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Artificial Intelligence-Driven Prediction and Diagnosis of Breast Cancer using Core Needle Biopsy: A Systematic Review

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***Abstract* - Innovations in artificial intelligence (AI) and machine learning have profoundly impacted breast cancers researches, especially in the area of core needle biopsy specimens analysis for diagnostic, histopathological characterization, treatment effectiveness prediction, and tumor prognosis risk stratification. Some researches have gave evidence that deep learning algorithms that analyzed digital histopathology whole-slide images from core needle biopsy tissues could effectively perform tumor identification, subtype classification and pathological complete remission prediction after neoadjuvant chemotherapy, when used alone or in combination/ with complementary imaging methods such as mammography, ultrasound, and magnetic resonance imaging. Besides, AI-based techniques have been highly effective in distinguishing breast lesions that are morphologically similar in biopsy samples, enhancing the reproducibility of histological grading, and addressing the variability between individual pathologists. Besides this, machine learning methods that combine biopsy-derived characteristics with structured clinical data and molecular information have been very helpful in improving the prediction accuracy and helping to plan personalized treatment.. Detailed literature review papers reflect the pros and cons of implementing AI in biopsy-based clinical workflows such as data heterogeneity, improving the prediction accuracy and helping to plan personalized treatment.Detailed literature review papers reflect the pros and cons of implementing AI in biopsy-based clinical workflows such as data heterogeneity, limited tissue sampling, model interpretability, generalizability, and need for strong clinical validation. On the whole, existing studies are strongly in favour of AI being increasingly used as a decision-support tool in core needle biopsy based breast cancer assessment but also underline the need for large-scale, multi-center studies and prospective validation for dependable clinical translation.**

Keywords: Breast cancer; Core needle biopsy; Diagnostic accuracy / Concordance; Artificial intelligence; Deep learning; Radiomics; Digital pathology Neoadjuvant chemotherapy.

I. INTRODUCTION

A. Background

Breast cancer ranks as the most commonly diagnosed type of cancer among women globally and remains one of the top causes of cancer deaths yet the number of deaths has been significantly reduced due to the development of new diagnostic and treatment methods. An early and precise

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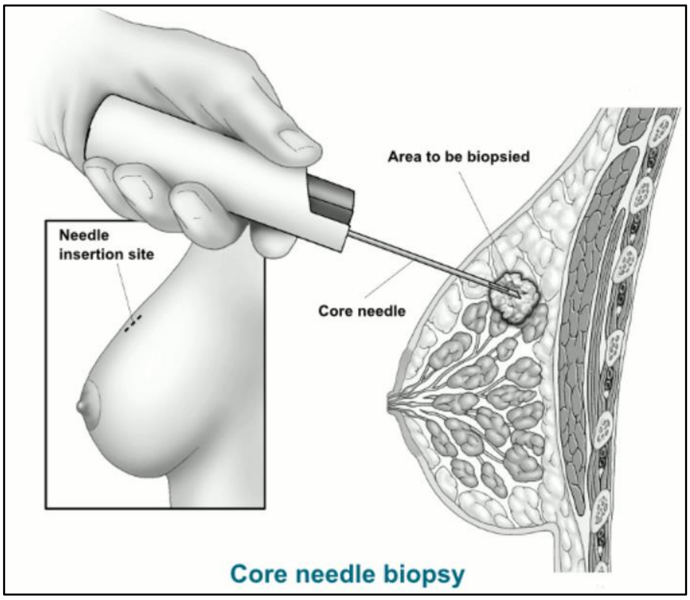

diagnosis is very important for effective treatment and better results. Core needle biopsy (CNB) is the main method of sampling tissue for histopathological diagnosis in a minimally invasive fashion. On one hand, the core needle biopsy (CNB) remains an invaluable clinical tool. On the other hand, the correct diagnosis of CNB specimens is not a simple task at all. Small tissue volume, sampling error, tumor heterogeneity, and staining inconsistency are some of the reasons that may lead to the loss of diagnostic accuracy and reproducibility. The differences in pathological interpretation resulting from these human factors can be so significant as to result in a completely different diagnosis or a postponement of clinical decisions. Since conditions diagnosed by biopsy are mainly used to tailor personalized treatment regimens, the availability of objective and reproducible diagnostic tools is a must. [3] [8] [11]

