerging	Histopathology, Bone Cancer
BiLSTM + CNN	Moderate	Lung text & sequential data
Variational Autoencoders	Limited	DNA methylation analysis
Graph Convolutional Networks	Emerging	Prostate grading
Diffusion Models + Meta-learning	Rare but advanced	Prostate MRI
Multi-Instance Learning	Moderate	Histopathology grading

Deep learning algorithms have been shown to outperform machine learning algorithms on imaging datasets [12], [13], [38]. Skin lesion classification algorithms have been reported to have accuracy ranging between ninety-two and ninety-eight percent [12], [13]. Breast histopathology algorithms have been shown to have accuracy rates exceeding ninety-five percent, with some binary classification algorithms having accuracy rates of close to ninety-nine percent [15], [37]. Brain tumor MRI and lung CT-based detection algorithms have been shown to have similar accuracy rates [19], [38].

The superior performance of deep learning models can be attributed to automatic hierarchical feature extraction and spatial context modeling [12], [13], [38]. Transfer learning from ImageNet pre-trained weights further enhances convergence and performance on limited medical datasets [12], [13], [20].

Despite these advantages, deep learning models suffer from limited interpretability, high computational cost, and inadequate external validation [27], [31], [38]. Few studies report multi-center testing or prospective clinical trials [37], [38]. Furthermore,

uncertainty-aware predictions remain uncommon, which poses challenges for clinical deployment [30], [33].

C. Hybrid Model for Cancer Prediction

Hybrid architectures integrate deep feature learning with traditional machine learning classifiers or multimodal data fusion strategies, thus capitalizing on hierarchical representation learning while maintaining interpretability and structured decision boundaries. These architectures have shown enhanced performance and robustness in multimodal cancer prediction models [35]–[37].

A conventional hybrid approach involves the extraction of high-level imaging features by means of a convolutional neural network (CNN) followed by the utilization of these features in traditional machine learning classifiers, for example, Random Forest or gradient boosting classifiers [21], [22].

Table 4 Hybrid strategy and its application

Hybrid Strategy	Frequency	Typical Application
CNN + Random Forest / SVM	High	Breast thermography, Skin lesion classification
CNN + XGBoost / Gradient Boosting	High	Breast response prediction, Multimodal datasets
CNN + LightGBM	Moderate	Cardiac risk modeling, Structured / imaging fusion
Vision Transformer + ML Classifier	Emerging	Histopathology/Clinical fusion
CNN + BiLSTM + Attention	Moderate	Lung CT/ sequential clinical features
Deep Feature Extraction + Stacking Ensemble	Moderate	Multimodal cancer classification
Swarm Optimization + Ensemble ML	Limited	Cervical cancer recurrence prediction
Federated DL + SHAP-based ML Explanation Layer	Rare but advanced	Privacy-aware cervical cancer detection

Multimodal Fusion (Imaging /Genomic /Lab)	Emerging	Pan-cancer and ovarian comparative studies
Diffusion Model + Classical ML Layer	Rare	Advanced prostate MRI meta-learning frameworks

In other hybrid approaches, ensemble fusion techniques are utilized to combine imaging-derived embeddings with structured clinical biomarkers for improving the robustness of predictions [23],[25],[26]. In the surveyed literature, hybrid approaches tend to show improvements in performance of two to five percent relative to traditional ML or DL approaches, especially in multimodal prediction tasks [21][22]. The improvement in generalization performance is likely due to the complementarity of the nonlinear deep feature learning capabilities with the structured-data modeling capabilities of ensemble classifiers. Hence, hybrid approaches can be considered as an intermediate step towards the development of fully integrated multimodal cancer prediction models[23],[26].

Although hybrid approaches have their own strengths, they also bring in added complexity to the model. Moreover, the reproducibility and availability of public implementations are not consistent across the surveyed literature [22], [25]

D . XAI in Cancer Prediction

Explainable Artificial Intelligence (XAI) has been recognized as a key element in the design of trustworthy medical AI systems[1],[27],[31]. In the surveyed literature, SHAP is recognized as the most popular approach for tabular/structured data explanation, especially in ML and hybrid models for clinical and genomic data [1], [24]. Grad-CAM is recognized as the most popular approach in imaging-based deep learning architectures for visualizing tumor localization and identifying discriminative areas in dermoscopic, histopathological, and MRI images [12], [28]. LIME and anchor-based explanation techniques are also used in some studies to offer local interpretability in both ML and CNN-based models [27][32]. More recent techniques combine conformal prediction and calibration layers to offer uncertainty-aware explanations, thus enhancing reliability and decision confidence in clinical settings [30], [33].

