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Revolutionizing Breast Cancer Detection with Artificial Intelligence and Machine Learning Breakthroughs in Imaging and Diagnosis: Literature Review

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Abstract

Cancer is a major global health challenge, with 19.3 million new cases and 10 million deaths in 2021. Breast cancer, with 2.3 million cases in 2022, is among the most common. Personalized treatment is vital for better outcomes but requires collaboration between clinicians and researchers. Traditional diagnostic methods, relying on manual histological examination, are slow and error-prone, worsened by a global shortage of pathologists, highlighting the need for more reliable diagnostic tools. The digitization of tissue slides has enabled artificial intelligence (AI) and machine learning (ML) integration into medical imaging, promising improved patient care. This study evaluates AI-based computational models for digital pathology, focusing on breast cancer diagnosis. These models aim to boost diagnostic accuracy and efficiency, overcoming limitations of conventional histopathological methods. We assessed various AI-based models for digital pathology, emphasizing their potential to enhance patient outcomes, treatment planning, and diagnostic accuracy in oncology, particularly for breast cancer. This paper reviews recent AI applications in oncology, highlighting their strengths and current challenges, and underscores their ability to improve the accuracy and efficiency of diagnostic processes.

Keywords: Artificial intelligence; Machine learning; Breast cancer; Digital pathology; Medical imaging; Oncology; Diagnostic accuracy
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1. Introduction

Globally, 19.3 million new instances of cancer were detected in 2021, and disease was responsible for 10 million deaths.[1] Overall, colon, prostate, stomach, lung, and breast cancers are the most common types of cancer.[2] Breast cancer remains one of the most severe and prevalent forms of cancer worldwide. The seriousness of breast cancer demands personalized care, with treatments customized to each patient's unique disease progression. This approach is achieved through close collaboration between doctors and researchers.[4] Conventional cancer diagnosis is based on manual techniques and eye observation, which leads to laborious and error-prone histological diagnosis. The subjectivity and unpredictability of expert assessments in histopathology analysis highlight the need for early detection and precise diagnosis to improve treatment success. The use of artificial intelligence (AI) to improve diagnostic accuracy is necessary because of the shortage of global pathologists. The digitization of histopathology slides and computer model analysis are two aspects of digital pathology. Prewitt and Mendelsohn created a technique in 1965 for scanning microscope images, turning optical data into a matrix of optical density values and using that information to determine if different cell types are present.[5] Introduced in 1956, AI includes machine learning (ML) techniques, in which computers learn from data to recognize patterns and anticipate outcomes without the need for explicit programming.[6] Deep learning (DL), a subset of ML, was made possible by the creation of artificial neural networks in the 1980s.[7] Owing to advancements in computational processing capability, DL has attracted interest

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in recent decades for its applications in digital pathology and other domains.[8–10]

Here, we provide a comprehensive quantitative comparative analysis of various AI and ML models, highlighting their performance metrics and specific applications in digital pathology for breast cancer detection. While previous reviews may have covered related topics[11–14] this paper aims to provide a comprehensive evaluation of key-performance metrics such as accuracy, sensitivity, specificity, and area under the receiver operating characteristic curve (AUC-ROC) and compare results from multiple studies to highlight the strengths and weaknesses of different ML approaches. This thorough review encompasses a wide array of studies, each contributing valuable insights and advancements in the field.

1.2 Survey methodology

To ensure a rigorous and unbiased literature review, a systematic approach was employed to select and evaluate the most recent and relevant studies on the application of AI and ML in breast cancer imaging and diagnosis. Multiple reputable databases, including PubMed, Elsevier, IEEE Xplore, Google Scholar, and other well-established scientific repositories, were searched because of their extensive collections of peer-reviewed articles, conference proceedings, and high-impact journal publications pertinent to the research topic. To maintain the timeliness and relevance of the analysis, the search was restricted to studies published within the last decade while also considering foundational works that have significantly contributed to the field.

The search strategy incorporated Medical Subject Headings (MeSH) terms, Boolean operators, and keyword-based queries to retrieve the most pertinent studies. An iterative refinement process was conducted to balance broad coverage with precise selection, ensuring the inclusion of studies directly related to breast cancer detection and diagnosis via AI/ML techniques. Studies were selected on the basis of predefined inclusion criteria, which encompassed the application of AI/ML methods in breast cancer diagnostics; the provision of performance metrics such as accuracy and area under the curve (AUC); the utilization of various imaging modalities (e.g., mammography, magnetic resonance imaging (MRI), and histopathology); and the employment of state-of-the-art AI/ML models, including convolutional neural networks (CNNs), vision transformers, random forests, and support vector machines (SVMs). Studies lacking sufficient performance metrics, validation methods, or clinical relevance were excluded.

To mitigate selection bias, two independent reviewers screened the identified studies on the basis of the predefined inclusion and exclusion criteria, with any discrepancies resolved through discussion or consultation with a third reviewer. Furthermore, citation networks and reference lists were examined to ensure that no critical studies were overlooked. Data extraction focused on key aspects, such as the AI/ML models utilized, imaging modalities, primary findings, performance metrics, and clinical significance. The extracted data were systematically compiled into tables for comparative analysis on the basis of common themes, strengths, and limitations, which are further discussed in detail.

By adhering to this systematic and comprehensive methodology, an objective and well-rounded synthesis of the literature was achieved, providing a robust foundation for subsequent analysis and discussion.

1.3 The growing global burden of breast cancer: A global health challenge

Breast cancer is recognized as the most frequently diagnosed form of the disease in women. Breast cancer continues to be one of the most prevalent malignancies affecting women worldwide, with an estimated lifetime risk of diagnosis affecting approximately one in eight women. In 2022, an estimated 666,000 women died of breast cancer, accounting for 15.4% of all cancer-related deaths among women, or approximately one in every six cases.[3] Breast cancer incidence rates are highest in countries with higher economic transitions, but mortality rates are disproportionately high in countries with lower human development indices (HDIs) because of limited access to early diagnosis and treatment. The World Health Organization (WHO) and the International Agency for Research on Cancer (IARC) emphasize the critical need for global efforts in early detection and treatment to reduce the growing burden of breast cancer. By 2040, the annual number of new breast cancer cases is projected to exceed 3 million, with more than 1 million deaths per year if current trends continue.[15,16]

1.4 Current state of breast cancer imaging

AI has proven highly effective in early cancer detection and prevention because of its ability to analyze tumor characteristics such as size, lymph node involvement, and protein expression. It excels in recognizing patterns and correlations between cancer subtypes, leveraging datasets of CT, MRI, mammography, and histopathology images to train ML models.

Recent advances in breast cancer research have seen significant improvements through deep learning (DL) models. These models outperform traditional methods in tumor detection, particularly CNNs and vision transformers, which increase diagnostic accuracy across various imaging modalities.[17,18] Furthermore, DL algorithms have advanced the automated classification and segmentation of breast cancer

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lesions, aiding radiologists in differentiating between benign and malignant tumors. Studies have shown that these algorithms achieve high sensitivity and specificity, often comparable to or exceeding the performance of human experts in certain contexts.[19,20] Moreover, AI and ML are instrumental in predicting treatment response and patient outcomes. By analyzing extensive datasets, these technologies identify patterns and correlations that facilitate personalized treatment plans, thus enhancing patient management and outcomes. The integration of AI into breast cancer research continues to evolve, offering advancements in early detection, risk assessment, and personalized treatment strategies.[11,21] Computer-aided diagnosis (CAD) systems benefit significantly from AI, improving diagnostic precision through advanced computational techniques.[22]

DL models, particularly in interpreting mammograms, ultrasounds, and MR images, frequently surpass those of human radiologists in detecting early cancer signs. AI-driven models also facilitate personalized treatment by analyzing genetic, histopathological, and clinical data, enabling better patient management. However, it is essential that AI tools complement, rather than replace, human expertise, with clinical oversight to ensure patient safety. As AI and ML continue to advance, they hold great promise in reducing mortality and improving the quality of life for breast cancer patients. Current evidence and examples are dominated by retrospective studies from high-income settings, which may not reflect global screening practices or care pathways. Future work should broaden data sources to underrepresented populations and health systems, and anchor evaluations to patient-centered outcomes and cost-effectiveness to guide real-world adoption.

2. Applications of AI and ML in breast cancer imaging

2.1 Image analysis and interpretation

AI and ML have significantly advanced image analysis and interpretation in breast cancer imaging. Deep convolutional neural networks (CNNs) enhance image quality by reducing noise and improving contrast, which is critical for detecting subtle anomalies. Google's DeepMind Health developed an algorithm that outperformed human radiologists in reading mammograms, significantly reducing the number of false positives and negatives.[23] The AI system developed by McKinney et al.[23] demonstrated a significant reduction in false positives of 5.7% in the USA dataset and 1.2% in the UK dataset. Similarly, false negatives were reduced by 9.4% and 2.7% in the USA and UK datasets, respectively. This improvement suggests that the AI system can enhance diagnostic accuracy by correctly identifying both the presence and absence of cancer more often than human readers do. The study also highlighted an increase in the AUC-ROC for the AI system compared with that of human radiologists. The AI system outperformed all six radiologists in a reader study, with an AUC improvement of 11.5% over the average radiologist's performance.