Artificial intelligence (AI) and machine learning (ML) have come a long way in recent years - these are the main reasons why we now have many new ways to tackle the above challenges. Using deep learning techniques for analyzing digital histopathology whole-slide images related to core needle biopsies, researchers have achieved good results in identifying tumours, classifying subtypes, helping grading, and even predicting pathological complete response after neoadjuvant chemotherapy. Similarly, AI-based examination of other imaging methods and the combination of clinical and pathological information have significantly improved our ability to diagnose and prognosticate. [10][13][17][14][18][22]

Despite some very promising results, AI-based biopsy analysis has seen only a limited clinical translation so far. The performance reported in the studies varies a lot because of differences in dataset size, annotation strategies used, pre-processing pipelines, and evaluation metrics. Besides, many models are trained on single center or retrospective datasets, which leads to robustness and generalizability concerns across institutions and patient populations. These problems highlight the necessity of well-validated biopsy-based AI systems that can be used with confidence for clinical decision-making in breast cancer diagnosis. [15] [19] [24] [16] [21].

B. Statement of Problem

Even with huge progress in breast cancer diagnostic techniques, interpreting core needle biopsy (CNB) specimens, is still a major challenge. This is due to the fact that only a small amount of tissue is sampled, tumour heterogeneity, sampling variability, and staining inconsistencies. In particular, these restrictions frequently cause inter-observer differences, inconsistencies in diagnosis, and postponement of clinical decisions, most especially in difficult cases. AI-based deep learning models have been able to help biopsy analysis however their clinical use is very limited due to their inconsistent results in different studies, dependence on single-center retrospective datasets, and absence of standard methods for preprocessing and validation. Therefore, a robust AI framework, mainly focused on biopsy, is of utmost importance to improve diagnostic accuracy, reproducibility as well as generalizability across different institutions and patient populations.

C. Purpose of the Research

The main aim of this research is to propose an AI-based system that can provide precise and dependable analysis of breast core needle biopsy (CNB) whole-slide images (WSIs). The objective here is to increase diagnostic accuracy by combining deep learning techniques with sophisticated image pre-processing and feature extraction tools, such as convolutional neural networks (CNN), textural analysis, and stain normalization procedures. The system will help pathologists not only in identifying tumours but also in tumour grading and molecular subtype classification, which are bound to result in better treatment planning and clinical outcomes for patients. [10] [13] [17] [14] [18] [22]

Besides, this research also aims at overcoming the limitations of existing AI models by enhancing the robustness and generalizability. Standardized data augmentation, evaluation of multi-center datasets, and rigorous validation strategies to reduce bias and prevent over fitting will be the ways to achieve this. The research is also geared towards reducing variability between observers and improving reproducibility, thereby leading to more consistent diagnostic decisions in breast cancer pathology.

The authors of this study also plan to examine how the combination of clinical and pathological metadata with image-based AI analysis can be used to create a comprehensive diagnostic support system. The authors of the study intend to combine image features with clinical variables such as age, hormone receptor status, and tumour markers so that the framework can be used to make prognostic predictions with greater accuracy and to make recommendations for personalized treatment. The integration of different modalities is expected to make the results of AI research more accessible and acceptable to clinicians, thereby facilitating the widespread use of AI in pathology. [14] [18] [22] [10] [13] [17]

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II. LITERATURE REVIEW

[1] One reason why core needle biopsy (CNB) of ductal carcinoma in situ (DCIS) frequently underestimates it is due to the missing invasive component and the current limited performance of clinic pathological and imaging based predictors that lead to the necessity of dependable preoperative modeling. [2] Lymph vascular invasion (LVI) is the major prognostic factor that is linked to tumor recurrence/local and metastasis; however, the identification and incorporation of LVI in the prognostic models is inconsistent which explains the considerable improvement of the models needed to accurately predict the prognostic value of LVI. [3] The major risk factor for breast cancer is breast density without quite a clear histological basis, at the same time, machine learning provides the way to quantitatively characterize morphological changes that are not feasible by the pathologist visually. [4] Although core needle biopsy (CNB) is our standard method for obtaining diagnostic tissue in female breast cancer, the level of accuracy of CNB in diagnosing male breast lesions is still uncertain because of their rarity which is why the importance of very careful sampling and follow-up is emphasized. [5] An excellent prognosis is predicted by a pathological complete response (pCR) to neoadjuvant chemotherapy (NAC). However, pathology remains the reference standard for pCR assessment and none of the imaging modalities is sufficiently reliable, while the reliability of core needle biopsy (CNB) after NAC remains a subject of debate. [6] The main limitation of conventional breast cancer diagnosis relying on pathological assessment is the high level of subjectivity whereas machine learning based diagnostic approaches have the potential of providing higher diagnostic accuracy by recognizing and analyzing very complex patterns of images that humans cannot perceive. [7] As a surrogacy of the multigene assays, immunohistochemical (IHC) based surrogate markers are suitable nevertheless the discordance between biopsy and surgical specimen may lead to the change of subtype classification and hence an impact on the disease outcome. [8] Despite the fact that CNB is widely used, very little evidence exists proving that CNB is superior to FNAC, therefore the necessity of performing diagnostic studies comparing these two methods becomes very evident. [9] Machine learning based on the radiomics approach not only assists the radiologist in accurate assessment of lesions, but also helps better categorize of BI-RADS and reduction of benign biopsies. [10] Digital pathology and artificial intelligence have the capability to overcome the challenges of the conventional histopathology, but the first generation of the algorithms suffered from the lack of big annotated data sets, validation and limited diagnostic capability. [11] Inevitably, there is a lack of standardization in methodological designs in breast cancer machine learning studies, and besides, such studies are often constrained by limited datasets, class imbalance, inconsistent metrics, and lack of external validation.