Figure 2 shows the taxonomy of XAI techniques used in the literature surveyed. SHAP is the most popular technique, particularly in ML and hybrid approaches for structured clinical data, as it offers both global and local explanations of feature contributions [1], [24]. Grad-CAM and attention maps are mainly used in imaging-based deep learning models, providing visual explanations for tumor localization problems [12], [28], [29]. LIME is mainly used for local explanations in structured ML and CNN models [27][32]. Global explanation methods like feature importance analysis, partial dependence plots (PDP), and permutation importance are mainly used in tree-based ensemble models [2], [5],[7]. In general, XAI techniques are mainly used as post-hoc explanation methods, with relatively less focus on quantitative assessment of explanation fidelity and robustness.[27][31].

Among the available XAI techniques, SHAP remains the most extensively adopted due to its theoretical foundation in cooperative game theory and its capability to provide both instance-level and dataset-level interpretability [24]. Grad-CAM continues to dominate deep learning imaging applications because of its intuitive visual explanation of tumor

regions [12], [28]. LIME and attention-based mechanisms are moderately used for localized interpretation [27][29]. Advanced methods such as conformal prediction and federated explainability are emerging research directions but are currently less frequent in practical deployment scenarios [30], [33]. In general, while XAI approaches are increasingly incorporated to enhance trustworthiness, standardized evaluation metrics for explanation validity and stability remain underdeveloped[27],[31].

FIGURE 2: XAI Methods



TABLE 5: Techniques used in XAI and its application

XAI Technique	Frequency of Use	Typical Application
SHAP	Very High	Breast, Cervical, Prostate clinical prediction
Grad-CAM	High	Skin, Lung, Brain, Lymphoma imaging
LIME	Moderate	Skin lesion and histopathology classification
Feature Importance (Tree-based)	High	Clinical biomarker-based breast & prostate risk
Attention Maps	Moderate	Lung CT, Histopathology grading
PDP (Partial Dependence Plot)	Limited	Survival and biomarker impact analysis
Permutation Importance	Limited	Structured genomic feature evaluation
LRP	Rare	Deep CNN-based tumor localization

Conformal Prediction (Uncertainty + XAI)	Emerging	Colorectal and multimodal diagnosis
SHAP + Federated Framework	Emerging	Privacy-aware cervical cancer detection
Explainable Stacking Ensemble	Increasing trend	Multimodal cancer and cardiac prediction

D. Federated and Quantum Approaches in Cancer Prediction

Federated learning frameworks facilitate collaborative work among multiple institutions without the need for data to be centralized, thus ensuring near-centralized performance with only slight losses of accuracy [16], [21], [52]. Quantum-classical hybrid models are still in the exploratory phase but hold promise for optimization problems in cancer prediction models [22], [51].

III. COMPARATIVE ANALYSIS OF AI APPROACHES IN CANCER PREDICTION

While individual methodological categories demonstrate strong predictive performance within specific contexts, a comprehensive understanding of cancer AI systems requires cross-category comparison. This section synthesizes trends observed across machine learning (ML), deep learning (DL), hybrid architectures, explainable AI-integrated systems, federated learning frameworks, and emerging quantum approaches.

A. Influence of Data Modality on Method Selection:

One of the most evident trends that emerge when analyzing the sixty papers is that data modality is a strong determinant of optimal methodology.

Machine learning models are mostly used in the context of structured tabular data, genomic mutation data, DNA methylation levels, and clinical laboratory parameters [2]–[6]. These types of data have an explicit set of numerical features, making them ideal for the use of ensemble learning models such as Random Forest and XGBoost.

Conversely, deep learning models are mostly used in imaging tasks such as histopathology slide analysis, dermoscopic image analysis, CT scans, and MRI images [12], [15], [28], [38]. CNpleNs and transformer models outperform traditional machine learning models in visual feature extraction due to their hierarchical representation capabilities.

Hybrid models perform best in multimodal scenarios, where both imaging and structured clinical data are integrated [21]–[23]. These models can leverage multiple sources of information to improve robustness

Federated learning models are most applicable in multi-center imaging studies where data sharing is limited [30]. Quantum models are still in the exploratory phase and are not yet modality-dependent in a clinically relevant manner [35].