Another example is the work of Kim et al.,[24] which used a deep learning model to enhance digital breast tomosynthesis images, improving lesion visibility and diagnostic accuracy. The study analyzed 29,107 digital mammograms, including 4,339 cancer cases, from five institutions. Images were selected for diversity in age, breast density, and equipment. The DIB-MG algorithm, a DCNN based on ResNet, was used to generate cancer probability scores for each case via four mammogram views. The model was trained via weakly supervised learning and evaluated on the basis of sensitivity, specificity, and AUC. DIB-MG achieved a sensitivity of 75.6--76.1%, specificity of 88.5--90.2%, and AUC of 0.903--0.906. The sensitivity is relatively high for masses and invasive cancers, and the performance varies by imaging equipment, with Siemens showing the highest sensitivity (88.8%).[24]

2.2 Tumor detection and classification

AI and ML algorithms are pivotal in detecting and classifying breast tumors. CNNs and SVMs have been extensively used to differentiate between benign and malignant lesions. Dhungel *et al*.[25] developed a CNN model that achieved high accuracy in classifying breast masses on mammograms by analyzing features such as shape, margin, and texture. Rodríguez-Ruiz *et al*.[26] reported that an AI system could match the performance of expert radiologists in detecting breast cancer in mammograms, significantly improving diagnostic accuracy. Moreover, Couture *et al.*[27] used deep learning models to classify breast cancer subtypes from histopathological images, aiding in personalized treatment planning.

2.3 Quantitative imaging

Quantitative imaging leverages AI to extract measurable features from breast cancer images, providing detailed and objective data for analysis. AI algorithms analyze image characteristics such as texture, shape, size, and intensity, which can be correlated with tumor aggressiveness and response to treatment. For example, Militello *et al.*[28] utilized radiomics to extract features from MRI scans and differentiated malignant from benign tumors with high accuracy. Another study by Yu *et al.*[29] developed and evaluated a deep fusion learning framework for mammographic image classification, with two models achieving high performance: Model 1, with 89.06% accuracy, and Model 2, with 87.5% accuracy, both of which improve tumor detection by integrating deep features and cross-channel information. These quantitative metrics support radiologists in tracking tumor progression and evaluating therapeutic interventions.

2.4 Predictive modeling

AI and ML play crucial roles in predictive modeling for breast cancer and in predicting disease progression, treatment outcomes, and recurrence risk. Predictive models such as logistic regression, random forests, and deep learning networks analyze diverse datasets, including images, genetic profiles, and clinical records, to generate personalized predictions. McKinney *et al.*[23] developed a deep learning model that accurately predicts breast cancer risk from mammograms, outperforming traditional risk assessment tools. Yala *et al.*[30] created a risk model using mammographic features and patient history, achieving higher predictive accuracy for future cancer development than existing methods do. Additionally, González-Castro *et al*.[31] explored the use of machine learning algorithms to predict 5-year breast cancer recurrence by analyzing both structured and unstructured health data from electronic records, demonstrating that integrating these data sources enhances prediction accuracy and supports personalized patient care.

2.5 Significance of immunohistochemistry in cancer research

The synergy between ML and immunohistochemistry (IHC) in cancer risk stratification represents a powerful approach to enhancing the understanding of cancer biology and improving patient outcomes. It enables the integration of complex data types, enhances predictive accuracy, and facilitates personalized risk assessment, ultimately leading to more effective cancer prevention and management strategies. ML leverages the analysis of IHC data to identify complex patterns and relationships, ultimately assisting in more accurate cancer risk stratification. This helps reduce data dimensionality, focuses on the most informative markers, and facilitates the classification of tissue samples into different risk categories. As new IHC data become available, models can be updated to incorporate the latest findings, ensuring that risk stratification remains up-to-date and accurate. Researchers continue to explore innovative applications and develop robust ML models to leverage the wealth of information embedded in IHC data.

2.5.1 Image analysis

To quantify the expression levels of certain proteins or detect patterns of protein expression linked to distinct cancer types or disease stages, ML algorithms can be trained to evaluate IHC images. Gurcan *et al*.[32] and Veta *et al*.[33] investigated the emergence of feature engineering and learning techniques in image pathology, particularly for tasks such as object identification, picture segmentation, and tissue categorization. Komura and Ishikawa[34] investigated the application of ML models in digital pathology, which includes computer-assisted diagnosis, content-based picture retrieval, and clinicopathological correlations. Researchers have discussed the use of deep learning models, their limitations, and the prospects for the field of diagnostic breast pathology in this work.[34] DL techniques have been successfully applied to numerous image analysis challenges.[35–38]

2.5.2 Tumor classification

IHC staining patterns can be used to train ML algorithms that categorize different types or subtypes of cancer. This can help with cancer diagnosis and patient outcome prediction. Numerous investigators have investigated an array of methods with the goal of attaining low-error and high-performance brain tumor identification and classification. Stacke *et al*.[39] demonstrated how to optimize images that maximally activate the neurons in a CNN to assess the network's generalizability in tumor classification via H&E (hematoxylin–eosin)-stained images. The study involved analyzing the representations generated by the network and documenting the features to which the network responded. To improve the accuracy of brain tumor classification via MR images, Tandel G. *et al*.[40] created five clinical multiclass datasets and used a CNN based on transfer learning. The usefulness of tumor classification techniques for classifying MR brain imaging characteristics into n/a, multifocal, multicentric, and gliomatosis was assessed in this work.[40] The statistical characteristics of the incoming photographs were analyzed as part of the classification process, and the data were methodically separated into several categories. These categorized data were then tested via ML techniques such as KNN (k closest neighbors), RF (random forest), SVM, and LDA (linear discriminant analysis).

2.5.3 Prognostic and predictive biomarker discovery

ML can help identify new prognostic or predictive biomarkers by analyzing IHC data alongside clinical outcomes.[41] These biomarkers can guide treatment decisions and predict patient responses. Biomarkers are recognized as molecular indicators that signify an increased likelihood of benefits or the potential for toxicity associated with a particular medicine.[42] Additionally, they can be defined as measurement variables linked to the outcome of a disease.[43] Prognostic biomarkers provide insight into the prognosis of cancer as well as the administration of therapy.[44] Predictive biomarkers serve as indicators of the probability of a patient's response to a treatment plan. They enable the categorization of patients into groups with higher or lower chances of responding to a specific regimen, thereby enhancing therapeutic precision and treatment effectiveness.[45] ML methods utilize both prognostic and predictive biomarkers to assess performance, validate models, and present key results pertinent to the research. One such study[46] aimed to predict a biomarker panel for lung cancer on the basis of autoantibodies. They employed recursive feature elimination with random forest modeling and utilized least absolute shrinkage and selection operation (LASSO) regression with repeated 10-fold cross-validation in their approach.[47] DL techniques were employed to analyze scanned sections of H&E-stained tissue, aiming to develop a biomarker for predicting patient outcomes after primary colorectal cancer surgery.[48] The approach involved the use of two CNNs: the first network delineated cancerous tissue, and the second network categorized patients into distinct prognostic groups. Risk stratification was carried out via both invariable and multivariable analyses. Prognostic biomarkers estimate the natural history of disease independent of therapy, whereas predictive biomarkers identify individuals more likely to benefit (or be harmed) by a specific intervention. Multi-omics strategies integrating genomic, transcriptomic, epigenomic, proteomic, metabolomic, and circulating biomarkers can capture complementary biology across DNA alterations, pathway activity, tumor microenvironment, and host response. When aligned with clinically meaningful endpoints (e.g., invasive disease-free survival, overall survival, pathologic complete response), multi-omics models offer the potential to enhance risk stratification beyond single-assay signatures and to inform therapy selection with greater precision. The ethics and regulatory areas are emphasizing data governance, privacy-preserving training, subgroup performance reporting, and lifecycle monitoring aligned with contemporary AI/medical-device guidance. This framing supports safe clinical translation and transparent post-deployment oversight.

2.5.4 Spatial analysis

ML methods can be used to analyze the spatial relationships between different cell types and protein expression patterns in IHC images. These findings provide insights into the tumor microenvironment and its impact on cancer progression.[49] This mini-review discusses recent progress in ML and AI concerning the spatial analysis of the tumor immune microenvironment in pathology slides. The integration of ML and AI algorithms with digital pathology is revolutionizing the histopathological analysis of the tumor immune microenvironment (TIME) in tumor samples.[50] Spatial assays, such as IHC, only permit targeted analyses involving a limited number of molecular markers.

2.5.5 Data integration

IHC data can be combined with other omics datasets, such as transcriptomics and genome data, using ML to gain a comprehensive understanding of cancer biology and identify possible therapeutic targets. Current AI frameworks, which rely only on ML techniques, have been applied to the combination of omics and phenotypic data to identify novel biomarkers.[51] Additionally, ML algorithms have been used extensively to classify cancer via a variety of data sources.[52] Computed tomography (CT) data along with radiomic features were utilized in two different studies to classify cancer patients, enhancing the prediction accuracy for lung cancer and pulmonary lesions.[53]

2.5.6 Quality control

ML algorithms can help in quality control by detecting staining artifacts, tissue irregularities, or other issues in IHC images, ensuring the reliability of the results.[54] In this article, computational pathology (CPATH) in diagnostic breast pathology and IHC were explored with the application of ML/AI-based tools and the use of AI applications in diagnostic breast pathology.[55]

Key gaps remain in cohort diversity, assay harmonization, and robustness to missing modalities, which may limit generalizability across settings. Foundational datasets and annotations remain heterogeneous, with class imbalance, missing data, and limited external validation reducing generalizability. Future work should prioritize multi-site prospective validation, standardized pre-analytics and equitable deployment assessments.