[12] Deep learning techniques have a lot of potential in the field of digital pathology. However, due to the great similarity in the appearance of fibroadenoma and phyllodes tumor, it is still very difficult to differentiate the two on CNB. [13] While CNB is the standard method in developed countries, its costly nature means it cannot be widely used in LMICs. As a result, the development of low-cost biopsy methods that are validated has been a priority. [14] The rate at which HER2 results on CNB match those of surgery is very much dependent on different factors. Considering the HER2-low category, it changes the examination for the cases that were previously negative according to the current cutoff. [15] High costs of CNB in LMICs are the major reason for the increased use of affordable biopsy methods that deliver accurate diagnostics without expensive systems. [16] Very little is known about how effective biopsy techniques used before surgery are in diagnosis because almost all studies are done on surgical specimens. [17] The rate at which breast cancer is found following the diagnosis of atypical ductal hyperplasia is highly varied, so it makes sense that things such as prediction tools might be used to decrease the number of unnecessary operations. [18] The bimodal AI systems that are capable of utilising pathology images along with clinical data give rise to breast cancer prediction performance that is at a higher level than that achieved by earlier single-modal methods. [19] Innovations in AI have helped to better detect classify predict treatment response to, and analyze the outcomes of triple-negative breast cancer through the mining of large datasets. [20] The level of androgen receptor expression might be very significant in the case of breast cancer, especially in TNBC. However, the assessment of these cases, as well as that of CNB, has not yet been standardized, and accuracy has not been examined. [21] The prediction models for DCIS upgrade that were developed at the time were based on either basic imaging techniques or deep learning methods, and their accuracy was quite limited.

[22] Since the diagnostic accuracy of FNAC varies greatly, especially for the nodules that are indeterminate, researchers have been evaluating CNB as a possibility. [23] Using antithrombotic drugs, patients undergoing CNB face a risk of bleeding which is still a matter of debate however recent studies have come up with solutions by using large multicenter data. [24] US-guided CNB well serves the purpose of the sampling of the axillary lymph nodes but still, a systematic review of the comparative study with FNA is required.

[25] Leveraging AI to analyze longitudinal axillary ultrasound data could potentially not only predict the response of a patient after NAC better but also help in less invasive staging. [26] Creating AI-based histopathology is very dependent on having large, quality, and well-annotated datasets however the existing public datasets are known to be biased and not very reproducible. [27] Applying deep learning on HE-stained biopsy images could get us digital biomarkers of early chemotherapeutic response (NAC) which combined with clinicopathological data, would considerably increase the power of the prediction. [28] Radiomics and machine learning are non-invasive tools for Ki-67 prediction; however, the role of features outside but near to the tumor has to be investigated. [29] Despite the limited patient cohorts and validation, deep learning radiomics in conjunction with clinical data significantly enhances the non-invasive prediction of axillary lymph node status. [30] Observers hardly agree on Nottingham grading, especially in the case of biopsies, which necessitates a deep learning approach to be used for early grading. [31] Genomic tests help in understanding the risk of recurrence

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though there is hardly any evidence that these tests can predict axillary involvement which would then lead to imagining and personalizing the surgical treatment. [32] Managing LCIS on CNB continues to be a puzzle for clinicians as the risks of progression to invasive carcinoma have not been consistently reported and LCIS resembles atypical lobular hyperplasia on many occasions. [33] Studies on CNB accuracy are comprehensive, but fare exceptionally low in terms of performance comparison across hospital services.