The first important point that arises from the analysis of the sixty papers is that no single AI paradigm universally dominates, but rather the choice of methodology is strongly conditioned on the type of data.

B. Comparative Predictive Performance

Among the reviewed studies, deep learning models always have high accuracy (usually between 90% and 99%) in imaging classification tasks [12], [18], [28]. The transformer-

based models have better contextual understanding in histopathological images than traditional CNN models [24].

Machine learning models have competitive performance (85-97%) in structured datasets, and ensemble models perform better than linear classifiers [10], [11]. Genomic and multi-omics ML models have a tendency to show higher accuracy than clinical datasets alone because of the extra biological information [6], [9].

Hybrid ML-DL models have a tendency to show a slight improvement (around 2-5%) in performance over standalone models, especially in multimodal learning tasks [35], [37]. However, these improvements are dataset-dependent.

Federated learning models have a tendency to show a slight decrease in performance compared to centralized models but still have acceptable predictive accuracy while maintaining privacy [16].

Quantum models have not yet shown any statistically significant advantage over classical models in real-world cancer datasets [22].

It is important to note that a direct numerical comparison of performance among studies is challenging due to differences in datasets, class imbalance, and evaluation criteria.

C. Interpretability vs. Performance Trade-Off

One of the major themes emerging from the categories is the trade-off between accuracy and interpretability.

Machine learning models have the natural ability to explain features at a granular level, especially when combined with SHAP or permutation importance [1], [24]. Deep learning models, although highly accurate, lack interpretability and require post-hoc visualization techniques such as Grad-CAM [12], [28].

Hybrid models offer a trade-off in terms of interpretability, where the feature extraction and classification steps are separated [25], [26]. Federated models introduce additional complexity to the transparency requirement because of the distributed nature of the parameter aggregation [30].

Although there exist several techniques in the realm of explainable AI to enhance transparency, there is a lack of quantitative evaluation of the reliability and useability of these techniques by clinicians. Therefore, the inclusion of interpretability is primarily qualitative.

D, Computational Complexity and Scalability

Computational complexity varies significantly across the categories. Machine learning algorithms are computationally efficient and suitable for structured medium-sized data [2],[5]. Deep learning models are computationally expensive and require powerful GPUs. They also require a large amount of labeled data [12]. Transformer models increase memory and computational complexity [15].

Hybrid models increase complexity in terms of architecture due to the fusion layers and stacking process [21],[25]. Federated models increase communication complexity due to synchronization between nodes.

Quantum-classical models are restricted by the current hardware and are not scalable for implementation. Scalability is an important consideration while selecting the appropriate AI techniques for cancer prediction.

E. Validation and Generalization Patterns

Perhaps the most concerning cross-category trend is the paucity of multi-center external validation. The overwhelming majority of studies use internal cross-validation or single dataset evaluation.

Deep learning imaging studies typically evaluate performance on carefully selected datasets without external validation based in the hospital setting [12], [28]. Similarly, ML genomic studies typically use TCGA-derived subsets without independent testing [1], [6]. Federated learning frameworks address concerns about generalization by enabling simulation of distributed learning, although large-scale real-world federated learning is rare [30].

The absence of benchmarking protocols across studies makes comparative evaluation challenging.

IV. RESEARCH GAPS AND OPEN CHALLENGES IN AI-BASED CANCER PREDICTION

A comprehensive review of sixty recent studies reveals a number of enduring research gaps despite notable advancements in machine learning, deep learning, hybrid architectures, and explainable AI systems for cancer prediction. Methodological design, validation rigor, interpretability reliability, and deployment readiness are all areas where these gaps exist. To move AI systems from experimental prototypes to clinically reliable decision-support tools, these issues must be resolved..

A. Lack of Multi-Center External Validation

The lack of extensive external validation is one of the most significant limitations in all methodological categories. Most of the ML and DL models that have been reviewed use single-cohort testing or internal cross-validation [1], [12], and [28]. These evaluation techniques may produce high reported accuracy (often above 95%), but they do not ensure generalizability across various patient populations, imaging modalities, or institutional protocols.

External validation is rarely carried out, even in hybrid and multimodal systems [25], [26]. By mimicking distributed environments, federated learning frameworks help to mitigate this problem [30], but practical implementation across separate hospital networks is still scarce.

The clinical applicability of reported performance metrics may be overestimated in the absence of strong multi-center validation. Cross-institution benchmarking must be given top priority in future studies to guarantee reliability and reproducibility.