3. AI/ML Applications in breast cancer imaging: methodology and key findings

The key studies included in the review are analyzed, with a focus on their strengths, limitations, distinguishing features, and methodologies that set them apart from other research in the field. The Table 1 below summarizes the methodology, strengths, weaknesses, and key characteristics of the reviewed studies.

Previous works highlighted considerable advancements in AI and ML for breast cancer detection and diagnosis, emphasizing the strengths of these technologies in improving diagnostic accuracy and efficiency. However, the practical implementation of these models in clinical workflows is still limited by factors such as the need for large datasets, computational demands, and the lack of interpretability. Future research should focus on addressing these challenges,

Table 1: Characterization of AI/ML methods in medical imaging: strengths, weaknesses, methods, and applications.

Category	Strengths	Weaknesses	Key Methods	Example Studies
Deep Learning Models for Image Analysis	- High accuracy in image classification tasks, often exceeding 90%. - Automatic feature learning reduces need for manual extraction.	-Requires large, labeled datasets. - Lack of interpretability ("black box" issue).	- Transfer Learning to leverage pre-trained models on large datasets. - Data Augmentation to enhance model generalization.	Dhungel *et al.* [25] Guan *et al.* [56]
Predictive Modeling & Treatment Planning	- Supports personalized medicine with predictions of treatment response and recurrence. - Integrates multiple data types (e.g., imaging, genetic profiles).	- Complexity in implementation in clinical workflows. - Requires advanced computational infrastructure.	- Random Forests and SVMs for robust high-dimensional data analysis. - Logistic Regression for binary outcome predictions.	McKinney *et al.* [23] Yala *et al.* [30]
Image Segmentation Techniques	- High precision in identifying tumors and anomalies in medical images. - Effective in segmenting microcalcifications.	- Computationally intensive, requiring advanced hardware for real-time analysis.	- U-Net Architecture for fine-grained detail capture in medical images.	Hossain *et al.* [57]

Category	Strengths	Weaknesses	Key Methods	Example Studies
Integration of Omics Data with Imaging	- Comprehensive risk assessment by integrating imaging with genomics, transcriptomics, and proteomics data.	- Challenges in data integration across diverse data types.	- Multi-Omics Integration for enhanced predictive power.	González-Castro *et al.*[31]
Clinical Applicability & Challenges	- Enhances diagnostic decision-making by improving diagnostic accuracy and reducing radiologist workload.	- Limited validation in real-world clinical settings. - Models often trained on retrospective data with limited generalization.	- Explainable AI (XAI) techniques such as Layer-wise Relevance Propagation (LRP) for interpretable decision-making.	Binder *et al.*[58]

integrating AI models into real-world clinical settings, and ensuring that they are explainable and accessible to healthcare professionals.

3.1 Advancements in diagnostic accuracy and prognostic prediction in breast cancer

Advancements in diagnostic accuracy and prognostic prediction for breast cancer in recent years have significantly transformed approaches to the detection and treatment of this disease. A crucial role has been played by the implementation of artificial intelligence (AI) and machine learning methods, which have greatly improved the precision of interpreting medical images such as mammography, ultrasound, and MRI. Modern deep learning algorithms are capable of automatically analyzing images, identifying suspicious areas, and even assessing their probable nature. This has helped reduce diagnostic errors and shorten analysis time.[59] Prognostic predictions have improved with multifactorial models that integrate genetic data, tumor profiling, clinical characteristics, and patient histories, enabling accurate outcome forecasts and personalized treatment selection.[60] In addition, significant progress has been made in the development of biomarkers that help detect cancer at early stages, long before clinical symptoms appear. For example, the use of circulating tumor DNA (ctDNA) or other liquid biopsies is becoming increasingly common in clinical practice.[61] A comprehensive approach that combines biomarker analysis, medical imaging, and clinical data enhances the chances of successful treatment and improves the quality of life for patients. These advancements are the result of an interdisciplinary approach involving the collaboration of experts in oncology, bioinformatics, genetics, and computer science. These findings highlight the importance of further research to improve the diagnosis and treatment of breast cancer.[62]

The detection of more aggressive and fatal subtypes of breast cancer, such as triple-negative and inflammatory breast cancers, remains a significant challenge for both radiologists and AI-based detection algorithms. These subtypes often exhibit atypical imaging characteristics, making them harder to identify. Furthermore, the effectiveness of AI tools is often hampered by a lack of continuous learning capabilities. To improve the diagnostic accuracy of AI systems, it is crucial to implement continuous learning frameworks that allow these tools to update and adapt on the basis of new cases and feedback from clinical use. Additionally, providing radiologists with feedback on missed cases can help address performance gaps, fostering an environment of ongoing learning and improvement.

ML, a branch of artificial intelligence, allows algorithms to recognize patterns in data and make predictions. It is generally divided into supervised and unsupervised learning. In supervised learning, models are trained via labeled datasets that pair input data with known outcomes. The model continuously adjusts its predictions on the basis of errors to improve accuracy. For example, in mammography, annotated images of cancerous lesions help the algorithm learn malignancy patterns, enhancing its diagnostic performance. Unsupervised learning, on the other hand, involves machine learning via datasets without predefined structures. In this type of learning, the neural network independently performs logical classification of the data.[63]

Compared with deep learning algorithms, classical ML methods, such as support vector machines, decision tree methods, random forests, and dimensionality reduction techniques such as principal component analysis, have relatively low computational requirements because these models involve fewer parameters. [64] Deep learning, a subset of machine learning, enables the training of models to predict outcomes on the basis of input data. Both supervised and unsupervised learning can be utilized to train deep learning networks. The basic principles of ML and its applications in cancer diagnosis, prognosis, and treatment are illustrated in Fig. 1. The application of ML spans various tasks throughout the spectrum of oncology, including diagnosis, prognosis, and treatment.

Several studies applying ML techniques for breast cancer diagnosis, prognoses, and treatment, particularly for histopathological image analysis, were reviewed (see Table 2). Breast cancer remains a leading cause of cancer-related mortality worldwide, necessitating advancements in diagnostic, prognostic, and treatment methodologies. ML and DL techniques have significantly contributed to automating histopathological image analysis, a cornerstone of breast cancer diagnostics. Among the classification methods used, support vector machines (SVMs) achieve the highest accuracy in diagnosing breast cancer.[78] For example, Hollon *et al.*[66] described a concurrent workflow that combines stimulated Raman histology (SRH), a label-free optical imaging technique, with deep convolutional neural networks (DCNNs). This integration facilitates the prediction of diagnoses at the bedside almost in real time through an automated process. Another study[79] introduced an automated predictive approach

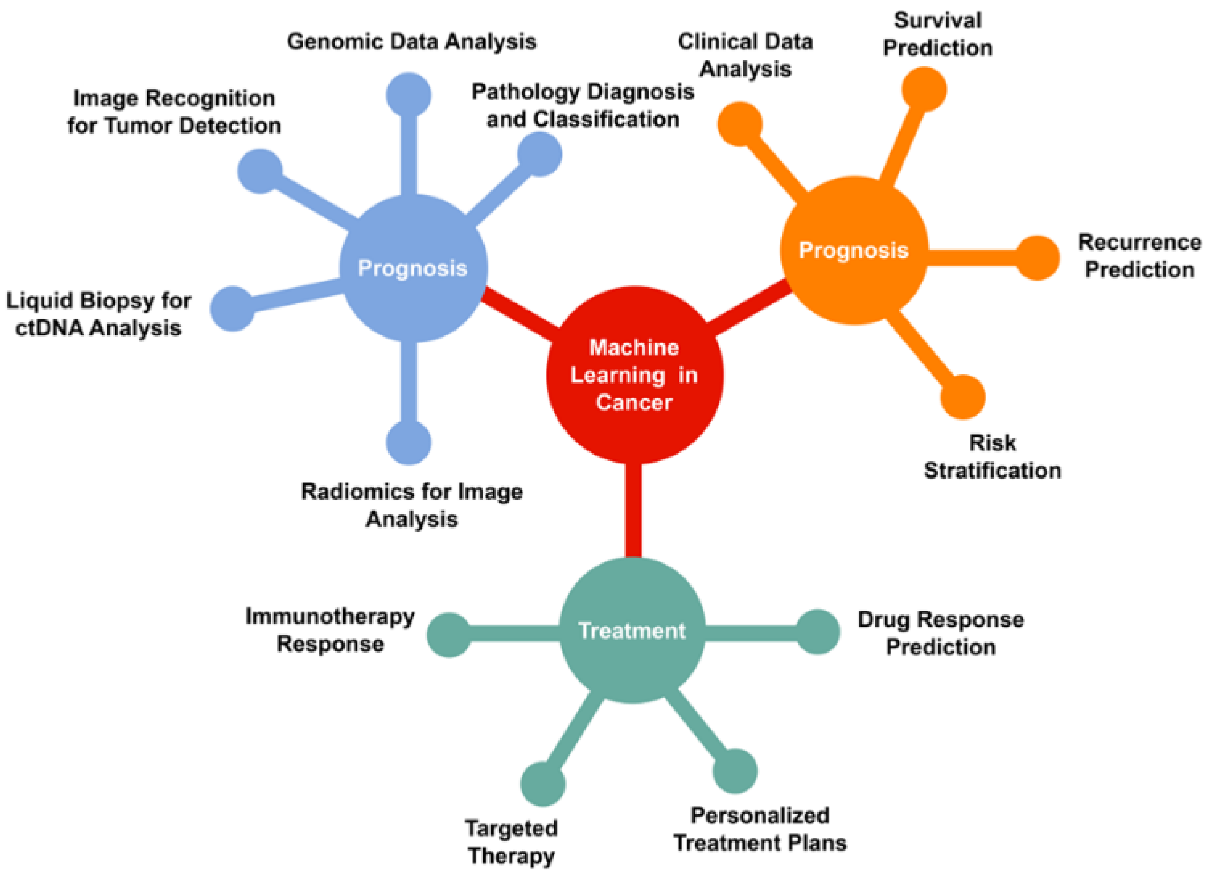

Fig. 1: A graphic representation to communicate effectively the diverse applications of machine learning in cancer.