The latest AI technologies have made a big impact on breast cancer diagnosis in various radiology and pathology modalities such as mammography ultrasound MRI, and histopathology. Analyzing whole-slide images without manual labeling can help reduce bias and annotation burden of neural network-based response prediction models for neoadjuvant chemotherapy (NAC). Though triple-negative breast cancer (TNBC) diagnosis mainly uses core needle biopsy (CNB) and MRI, very few researchers have combined MRI features with machine learning for predictive modeling. Current histopathological AI systems face challenges on extracting global features and working efficiently as they are very complex models. There is still biomarker inconsistency between CNB and surgical specimens especially for hormone receptors and molecular subtypes. Even though the significance of HER2-low tumors is increasing, there is still insufficient evidence on the accuracy of CNB for these tumors. The Wisconsin Breast Cancer Diagnostic dataset is commonly used as a machine learning benchmark for classifying breast tumors.

III. OBJECTIVE

A. *Main Objective:*

The key goal of this research is to thoroughly review and integrate prior investigations on employing AI and machine learning methods for breast cancer diagnosis and prediction, especially using mammography, core needle biopsy, histopathology, and multi-modal imaging data. With this review, the authors intend to assess the diagnostic precision, predictive effectiveness, and clinical dependability of AI systems on various datasets and at the same time pinpoint the drawbacks, inconsistencies, and obstacles that hamper their practical clinical usage.

B. *Specific Objectives*:

- To assess different AI models and deep learning frameworks in breast cancer detection and diagnosis- Research AI implementations in breast biopsy and imaging such as CNN-based models, radiomics, and ensemble learning.
- To compare, evaluate datasets and diagnostic methods- Debate the advantages and disadvantages of public datasets (e.g. Wisconsin Breast Cancer Dataset) and clinical datasets obtained from core needle biopsy ultrasound MRI, and histopathology images.
- To look at diagnostic accuracy and prediction outcomes in different papers- Assess results of lesion classification, BI-RADS prediction, HER2 status detection, lymph node metastasis prediction, and pathological complete response (pCR) prediction.
- To find reasons for limitations and discrepancies between biopsy and surgical findings- Explore, for example, the phenomenon of biopsy underestimation, the discordance between core needle biopsy and surgical specimen, and the risk of malignant upgrade.
- To investigate challenges for clinical applicability and integration of AI in breast cancer workflows- Analyze studies of AI validation in real-world, ethical issues, and clinical limitations for AI implementation in breast screening and diagnosis.

IV. METHODOLOGY/ SURVEY FRAMEWORK

It goes without saying that core needle biopsy remains the gold standard for breast cancer diagnosis, since it can provide samples of cancer cells, tissue architecture and their environment. The earliest cores were examined using conventional methods like hematoxylin and eosin-stained sections viewed under a microscope. Still, in a big data era, we can leverag the multi-modal properties of breast cancer like a cluster of cell types, immune profiling, tumor morphology, genomic alterations, proteomic characteristics, and other forms of tumor heterogeneity. Numerous other methods that focus on specific tumor features have been developed to diagnose breast cancer.

A. *Literature Identification and Selection*

The content was gathered from a wide view of academic journals - articles that examined old cases, followed patients over time, compared different testing methods, or reviewed findings about the use of needle biopsies for detection and prognosis of breast cancer. These studies touched on statistics, traditional algorithm-based tools as well as recent neural networks, all utilized on tissue slides, imaging data, and integrated patient records.

Core needle biopsies were examined in some studies as a diagnostic tool in conjunction with surgery, while others investigated the potential of these biopsies to provide data for various prediction models such as CNNs SVMs random forests, combined models, or mixed-method setups [1], [3], [9], [10], [18], [27].

Review papers were part of the selection as well - these allowed for the identification of frequently used methods, shortcomings, and recurring patterns in different datasets [11], [24], [26].

B. *Inclusion and Exclusion Criteria*

Some studies made the cut by meeting just one of these conditions

1) Doctors were able to determine the type of breast cancer by examining a tiny piece of tissue. Using the same piece, they figured out the speed of the cancer growth. The laboratory carried out tests for certain

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markers to classify it into a category. Results yielded some predictions about the future as well.

2) Accuracy, sensitivity, and specificity are figures that indicate the degree of the model's success. They also examined performance by using AUC scores along with concordance values. Kappa statistics help understand how much two things agree beyond mere chance. Each metric shows results from a slightly different angle. Such measures allow the comparison between models in a standardized manner.