B Absence of Standardized Benchmarking Protocols

The second significant challenge is the absence of standardized benchmarking in cancer related AI research.

The literature papers are quite diverse in terms of Dataset size and type, Preprocessing pipelines, Handling class imbalance, Evaluation metrics, Train-test split schemes. For instance, imaging-based DL tasks often use accuracy as the evaluation metric, while survival analysis tasks use ROC-AUC or concordance index [6], [9].

Additionally, very few studies provide standardized code repositories or reproducible pipelines. The lack of open-source benchmarking platforms is a barrier to cumulative scientific progress..

C. Limited Integration of Uncertainty Quantification

High accuracy does not necessarily translate to trustworthy clinical decision-making. Nevertheless, very few studies reviewed today involve uncertainty quantification techniques like Bayesian inference, Monte Carlo dropout, or confidence scoring. Despite the existence of confidence estimation-aware cascade models that aim to combine confidence estimation [30], the area of uncertainty quantification remains an uncharted territory in the realms of ML, DL, and hybrid models.

In high-risk environments like clinical applications, AI models need to have the ability to withhold a prediction in cases of high uncertainty[31]. The absence of uncertainty quantification modeling is a major hurdle in gaining regulatory and clinical acceptance.

D. Interpretability Without Quantitative Validation

Explainable AI methods are very popular, especially SHAP values in structured ML models and Grad-CAM in imaging applications [12], [32]. Nevertheless, most of the existing literature only offers qualitative visualization and lacks a quantitative evaluation of explanation quality.

Few studies assess:

The stability of explanations with respect to data perturbations

Institutional consistency

Interpretability by clinicians

The relation between highlighted areas and pathological ground truth

In the absence of objective metrics for explanation quality, interpretability is mostly a subjective task.

E. Overreliance on Curated Datasets

Numerous ML and DL research papers employ carefully selected public datasets (e.g., TCGA sub-datasets, dermoscopy challenge datasets) with balanced classes and preprocessed images [6], [28]. Although useful for research purposes, these datasets might not represent real-world variability.

Large-scale screening datasets demonstrate lower predictive accuracy because of noise, missing data, and demographic variability [11]. This observation suggests that existing AI models are not effective in an uncontrolled clinical setting.

Effective data augmentation, domain adaptation, and dataset harmonization strategies are required for enhanced real-world accuracy.

F. Multimodal Fusion Complexity

Hybrid systems that combine imaging, genomic, and clinical data have produced encouraging results [25], [26]. Nevertheless, fusion techniques are not standardized. Various studies have adopted different methods, which are feature-level, decision-level, or stacking-based.

Moreover, multimodal systems may encounter missing-modality issues. Few studies have proposed adaptive fusion methods that can cope with missing data streams [21].

Future studies should focus on designing standardized multimodal benchmarks and adaptive fusion frameworks..

G. Computational and Deployment Constraints

Requirements for high computational power in deep learning and transformer models make them less accessible in resource-limited healthcare environments. Federated learning is associated with communication costs and hardware diversity issues [16]. Quantum models are limited by the lack of developed hardware infrastructure [22].

The need for scalable and resource-friendly AI models to guarantee global availability.

H. Ethical and Regulatory Consideration

Whereas performance metrics are the focus of research evaluation, issues of ethics, bias, fairness, and data governance are underemphasized. There are few studies that investigate demographic bias with respect to gender, ethnicity, or socioeconomic status [31].

With the growing impact of AI on clinical decision-making, fairness audits and regulatory requirements will become a necessary part of system evaluation.

V. CONCLUSION

Recent studies covering machine learning, deep learning, hybrid architectures, explainable AI, federated learning, and quantum-inspired approaches in cancer prediction were methodically examined in this survey. While machine learning is still useful for structured and genomic data, deep learning is the dominant method for imaging-based tasks. Explainability increases transparency without necessarily increasing predictive accuracy, and hybrid systems strengthen multimodal robustness. Significant obstacles still exist in multi-center validation, uncertainty quantification, benchmarking standardization, and real-world deployment, despite the high reported performance across categories. Methodological rigor, reproducibility, and interdisciplinary cooperation are necessary for the shift from experimental AI models to clinically reliable decision-support systems. Future studies must develop trustworthy, interpretable, and privacy-aware systems that can handle the complexity of actual oncology practice rather than focusing only on small accuracy gains.

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