Table 2: Overview papers on ML algorithms in diagnosis, prognosis, and treatment response in cancer.

Type of cancer	Study goal	Model	Model Output	Study
Breast cancer	To evaluate the suitable classifier by comparing the performance of different ML algorithms for risk prediction and diagnosis of breast cancer	SVM (Support Vector Machine), K Nearest Neighbors (K-NN), Naive Bayes (NB), CART (Classification and Regression Tree)	The SVM model achieved highest accuracy 98.14% with lower error rate.	Ray A *et al.*[65]
Brain cancer	Assessing brain tumor pathology slides in intra-surgery evaluation.	CNN	Prospective clinical trials of stimulated Raman histology (SRH) images revealed higher diagnostic accuracy than conventional histologic images (94.6% vs 93.9%)	Hollon T.C. *et al.*[66]
Breast cancer	Automated predictive method for scoring whole-slide images (WSI) of HER2 slides based on a deep-learning network.	Deep learning network	The automated scoring achieved an overall accuracy of 97.9% for slide-level classification. The proposed method demonstrated excellent specificity, particularly for all IHC 0 and 3+ slides and the majority of 1+ and 2+ slides.	Che Y *et al.*[67]
Breast cancer	To identify of lymph node metastasis	CNN	Sensitivity/specificity of 85%/73% compared with trained radiologists (sensitivity/specificity 73%/63%)	Zhou *et al*[68]
Breast cancer	Diagnosis of carcinoma and non-carcinoma using histopathology images	Ensemble of fine-tuned VGG16 and VGG19	Accuracy: 95.29%, Sensitivity: 97.73%	Hameed *et al.* [69]
Breast cancer	Four-class classification (normal, benign, in situ carcinoma, invasive carcinoma)	CNN	Accuracy: 77.8% for four-class, Sensitivity: 95.6% for carcinoma	Araújo *et al*[70]
Breast cancer	Cancer prognosis and prediction	SVM, artificial neural networks (ANN), Naive Bayes classifier, and AdaBoost tree	Decision trees, regression trees, and so on, an artificial neural network (ANN) was found to be the most popular one.	Kharya S *et al*[71]
Brest cancer	Binary and multi-class classification of histopathological images	SE-ResNet module integrated CNN	Binary accuracy: 98.87%-99.34%, Multi-class accuracy: 90.66%-93.81%	Jiang *et al*[72]

Type of cancer	Study goal	Model	Model Output	Study
Breast cancer	Multi-stage classification of histopathology images	Patch-based model with ensemble learning	Accuracy: 97.5% for four-class, 98.6% for two-class	Bagchi *et al.*[73]
Breast Cancer	Review of early breast cancer detection methods	SVM, RF, ANN	Accuracy ranging from 90% to 97%, AUC > 0.90	Gupta *et al*[74]
Breast Cancer	Multiscale deep learning model for breast cancer classification	msSE-ResNet34	Accuracy: 88.87%, AUC: 0.9541	
Breast Cancer	Comparative study of ML techniques for breast cancer prediction	SVM, KNN, RF, ANN, LR	ANN achieved highest accuracy of 98.57%	Alqahtani *et al.*[75]
Breast Cancer	Classification using traditional classifiers with pre-trained CNNs	CNN with Logistic Regression (ResNet50)	Highest accuracy among configurations	Gupta *et al.*[76]
Breast Cancer	Binary classification of benign vs malignant histopathological images	DenseNet with SENet integration	Accuracy: 99.28% (BreakHis dataset)	Wakili *et al.*[77]

for scoring whole-slide images (WSIs) of human epidermal growth factor receptor 2 (HER2) slides via a deep learning network. Zhang et al. detailed the use of ultrasonography for the detection of biopsy-confirmed nodal metastasis in patients with breast tumors.[80]

In the context of next-generation sequencing, where conventional statistical methods may have limitations, a recommendation system inspired by those employed in online marketing has demonstrated the ability to predict nonresponse to treatment in patients with myelodysplastic syndromes. In observational research, an assessment was conducted to compare the accuracy of the support vector machine, artificial neural network (ANN), naive Bayes classifier, and AdaBoost tree to identify an effective model for predicting breast cancer.[81]

Machine learning has revolutionized breast cancer analysis by introducing innovative approaches that increase diagnostic precision and efficiency[69] laid a strong foundation by proposing an ensemble model that integrated fine-tuned VGG16 and VGG19 architectures, achieving remarkable accuracy (95.29%) and sensitivity (97.73%) for classifying carcinoma and noncarcinoma cases. In addition, Araújo *et al.*[70] demonstrated the power of convolutional neural networks (CNNs) for more nuanced four-class classification of histopathological images, achieving 77.8% accuracy and highlighting the hierarchical feature extraction capabilities of CNNs. Furthermore, Jiang *et al.*[72] introduced a novel CNN incorporating SE-ResNet modules, achieving binary classification accuracies as high as 99.34% and robust multiclass performance, thereby demonstrating the adaptability of deep learning models for diverse classification tasks.

The focus on multistage classification was exemplified by Bagchi *et al*,[73] who utilized a patch-based ensemble learning approach to analyze the ICIAR BACH dataset. This method achieved 97.5% accuracy for four-class classification and 98.6% accuracy for binary classification, underscoring the value of localized patch analysis in capturing critical features. Gupta *et al.*[77] took a complementary route by combining pretrained Res-Net50 features with traditional classifiers such as logistic regression, achieving superior binary classification performance and demonstrating the synergistic potential of integrating deep learning with traditional ML techniques. Finally, Wakili *et al.*[75] employed a DenseNet-based model interleaved with SENet modules, leveraging transfer learning to achieve an outstanding accuracy of 99.28% on the BreakHis dataset. This approach addresses computational inefficiencies while ensuring robust generalization, highlighting the advancements in optimizing computational workflows for histopathological analysis.

ML models, particularly supervised algorithms such as support vector machines (SVMs) and deep neural networks, can recognize patterns in IHC data and classify tissue samples into different categories on the basis of protein expression profiles.[82]

Several case studies have demonstrated the effectiveness of software tools in cancer risk stratification, helping clinicians make informed decisions about treatment options for cancer patients.[83] For example, Oncotype DX is a genomic test used in breast cancer risk stratification. The expression of 21 genes in tumor tissue was analyzed to predict the likelihood of breast cancer recurrence and the potential benefit of chemotherapy.[84] This study describes the effectiveness of Oncotype DX in guiding chemotherapy decisions for breast cancer patients. Cardoso et al. evaluated the clinical utility of the MammaPrint genomic test in guiding adjuvant chemotherapy decisions for early-stage breast cancer patients. The expression of 70 genes in tumor tissue was assessed to classify patients as either "low risk" or "high risk" for distant metastasis.[85] Obtaining high-quality and sufficient quantities of data, including clinical, genetic, and lifestyle information, is essential for accurate risk stratification. Data for cancer risk stratification are collected through a combination of epidemiological studies, clinical trials, and genetic research. This information includes information on demographics, lifestyle factors (e.g., smoking, diet, physical activity), and family history of cancer. Genetic studies involve the collection of DNA samples from individuals to identify genetic markers associated with cancer risk. Clinical trials collect data on cancer patients, including treatment outcomes, side effects, and genetic information. These data help in understanding how genetic factors influence treatment response.

Together, these studies illustrate the transformative impact of machine learning on breast cancer diagnosis and prognosis. By employing diverse strategies, from ensemble learning and deep feature extraction to patch-based analysis and transfer learning, researchers not only improve accuracy but also unlock new possibilities for automation and scalability in cancer management. These innovations mark a significant leap toward a future where ML-driven tools become indispensable in clinical decision-making, offering timely and reliable insights for improved patient outcomes.

However, current imaging-AI evidence is dominated by retrospective, single-site datasets with heterogeneous acquisition, which limits generalizability. Domain shift across scanners and vendors, reader and workflow variability remain under-addressed. Future work should prioritize multi-site prospective studies with patient-relevant endpoints, plus calibration and decision-curve analyses. Transparent reporting, public benchmarks with standardized preprocessing, and post-deployment drift monitoring are needed.

4. Quantitative comparative analysis of ai and machine learning models for breast cancer detection via digital pathology

In this section, we conduct an in-depth review of a body of research focused on predicting and diagnosing breast cancer risk in digital pathology through the application of ML techniques. The integration of AI and ML in digital pathology has revolutionized breast cancer detection and diagnosis.