3) Works stat has, ML, or deep learning methods that should have been used on tissue slices, scans, or patient files taken from biopsies. Even though the individual methods were different, repeating models under newly altered conditions again and again brought about common features of datasets.

Re-examining old cases while also monitoring new ones contributed to molding the evaluation, extracting information either from a single hospital or from multiple ones [4], [5], [7], [14], [24]. Studies that compiled the previously obtained results or simply described the ways in which AI was used have helped in locating the current achievements as well as the difficulties which are yet to be addressed [11], [26], [34].

Some studies were excluded because there was no information about tissue samples from biopsies. Also, articles that lacked the essential diagnostic or predictive details were excluded. Only research based on surgical samples was considered if the core needle biopsy was part of the procedure. Patient case reports, personal views, and incomplete descriptions of the methods? They were removed as well [11], [26], [34].

C. Data Extraction

Sequentially, the qualifying papers revealed preparations methodologically one by one. Study layout was leading the way, then how many people took part, followed by their medical profiles. Rather than just naming tools, detailed information about the kind of scan or tissue check used was carefully recorded. The manner in which data features were extracted had a significant impact - hence it was documented as well. Since result analysis techniques help in forming understanding, those methods have been included. Artificial Intelligence (AI) used concept was reflected in the records as the model's blueprint. Training routines were presented along with testing plans. Data group splits varied, but each division was documented. Performance statistics, once made available to the public, were incorporated here as well [3], [9], [10], [12], [27], [29].

Measures such as diagnosis agreement, post-surgery changes in diagnosis, matching of biopsy and operation samples, and molecular type consistency, among others were recorded [7], [8], [14], [38], [39].

Certain papers listed limitations - few patients, use of only historical data, lack of external validation, problems with interpreting results - which also got documented for reference [1], [5], [12], [18], [34].

D. Comparative Analysis Strategy

A comparative study was done to evaluate trends and variations in methodologies. Statistical and conventional machine learning methods were compared with deep learning and multimodal fusion models in terms of prediction efficacy, robustness, and clinical readiness [2], [6], [9], [27], [36]. The diagnostic accuracy of CNB has been verified across several clinical situations, such as the detection of invasive cancer, the involvement of lymph nodes, molecular subtyping, and the prediction of treatment response [4], [5], [14], [24], [31].

Particularly emphasized was how the size and diversity of the dataset, as well as the method of validation, affected the results communicated. Besides, the consistent tendency of hybrid models combining clinical and imaging characteristics to outperform single-modality methods was highlighted [18], [27], [29], [35]. The comparison of limitations like inter-observer variability, domain shift, and no use of external validation helped in pinpointing the enduring challenges and areas of research still needing focus [11], [26], [34].

Figures and Tables

Ref. No.	Study Focus	Data / Modality	Methodology/ Model	Key Performance Metrics
4	CNB diagnostic accuracy	US-guided CNB vs excision	Retrospective diagnostic accuracy analysis	Accuracy 99.6%, Sensitivity 98.9%, Specificity 100%
9	BI-RADS classification	Breast ultrasound radiomics	Ensemble SVM (majority voting)	Sensitivity>94%,PPV↑,↓ unnecessary biopsies 15–18%
10	Invasive carcinoma & DCIS detection	Whole-slide histopathology images (H&E/HES)	CNN ensemble (Inception + ResNet)	AUC > 0.98, high sensitivity & specificity

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13	Low-cost biopsy validation (LMICs)	Vacuum-assisted CNB	Diagnostic accuracy evaluation	Accuracy 92.98%, Sensitivity 92%, Specificity 100%
15	Frugal VACN Btechnique	CNB(low-cost system)	Prospective diagnostic study	Accuracy 92.98%, PPV 100%
18	Axillary LN metastasis prediction	WSI+ clinic pathological data	Multimodal MIL-based deep learning	AUC0.809,outperforming single-modality models
24	Axillary LN diagnosis	US-guided CNB	Systematic review &meta- analysis	Sensitivity0.90,AUC 0.98, Specificity 0.99
25	NAC response prediction	Longitudinal ultrasound radiomics	SVM fusion model	AUC0.899,Accuracy↑to 79.2%
29	Axillary LN metastasis	US radiomics + clinical factors	Deep learning radiomics nomogram	AUCupto0.95(external validation)
30	Tumor grading (NHG)	Biopsy whole-slide images	CNN ensemble (DeepGrade)	AUC≈0.91,significant prognostic stratification
35	Image–clinical fusion	Imaging + clinical metadata	Deep learning fusion model	Accuracy 92.3%, performance dropped