Histopathology involves examining tissue samples fixed in formalin, embedded in paraffin, and mounted on glass slides.[86,87] While mammography is the most common screening method for breast cancer,[88] it faces limitations such as reduced sensitivity due to breast density.[89] Histopathological image analysis remains the gold standard for breast cancer diagnosis. AI has advanced breast cancer detection, especially in digital mammography (DM), improving image interpretation, reducing false positives, and increasing diagnostic accuracy. AI techniques have been refined to enhance disease detection, predict outcomes, and support clinical decision-making.[90-92]

One study applied a 3D RetinaNet model to detect breast cancer in TWIST DCE-MRI images, achieving an AUC of 0.90 and a sensitivity of 0.95.[19] This high detection rate underscores the model's efficacy in accurately identifying cancerous lesions, making it a valuable tool in clinical settings. Feng *et al.*[18] implemented the knowledge-driven feature learning and integration (KFLI) model, which uses DWI and DCE-MRI data from 100 high-risk female patients, improving diagnostic performance with an accuracy of 0.85. By incorporating a sequence division adaptive weighting module, the KFLI model improved diagnostic performance and provided significant insights for radiologists. Transfer learning in CNNs has also significantly improved breast cancer detection in histopathological images, achieving over 96% accuracy with limited datasets (56). Additionally, a U-Net segmentation network was employed for microcalcification detection in mammograms, achieving AUC values between 0.94 and 0.96.[57] In another significant study, Senapati *et al.*[93] applied a hybrid approach using kernel particle swarm optimization (KPSO) to design a radial basis function neural network (RBFNN) to classify breast cancer in pathology images. The model achieved AUC values over 0.90 and accuracy rates between 90% and 94%, demonstrating reliable classification performance and robustness. Botlagunta's research[94] utilized ensemble learning techniques, specifically random forests, for the clinical and diagnostic prediction of breast cancer metastasis via clinical data. The model achieved high robustness and accuracy, with AUC values exceeding 0.95 and accuracy rates ranging from 94% to 97%.

Yassin *et al.*[95] reviewed various ML techniques for CAD of breast cancer using different modalities. Techniques such as SVM and random forests achieved accuracy rates above 94%, with sensitivity and specificity exceeding 93%. This study underscores the enhanced diagnostic capabilities of ML techniques. Gupta *et al.*[74] reviewed methods and systems for early breast cancer detection. Various ML techniques were evaluated, achieving accuracy rates ranging from 90% to 97% and AUC values over 0.90. This study emphasized the critical role of early detection and highlighted how ML enhances diagnostic accuracy. This comparative study[96] analyzed the diagnostic accuracy of digital versus film mammography. Compared with film mammography, digital mammography, which has accuracy rates above 92%, has superior performance, achieving accuracy rates exceeding 95%. This study provides substantial evidence supporting the preference for digital methods in breast cancer screening. In a comprehensive study using the Wisconsin Breast Cancer dataset, the ANN achieved the highest accuracy (98.57%), outperforming the SVM and KNN, both of which also performed well. These findings support the integration of advanced ML techniques in clinical practice to improve diagnostic accuracy and patient outcomes.[97] Labilloy *et al.*[98] investigated the factors associated with nonadherence to timely surgery for breast cancer patients by applying ML techniques to electronic health records and tumor registry data. The study included 1,004 women diagnosed with stage 0 through III breast cancer between 2014 and 2019 at UF Health, Jacksonville. Other studies explored the factors influencing nonadherence to timely surgery, while novel frameworks such as EACO–ResNet101 improved breast cancer detection by optimizing CNN hyperparameters.[99] Research by Makhlouf *et al.*[100] provides a comprehensive roadmap for the development of AI tools in digital pathology. The authors emphasize the importance of collaboration between AI scientists and pathologists throughout the entire development process, from hypothesis formulation to deployment. Alaa *et al.*[103] presented the Adjutorium model, which was designed to guide the use of adjuvant therapies for breast cancer by predicting patient survival and therapeutic benefits via an ensemble of ML models optimized through Bayesian techniques. Binder *et al.*[58] combined CNNs and layerwise relevance propagation (LRP) to integrate morphological and molecular data, offering explainable insights into breast cancer profiling. This study by Boeri et al. provides a primary evaluation of the application of ML techniques, specifically ANNs and SVMs, to predict breast cancer prognosis. This research focused on predicting cancer recurrence (both locoregional and systemic) and death from the disease within 32 months postsurgery. Ming *et al.*[102] assessed the effectiveness of ML models for breast cancer risk prediction and compared them with traditional models such as the Breast Cancer Risk Assessment Tool (BCRAT) and BOADICEA to improve the accuracy of risk stratification. This paper by Spanhol *et al.*[103] introduces the BreaKHis dataset, a comprehensive collection of 7909 breast cancer histopathological images acquired from 82 patients, aimed at advancing the field of breast cancer image analysis. The dataset includes both benign and malignant images captured at four different magnification levels (40x, 100x, 200x, and 400x) and provides a valuable resource for the development and evaluation of computer-aided diagnosis systems. This study by Cai *et al.*[104] introduces a novel phase-based texture descriptor named the phase congruency-based binary pattern (PCBP), which is designed to enhance the classification of breast ultrasound images (BUSs). PCBP combines the phase congruency approach with the local binary pattern (LBP) method to capture local structural and textural information from BUS images, facilitating discrimination between benign and malignant tumors. A study by Viswanatha Reddy Allugunti[105] presented a CAD system for classifying breast cancer via thermographic images, whereas Khalid et al.[108] focused on developing computationally efficient ML models for detecting and preventing breast cancer via mammographic images. A study by Mohamed and colleagues[107] proposed a fully automatic breast cancer detection system using U-Net for segmentation and a CNN for classifying breast tissues in thermographic images. Arefan and colleagues[108] investigated the use of deep learning models to predict short-term breast cancer risk via prior normal mammograms. The research compares two deep learning-based approaches: an end-to-end CNN model (GoogLeNet) and a GoogLeNet model combined with linear discriminant analysis (GoogLeNet-LDA). Alqahtani and colleagues[81] proposed msSE-ResNet, a deep learning model designed to improve breast cancer detection accuracy by recalibrating feature channels at multiple scales.

To enable convenient reference and access to the details of these studies, a summary of their key characteristics and findings is presented in Table 3. This table serves as a valuable resource for comprehending extensive and in-depth investigations into breast cancer risk assessment, particularly emphasizing the application of AI and ML techniques. Table 2 also addresses the diversity of tasks solved across the studies, including tumor detection, image segmentation, diagnostic prediction, and treatment response guidance. Different ML techniques are applied across these studies, ranging from CNNs for image analysis to ensemble learning methods for diagnostic predictions. Most studies report high performance, with accuracy values typically above 90%. This consistency in results underscores the robustness of modern AI/ML models in cancer detection and diagnosis.

Table 3: An overview of the AI and ML models for analysis of breast cancer risk assessment using medical images.

Study	Characteristics	Descriptions	Data	Technique	Results	Prognosis	Task
Ayatollahi *et al.*[19]	Deep Learning, Image Analysis	3D RetinaNet for detecting breast cancer in ultrafast TWIST DCE-MRI images	572 images from 462 patients	CNN (3D RetinaNet)	AUC: 0.90, Sensitivity: 0.95	High accuracy in tumor detection and classification	Tumor detection and classification
Feng *et al.*[18]	Deep Learning, Knowledge Integration	KFLI model using DWI and DCE-MRI data	100 high-risk female patients	CNN (KFLI)	Accuracy: 0.85	Improved diagnostic performance and feature integration	Enhanced diagnostic performance

Study	Characteristics	Descriptions	Data	Technique	Results	Prognosis	Task
Guan *et al.*[56]	Transfer Learning, Image Analysis	Transfer learning in CNNs for breast cancer detection	Histopathological images	CNN (Transfer Learning)	Accuracy: >96%	Effective with limited datasets	Breast cancer detection
Hossain *et al.*[57]	Deep Learning, Segmentation	Microcalcification segmentation using U-net segmentation network	Mammogram images	U-Net	AUC: 0.94-0.96, Accuracy: 93-96%	Enhanced model robustness and training data	Microcalcification segmentation
Senapati *et al.*[93]	Machine Learning, Classification	Hybrid approach using KPSO and RLS for RBFNN design	Pathology image datasets	RBFNN	AUC: >0.90, Accuracy: 90-94%	Reliable classification performance	Classification of breast cancer
Botlagunta *et al.*[94]	Ensemble Learning, Diagnostic Prediction	Classification and diagnostic prediction of breast cancer metastasis on clinical data	Clinical data	Random Forests	AUC: >0.95, Accuracy: 94-97%	High robustness and accuracy	Diagnostic prediction
Yassin *et al.*[95]	Machine Learning, CAD Systems	ML techniques for breast cancer CAD using different image modalities	Various image modalities	SVM, Random Forests	Accuracy: >94%, Sensitivity: >93%, Specificity: >93%	Enhanced diagnostic capability	Computer-aided diagnosis (CAD)
Gupta *et al.*[74]	Machine Learning, Early Detection	Review of early breast cancer detection methods and systems	Multiple datasets	Various ML techniques	Accuracy: 90-97%, AUC: >0.90	Improved early detection accuracy	Early breast cancer detection
Pisano *et al.*[96]	Diagnostic Accuracy, Comparative Study	Comparison of digital vs. film mammography for diagnostic accuracy	Mammography images	Digital Mammograph, Film Mammography	Accuracy: Digital: >95%, Film: >92%	Enhanced diagnostic perfo digital methods	Diagnostic accuracy comparison
Islam *et al.*[97]	Comparative Study, ML Techniques	Comparison of SVM, KNN, RF, ANN, and LR for breast cancer prediction using the Wisconsin Breast Cancer dataset	Wisconsin Breast Cancer dataset from UCI Machine Learning Repository	SVM, KNN, RF, ANN, LR	ANN: Accuracy 98.57%, SVM: Accuracy 97.14%, KNN: Accuracy 97.14%, RF: Accuracy 95.71%, LR: Accuracy 95.71%	ANN outperformed other techniques in prediction accuracy	Prediction of breast cancer
Labilloy *et al.*[98]	ML application in clinical pathological prediction.	Identification of factors leading to non-adherence to timely surgery	1,004 women diagnosed with stage 0-III breast cancer from UF	Various ML methods including AdaBoost, CatBoost,	Accuracy: 0.78; AUC: 0.82; Sensitivity: 85-95%;	The study identified the Area Deprivation Index (ADI)	Adherence prediction to timely surgery

Study	Characteristics	Descriptions	Data	Technique	Results	Prognosis	Task
		using ML techniques.	Health, Jacksonville.	Gradient Boosting, and Random Forest. Best performance was AdaBoost	Specificity: >90%	as the most significant predictor of non-adherence to timely surgery, followed by cancer stage and race. These findings underscore the importance of social determinants in patient adherence to treatment schedules and highlight the need for targeted interventions	
Thirumalaisamy *et al.*[99]	The study integrates deep learning with a metaheuristic optimization technique.	Combining CNN with Enhanced Ant Colony Optimization (EACO) for breast cancer classification	MIAS and CBIS-DDSM mammographic datasets	CNN (ResNet101) with EACO optimization	CBIS-DDSM: Accuracy 98.63%, Sensitivity 98.76%, Specificity 98.89%; MIAS: Accuracy 99.15%, Sensitivity 97.86%, Specificity 98.88%	High accuracy in tumor detection, optimized hyperparameters improve performance	Tumor detection and classification
Makhlouf *et al.*[100]	Development of AI Tools, Human-AI Interaction	Framework for developing AI tools in digital pathology, emphasizing collaboration between AI scientists and pathologists	Various datasets from pathology and clinical studies	AI and ML techniques for image analysis and diagnosis	AUC and other metrics depend on specific implementations and applications	Enhanced diagnostic workflows, improved patient outcomes through AI integration	AI tool development for digital pathology
Alaa *et al.*[101]	AI and ML for Adjuvant Therapy Guidance	Development of Adjutorium, an AI-based model to predict survival benefits from adjuvant therapies in breast cancer	Data from nearly one million women from the UK and US cancer registries	AutoPrognosis: ensemble of ML models optimized with Bayesian techniques	Internal validation: AUC-ROC 0.825 for breast cancer-specific mortality at 10 years, External	Improved accuracy in predicting survival and treatment benefits, better decision-making for	Adjuvant therapy guidance for breast cancer

Study	Characteristics	Descriptions	Data	Technique	Results	Prognosis	Task
					validation: AUC-ROC 0.803 for breast cancer-specific mortality at 10 years	adjuvant therapy	
Binder *et al.*[58]	Explainable ML for Cancer Profiling	Combines morphological and molecular data to profile breast cancer using explainable machine learning	TCGA and B-CIB (Berlin Cancer Image Base), over 200,000 manually annotated patches	CNNs, LRP (Layer-wise Relevance Propagation)	Balanced accuracy for protein prediction: up to 65%, somatic mutations: 71%, CNVs: 70%, gene expression: 77%, gene methylation: 78%	Improves understanding of the relationship between morphology and molecular features, aids in diagnosis and treatment planning	Cancer profiling through explainable ML
Boeri *et al.*[109]	The study focuses on using AI and ML models to predict breast cancer prognosis.	Evaluation of machine learning models (ANN and SVM) to predict breast cancer recurrence and mortality	Data from 610 female patients who underwent surgery for breast cancer	Artificial Neural Network (ANN) and Support Vector Machine (SVM)	ANN: AUC 0.804-0.916, Accuracy 95.29%-96.86%, Sensitivity 0.35-0.64, Specificity 0.97-0.99; SVM: AUC 0.896-0.849, Accuracy 95.72%-96.86%, Sensitivity 0.48-0.56, Specificity 0.98-0.99	Models provide accurate and specific predictions but need improvement in sensitivity	Prediction of breast cancer recurrence and mortality
Ming *et al.*[102]	The study focuses on using AI and ML models to enhance the accuracy of breast cancer risk predictions	Comparison of various ML techniques with established models (BCRAT and BOADICEA) for predicting breast cancer risk	Simulated datasets and two retrospective samples: US population-based sample (n=1143) and Swiss clinic-based sample (n=2481)	ML methods (*e.g.*, ADA, RF, MCMC GLMM) vs. BCRAT and BOADICEA	US sample: ADA AUC 88.28%, RF AUC 88.89%, BCRAT AUC 62.40%; Swiss sample: ADA AUC 90.17%, MCMC GLMM AUC 89.32%, BOADICEA AUC 59.31%	ML models significantly outperform BCRAT and BOADICEA, providing more accurate risk stratification	Breast cancer risk prediction
Spanhol *et al.*[103]	The study focuses on creating a	Introduction of BreaKHis dataset,	7909 breast cancer histopathology	SVM, RF, QDA, 1-NN classifiers	Accuracy: 80% to 85% depending on	Significant potential for improvement	Histopathology image classification

Study	Characteristics	Descriptions	Data	Technique	Results	Prognosis	Task
	large, publicly available dataset for breast cancer histopathological image classification and evaluating baseline pattern recognition systems.	evaluation of baseline classification systems for breast cancer histopathology	images from 82 patients (benign and malignant)	with various feature extraction techniques (LBP, CLBP, LPQ, etc.)	magnification factor	in classification accuracy through advanced feature extraction and classifier ensemble methods	
Cai *et al.*[104]	The study focuses on developing an advanced texture descriptor for BUS image classification, emphasizing robustness and efficiency.	Development of a novel phase-based texture descriptor for efficient classification of breast ultrasound images (BUS)	138 BUS images (69 benign, 69 malignant) from Huashan Hospital, Shanghai, China	Phase Congruency-Based Binary Pattern (PCBP) with SVM	AUC: 0.894, Accuracy: 86.96%, Sensitivity: 86.96%, Specificity: 86.96%	Provides robust and efficient classification of BUS images, potentially useful for CAD systems	Breast ultrasound (BUS) image classification
Allugunti[105]	The study focuses on developing a robust CAD system using deep learning and machine learning techniques to analyze thermographic images for breast cancer detection.	Development of CAD system for breast cancer detection using thermographic images	1000 thermographic images from 150 patients (Kaggle dataset)	CNN, SVM, Random Forest (RF)	CNN: Accuracy 99.65%, SVM: Accuracy 89.84%, RF: Accuracy 90.55%	High accuracy in detecting breast cancer using CNN, promising for CAD systems	Computer-aided diagnosis (CAD)
Khalid *et al.*[106]	Machine Learning for Breast Cancer Detection and Prevention	Development and comparison of multiple machine learning models for detecting breast cancer in mammograms	3002 mammograms from 1501 individuals collected between 2007-2015	Random Forest (RF), Decision Tree (DT), K-Nearest Neighbors (KNN), Logistic Regression (LR), Support Vector Classifier (SVC), Linear SVC	Accuracy: RF - 97.23%, DT - 94.67%, KNN - 96.34%, LR - 94.56%, SVC - 95.78%, Linear SVC - 95.02%	High accuracy in detecting breast cancer using machine learning models, potential for improving CAD systems	Breast cancer detection using mammograms

Study	Characteristics	Descriptions	Data	Technique	Results	Prognosis	Task
Mohamed *et al.*[107]	Fully Automated Breast Cancer Detection	Development of a fully automatic deep learning system for breast cancer detection using thermograms	DMR-IR database, 1000 thermogram images (500 normal, 500 abnormal)	U-Net for segmentation, CNN for classification	Accuracy: 99.33%, Sensitivity: 100%, Specificity: 98.67%	High accuracy and sensitivity make it promising for clinical use	Fully automatic breast cancer detection
Arefan *et al.*[108]	The study aims to develop and evaluate deep learning models for predicting breast cancer risk based on normal mammograms.	Development and comparison of two deep learning models to predict breast cancer risk using normal mammograms	Case-control cohort of 226 women (113 with breast cancer, 113 controls)	End-to-End CNN (GoogLeNet) and GoogLeNet-LDA	GoogLeNet-LDA AUC: 0.73 (whole-breast CC view), 0.72 (dense tissue MLO+CC view); GoogLeNet AUC: 0.67 (dense tissue MLO+CC view)	Promising results for predicting short-term breast cancer risk; higher performance of GoogLeNet-LDA model	Prediction of breast cancer risk
Alqahtani *et al.*[75]	The study focuses on the development of a deep learning model (msSE-ResNet) that utilizes multiscale channel recalibration to enhance the classification of breast cancer pathology images.	Development of a deep learning-based classification strategy using a multiscale channel recalibration model (msSE-ResNet) for breast cancer pathology images	BreaKHis dataset: 7909 breast cancer pathology images from 82 patients (24 benign, 58 malignant)	msSE-ResNet34, msSE-ResNet18		Demonstrates robustness and improved classification accuracy for various magnifications, potential for clinical application	Pathology image classification

This comprehensive review outlines the importance of integrating ML techniques in predicting breast cancer risk and outcomes via digital pathology data. Combining clinicopathological features and quantitative omics data analyzed through advanced ML methods leads to improved diagnostic accuracy and personalized treatment strategies, ultimately contributing to better patient outcomes. Studies highlight advancements such as the EACO–ResNet101 framework for early diagnosis, the importance of collaborative AI tool development and the use of explainable AI to increase understanding and diagnostic capabilities. The potential of advanced ML models in adjuvant therapy decision-making, as well as the creation of robust datasets and feature extraction methods, demonstrates the broad impact of ML across various aspects of breast cancer detection and treatment. The application of ML techniques in breast cancer detection and diagnosis has demonstrated substantial potential in enhancing diagnostic accuracy and supporting clinical decision-making. Each ML method offers unique advantages and limitations.