V. DISCUSSION

A. Performance Trends Across AI Models

It is clear from looking at previous research how far we have come - the transition from traditional machine learning techniques to advanced deep learning tools when detecting breast cancer. Not very long ago, simple classifiers achieved relatively good results but faced difficulties mainly because they were dependent on manually selected features and had weak pattern recognition capabilities [6 11 37, 40]. So what happened? It was the neural networks that analyze images and tissue samples which started identifying complex shapes and structures independently, thus outperforming the older techniques [10 12 18 27 30]. Nevertheless, results vary widely - different architectures, types of data, methods of testing continue to make results inconsistent [11,26]. When multi-modal data sources and state-of-the-art models combine, they outperform single modality model setups every time - although there is still a lot of variation in working across the board [18 27 37].

B. Influence of Dataset Size, Diversity, and Quality

Comprehensive sets of varied and thoroughly labeled examples determine a major factor in the performance of artificial intelligence systems. Often, a small dataset from a single location is used in research that causes the system to memorize instead of learning, and the results become less transferable to other areas [11 26 29]. Publically available data that are used to assess models vary considerably - while some have very thorough information, others lack vital details or have images of poor quality; all these aspects result in tests yielding very different outcomes and also pose difficulties in trying to repeat them [26,40]. Insufficient labeling, unequal proportions, and lack of verification by independent sources are some of the major obstacles that these AI tools continue to face before they can be used in real medical environments [11 26 29]. What is increasingly evident is that robust, reliable AI requires a vast, diverse, and well-documented data source.

C. Role of Transfer Learning and Data Augmentation

Generally, obtaining meaningful results from small breast cancer image datasets depends heavily on transfer learning of pre-trained models. When one re-uses older network architectures, they usually extract the most distinguishing features with greater ease, require less training time and eventually achieve higher accuracies. These improvements are strongly measurable in operations like determining tumor stages, assessing responses to chemo, and classifying microscopic tissue types [18 27 30 35 37]. Performing a controlled transformation of the data helps the model to better deal with unbalanced distributions and to be less sensitive to noise [11,28]. Incorporating prior knowledge and re-processed data together results not only in a reduction of annotated data requirement, but also in a very promising performance in limited data scenario such as biopsy or histopathology images [27,35].

D. Interpretability and Clinical Applicability

Doctors often stall even when AI makes accurate predictions because the inner workings stay hidden - like a black box with no clear path to answers. Instead of logical steps, the models spit out results based on code they don't explain. In areas like tissue review and scans, clinicians need to trace decisions step by step. Adding real-world patient info helps ground the

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machine's findings in something tangible. Trust builds not just from being right, but from fitting inside built thinking. Tools that mirror how experts normally decide feel less foreign over time. When tech adapts to current practices instead of forcing change, it slides into workflows easier. Clarity isn't secondary, it's just as vital as precision here.

E. Limitations and Future Challenges

Results vary widely due to inconsistent sample divisions and patchy tracking protocols across departments [11,26,29]. Some labs catch things others miss, leading to erratic model outputs during cross-test evaluations [1,7,14,38]. Centralized workflows among medical centers, uniform auditing processes. Openly shared datasets built on strict norms could shift outcomes [26]. What matters more than individual tech upgrades is combining patient images, clinical logs, and clear algorithm designs through repeated analysis [18,25,27,29]. That said, progress ends up being messy without alignment across teams.

VI. CONCLUSION & FUTURE SCOPE

A. Conclusion

Decisions about treatment severity often rely on outdated data from single hospitals. That information tends to date back years, feature limited patient groups, or skip external validation steps. Even as algorithms can now review tissue slides, tumor images, and lab outcomes to catch key signs of cancer progression and possible drug responses, the tools don't yet operate evenly across care centers. So far, digital analysis supports doctors in the lab but doesn't show strong performance in daily clinical settings. In the end, broader testing and reliable standards are needed for true adoption. For now, trust still rests heavily on small-scale studies

B. Future Scope

Through combining scans, tissue samples, medical records. Genetic signs, researchers aim to create sharper forecasts for diseases. As it happens, tracking patients over years in multiple hospital settings helps build stronger patterns. With models showing step-by-step logic, clinicians can trust the outputs more easily. In real-world clinics, tools must prove reliable under daily pressures. That said, fairness and safety end up being just as vital as hitting high accuracy levels.

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