Future research should focus on developing AI and ML models that integrate smoothly into clinical workflows, making them user friendly and accessible to healthcare professionals. Optimizing models for specific medical datasets will increase their accuracy and reliability in real-world settings. To build trust among clinicians, these models must be interpretable, with clear decision-making processes. Collaboration among AI researchers, clinicians, and pathologists is crucial for creating effective diagnostic tools that meet clinical needs.

As AI and ML continue to evolve, ongoing validation and updates are essential to maintain performance and incorporate new advancements. Large, diverse datasets are key for training and validating models, ensuring that they work across different clinical scenarios. Research should also explore tailoring treatment plans to individual patients on the basis of their clinical and pathological characteristics to improve effectiveness and outcomes. Combining data from multiple imaging modalities can provide a more comprehensive view of breast cancer, enhancing diagnosis. Since early detection is critical for improving survival rates, it should remain a priority in model development. Addressing these areas will strengthen the role of AI and ML in breast cancer prognosis, detection, and treatment, ultimately improving patient care.

A comparative analysis of the reviewed models reveals consistent performance patterns across imaging modalities. Convolutional neural networks (CNNs) and transformer-based architectures consistently demonstrate the highest diagnostic accuracy (often exceeding 95%) in image classification and lesion segmentation tasks, particularly when applied to mammography and histopathology data. However, their "black box" nature and dependence on large labeled datasets limit interpretability and scalability in clinical environments.

In contrast, classical machine learning algorithms such as support vector machines (SVMs) and random forests exhibit slightly lower accuracy (typically 88–93%) but offer greater transparency and computational efficiency. These models remain advantageous in settings with smaller datasets or limited computing infrastructure. Hybrid and ensemble Across modalities, digital mammography benefits most from CNN-based models due to high-resolution structured data, while MRI and ultrasound analysis face greater variability due to imaging heterogeneity. Histopathological applications have advanced rapidly, with deep learning models excelling in both tumor grading and subtype classification. Overall, ensemble and hybrid strategies appear most promising for real-world integration, offering robust performance and interpretability suitable for regulatory acceptance and clinical decision support.

Overall, CNN-based architectures demonstrate superior performance for image-based tasks such as segmentation and lesion classification, particularly in mammography and histopathology. Ensemble methods and random forests excel in prognostic modeling and multi-omics integration. However, performance varies by imaging modality—MRI and ultrasound analyses still face variability due to smaller datasets and signal noise. In summary, the significant

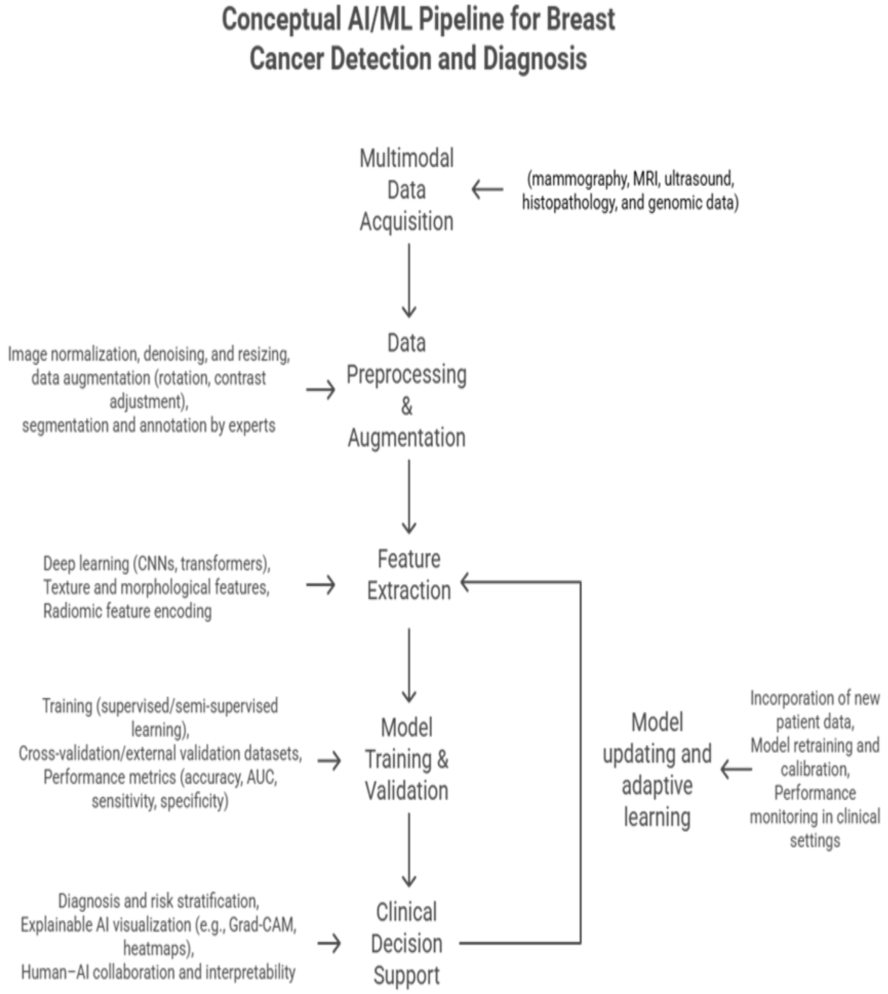

Fig. 2: Conceptual AI/ML Pipeline for Breast Cancer Detection and Diagnosis.

advancements made in AI and ML models have been applied to breast cancer detection, diagnosis, and treatment guidance. The consistent reporting of exact performance metrics (such as accuracy, sensitivity, and AUC) across different studies enhances comparability and demonstrates the reliability of these models. CNNs have emerged as the dominant technique for image-based tasks because of their ability to extract complex visual features, whereas ensemble models offer robust performance in diagnostic and prognostic tasks. The studies presented in Table 3 highlight the growing application of AI in real-world clinical settings, with several models already integrated into diagnostic workflows and personalized treatment strategies. The use of large, well-curated datasets further strengthens the predictive accuracy and clinical utility of these models.

However, it is important to remember that AI algorithms are still in the early stages of development, and validation on a large volume of data is needed to confirm their diagnostic and prognostic value. While machine learning-based methods will not replace histological verification in the near future, their integration into clinical practice will become one of the key and promising tasks for reducing breast cancer mortality. In the future, the use of AI technologies will allow a transition from simple clinical decision support systems to truly independent reading.

To provide readers with a clear conceptual overview of the methodological flow, a schematic representation of the AI/ML pipeline for breast cancer detection and diagnosis (Fig. 2) has been added. The diagram summarizes the sequential stages of data acquisition, preprocessing, model training, validation, and clinical integration, emphasizing explainable and adaptive learning processes that underpin successful real-world implementation.

4.1 Clinical translation and real-world integration

The successful implementation of AI and ML systems in clinical oncology requires not only high diagnostic performance but also practical, ethical, and regulatory readiness. Despite significant algorithmic progress, real-world integration remains limited due to issues of interpretability, data governance, and system interoperability.

Explainable AI (XAI) plays a pivotal role in enhancing clinical trust by providing transparency in model decision-making. Techniques such as saliency maps, Grad-CAM, and layer-wise relevance propagation allow clinicians to visualize the features influencing AI predictions, thereby improving confidence and accountability. Embedding these visualization tools into diagnostic interfaces facilitates collaborative decision-making between human experts and AI systems.

Continuous learning frameworks represent another critical step toward clinical viability. By allowing models to adapt to new data over time, these systems maintain performance stability as imaging modalities, patient populations, and diagnostic criteria evolve. However, the implementation of adaptive models must comply with regulatory requirements that ensure traceability, version control, and patient data security.

Regulatory and ethical considerations are equally vital. Compliance with frameworks such as the European Union's AI Act, the U.S. FDA's software-as-a-medical-device (SaMD) guidelines, and local data protection laws (e.g., GDPR, HIPAA) ensures model accountability and patient safety. Ethical deployment further demands fairness testing to prevent algorithmic bias and unequal outcomes across demographic groups.

In low-resource healthcare settings, the use of computationally efficient, lightweight AI models offers a practical solution for early breast cancer detection where expert pathologists or advanced imaging infrastructure may be scarce. Cloud-based diagnostic platforms, mobile imaging units, and federated learning strategies can facilitate equitable access to AI-assisted care without compromising patient data privacy.

Overall, successful clinical translation depends on sustained collaboration among clinicians, computer scientists, regulators, and policymakers. Such interdisciplinary partnerships will ensure that AI tools complement rather than replace human expertise, advancing precision oncology while maintaining ethical and equitable standards of care.

Multi-omics biomarkers are constrained by small or non-representative cohorts, batch effects, and missing modalities that can inflate performance estimates. Priorities include cross-platform harmonization, independent multi-center validation, and longitudinal designs linking ctDNA/imaging dynamics to hard clinical outcomes. Future studies should pre-specify context of use and decision thresholds and formally test treatment–biomarker interactions.

5. Challenges in AI applications

The effectiveness of any AI-based method is mainly determined by the volume and quality of the input information. To obtain the highest prediction performance, the data used to train an AI system must be clean, curated, have the highest signal-to-noise ratio, and be as accurate and thorough as possible. Similar comprehensive reviews have highlighted the challenges that are encountered during breast cancer detection. Nousrat and colleagues[13] highlighted challenges such as the limited availability of high-quality labeled datasets, ethical constraints, and the need for models that generalize better to real-world, complex medical datasets. For example, the effectiveness of an AI system in segmenting a specific biological structure found in a WSI depends heavily on the accuracy of the reference annotations made by experienced pathologists in the learning set. The study of Doyle *et al.*,[110] who created an ML-based AI technique to automatically identify locations of prostate cancer in WSIs, highlights the significance of highly selected data. An AI approach might be used to locate specific spots on the slides for later imaging with super resolution techniques, enabling the scanning of important structures and locations in the image at a much greater resolution while also generating less digitally scanned data overall. Following this strategy, Kleppe et al. employed an ML-based algorithm and reported that patients whose chromatin was homogenous had better survival outcomes than those whose chromatin was heterogeneous across several solid tumor types.[111]

Deep neural networks have been criticized for their lack of interpretability and for being less intuitive than hand-crafted networks, despite their great accuracy and simplicity of use. This could be a barrier to their use in therapeutic settings. The goal of a few studies has been to provide biological interpretability to DL tools via contemporary techniques, such as post hoc procedures or supervised ML models, to explain the results after the DL model has already made its prediction.[112,113] Because pathologists and oncologists spend much time developing these methods, engineering hand-crafted features is frequently difficult and time-consuming. Fusion techniques that integrate DL and custom strategies have gained popularity in recent years. These tactics might rely on handcrafted ML approaches for prediction after DL algorithms are used for the initial detection of cells or elements, thereby utilizing domain expertise to guarantee the approach's biological interpretability. The generalizability of the methods must be ensured via multi-institutional data before AI- and ML-based solutions are adopted in clinical settings. Training and validation sets are frequently created using the data that are available for developing an AI strategy. Examples from the categories of interest are typically evenly represented in the initial dataset, which is also known as a training, learning, or discovery set. Once the model has been trained and finalized on the learning set, it is typically validated without further optimization on a test set. This test set is either derived from the original set of cases or obtained from a different institution. Digital pathology-based companion diagnostic tests for oncologists may offer additional helpful data for disease risk classification and patient selection for specialized treatments. With a turnaround time of roughly two weeks, genomic companion diagnostic tests require the delivery of tissue to a central site. AI-based technologies will mostly be required for pathologists to identify structures or particular regions of interest in digitized WSIs. To enable short turnaround times and the capacity to control the clinical process, the digital slide scanner has thus become a crucial component in the development of such systems. Despite these difficulties and limitations, the future of AI techniques for digital pathology is encouraging. Many organizations worldwide have made the decision to digitize their whole pathology practice in recent years.

Ethical and regulatory frameworks for AI/ML are evolving, and many studies lack subgroup performance reporting, clear data-governance plans, and lifecycle monitoring. Next steps include bias audits across demographics and sites, privacy-preserving multi-site training with auditable data lineage, and change-control and drift-detection processes aligned with contemporary device AI expectations. Human factors and cost-effectiveness evaluations should accompany technical validation.

6. Limitations of using AI/ML applications in medical imaging

AI and ML systems in medical imaging face key challenges, particularly their reliance on large, high-quality datasets. Issues such as labeling errors, inconsistent imaging protocols, and a lack of diverse populations can harm model performance. Biases in training data raise concerns about fairness, as models may work well for some populations but poorly for others. Additionally, AI models are often criticized for their "black box" nature, making their predictions hard to interpret, which limits their clinical adoption. Explainable AI methods, such as layer wise relevance propagation, aim to address this issue but are not yet widely used. Overfitting is another concern, especially with small or unbalanced datasets, where models may fail to generalize to new data. This highlights the need for robust validation using large, diverse datasets. Ethical concerns also arise, including accountability when AI makes incorrect predictions and issues of patient privacy and data security. Finally, real-world integration is difficult because of the need for advanced computational resources, which are not always available, particularly in low-resource settings.

The limitations regarding data availability and the need for large, annotated datasets are particularly evident in the work of McKinney *et al*.[23] on breast cancer risk prediction via deep learning. They noted that the model's performance is contingent on the quality and quantity of training data, which remains a challenge, especially for institutions with limited access to diverse datasets.

Similarly, the lack of interpretability is a challenge highlighted in the deep learning models discussed by Dhungel *et al.*,[25] where high accuracy was achieved in classifying breast masses, but the model's decision-making process remained opaque, which poses issues for clinical adoption.

With respect to research aimed at overcoming these challenges, works such as Kim *et al*.[24] have made strides in addressing interpretability by employing weakly supervised learning techniques, which attempt to make the model's decisions more transparent to clinicians. Similarly, efforts such as those by Yala *et al.*[30] are working toward enhancing data efficiency through transfer learning and data augmentation strategies to reduce reliance on large, labeled datasets. For example, González-Castro *et al.*[31] explored integrating multiomics data with imaging to enhance predictive modeling, which attempts to address the challenge of data integration across diverse datasets. Additionally, recent efforts in explainable AI (XAI), such as those outlined in Binder *et al.*,[58] have made strides in addressing the interpretability of deep learning models, ensuring their transparency and adoption in clinical settings.

A major challenge for AI/ML models in breast cancer diagnosis is ensuring generalizability across diverse populations and clinical settings. Many models are trained on datasets that overrepresent certain groups, such as European American women, while they underrepresent others, such as African American or Hispanic women. This can lead to models that work well for some but poorly for others, raising fairness concerns. To address this, future research should focus on larger, diverse, multi-institutional datasets.

Reproducibility is another issue, as studies often use proprietary datasets and nonstandard protocols. Open-access data, standardized methods, and collaboration across institutions are crucial for overcoming this problem.

Bias in training datasets, such as an imbalance between benign and malignant cases, can lead to inaccurate and potentially harmful predictions, particularly for underrepresented groups.

7. Future prospective and conclusion

The advent of whole-slide digital scanning and the parallel expansion of DL-based neural networks for analyzing digital images of slides have propelled a surge in the popularity of digital pathology technologies. Despite the challenges and uncertainties related to regulatory measures, reimbursement, and implementation, there is growing interest within the pathology and cancer communities in the development and application of these technologies. Recent innovations include open-top light sheet microscopy, which generates 3D images of tissue samples without the need for destructive sectioning or slide preparation. To analyze and interpret these vast amounts of data, pathologists and oncologists require the assistance of AI methods.

In the foreseeable future, there is potential for the development of AI algorithms that not only support pathologists but also aim to alleviate the burden of mundane, repetitive tasks to increase diagnostic accuracy and grading. With the advent of the new era of deep learning-assisted pathology, data banking, integration, and cloud laboratories are emerging as essential elements of daily pathology practice. Furthermore, pathologists, data scientists, and enterprises are increasingly collaborating to amalgamate genomics, proteomics, bioinformatics, and computational algorithms into vast and complex clinical datasets.

This convergence of disciplines is paving the way for computational pathology to provide critical insights into disease diagnosis, prognosis, and treatment. Through this approach, computational pathology has the potential to revolutionize the field by offering a comprehensive understanding of diseases at the molecular level, thereby enabling personalized and precision medicine. Recent molecular studies further underscore the importance of integrating biological insights with computational approaches in advancing precision oncology.[116,117]

Although most studies report high accuracy and AUC values, many are based on single-institution or limited datasets, often leading to overfitting and reduced generalizability. Dataset imbalance and lack of multi-institutional validation remain significant barriers to clinical translation. Future work should prioritize open-access, annotated datasets and external validation across diverse populations to ensure reliability and reproducibility.

However, it is important to acknowledge that numerous technological and ethical challenges must be addressed to fully realize the potential of computational pathology. These challenges include ensuring data privacy and security, standardizing data formats, and developing robust and interpretable AI models. As a synergistic system, computational pathology promises to increase workflow efficiency, enabling clinical teams to share and analyze imaging data across a broader platform, thus fostering collaboration and innovation.

In this context, we critically assess the current state of research in computational pathology and outline directions for future developments. It is imperative to address the obstacles to the widespread integration of AI in cancer care to unlock the full potential of these technologies in improving patient outcomes. In summary, this research highlights the importance of embracing the opportunities and challenges presented by AI and computational pathology to advance the field and ultimately enhance patient care in oncology.

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Conflict of Interest

The authors declare that they have no competing interests.

Supporting Information

Not applicable.

Abbreviations

AI: Artificial intelligence; ML: machine learning; AUC-ROC: area under the receiver operating characteristic curve; MRI: magnetic resonance imaging; CNNs: convolutional neural networks; SVM: support vector machines; HDI: human development indices; WHO: World Health Organization; IARC: International Agency for Research on Cancer.

CRediT Statement

Zamart Ramazanova: Drafted the review paper. **Bakhyt Matkarimov:** Coordinated the team. **Zhanas Baimagambet, Yeldar Baiken, Bauyrzhan Aituov, Askhat Myngbay** and **Arshat Urazbaev:** Helped collect data and Draft the review paper. **Zamart Ramazanova, Yeldar Baiken, Askhat Myngbay** and **Arshat Urazbaev:** The lead authors have final responsibility for the decision to submit the manuscript for publication. All authors reviewed the manuscript.

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