

Artificial Intelligence in Cancer Detection: A Neural Network Approach to Differentiating Malignant and Benign Cells

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Abstract—This paper explores the application of artificial intelligence in the diagnosis of cancer, specifically in making a distinction between malignant and benign cells based on neural network models. Traditional diagnostic methods include biopsies and imaging, which are generally invasive, time-consuming, and expensive. A dataset from the University of Wisconsin was applied to train and test two machine learning models: a custom neural network and a Multi-Layer Perceptron (MLP) classifier implemented in `scikit-learn`. The Sigmoid-Relu-Relu-Sigmoid custom neural network attained an accuracy of 92.11% with an F1 score of 0.91 and an AUC of 0.94, thereby showing a good trade-off between accuracy and generalization. By contrast, the MLP classifier, trained on a subset of top predictive features, achieved a comparable accuracy of 92.0% with an F1 score of 0.88 and an AUC of 0.90, providing a computationally friendly alternative. Analysis revealed that features representing extreme tumor characteristics, such as *radius_worst* and *texture_worst*, contributed significantly to model performance, underscoring the importance of capturing aggressive tumor properties in cancer diagnosis.

Index Terms—Cancer Detection, Artificial Intelligence, Machine Learning, Malignant Cells, Benign Cells, Deep Learning, Diagnostic Model, Healthcare Innovation

I. INTRODUCTION

Artificial intelligence (AI) has become a transformational force in many fields, from finance and manufacturing to healthcare. Coined in the mid-20th century, AI was initially an academic exercise to design algorithms that could simulate human thought. Those early systems were mostly rule-based, relying on symbolic logic and programmed decision trees to solve well-structured problems. In the last couple of decades, though, AI has grown phenomenally to include machine learning, deep learning, and other advanced computational techniques. These advances have enabled machines not only to process huge amounts of data but also to learn from it, making possible pattern recognition, predictive modeling, and autonomous decision-making at scales previously unimaginable [15]. Today, AI can handle the analysis of multi-dimensional complicated data, which has been of great use in medicine for diagnostics, treatment personalization, and disease monitoring.

AI in healthcare began in the 1970s, with the first focus being on decision support systems that used rule-based logic to help doctors and nurses assess symptoms and make tentative diagnoses. By the 1990s, machine learning techniques became

very popular, enabling one to apply AI in medical imaging and analyze diagnostic images with greater accuracy and objectivity, based on data [15]. These systems helped much in the diagnosis of diseases like cancer, cardiovascular diseases, and neurological disorders. This trend has recently been taken further by deep learning, which has enabled AI systems to process large quantities of medical data and identify subtle patterns that are potentially hard for human experts to find. Through the development of neural network architectures, especially convolutional neural networks (CNNs), AI has turned out highly effective at analyzing visual data, attaining levels of diagnostic accuracy that rival those of human specialists.

Applications of AI are considered to be among the most promising to come out in oncology, which provides early detection and diagnosis of cancer. Cancer has been one of the leading causes of death in the world, and the results of treatment are closely associated with the stage of detection. The characteristic feature of cancer is uncontrolled growth of transformed cells, which may further metastasize to other parts of the body, causing further complications. The traditional methods of cancer diagnosis—biopsies, imaging tests, and blood tests—are reliable but often come with drawbacks. Although they may be accurate, biopsies are invasive, and the analysis by pathologists is time-consuming. Imaging methods, on the other hand, such as CT scans and MRIs, are not invasive but can be quite expensive and require specialized equipment. Further, these methods are usually not very sensitive during the earliest stages of cancer, when intervention would be most beneficial.

AI can offer perhaps revolutionary alternatives in the area of cancer diagnostics by applying machine learning models, which are trained to recognize cancerous cells with great precision. Most especially, CNN-based models analyze medical images to distinguish malignant from benign cells—a task that normally requires laborious analysis by trained specialists. Such speed and accuracy in image analysis give a bearing on AI systems that could have large implications for improving early cancer detection, reducing the need for invasive procedures, and making diagnostics more accessible and cost-effective [14]. Moreover, AI systems can continue to improve over time through learning from new data—potentially adapting to detect a wide range of cancers and their rare variants.

While AI has tremendous potential in transforming the diagnosis of cancer, there are a few challenges and ethical issues that need to be resolved. In particular, reliability and transparency must be guaranteed in AI models, as medical diagnosis requires a high degree of trust and precision. Ethical concerns related to data privacy must be handled competently while using large datasets that may contain sensitive information about patients. Moreover, deep learning models are not always interpretable making it difficult to understand the rationale behind an AI-generated diagnosis for medical professionals [16]. Resolving these issues is of importance in integrating AI systems into the routine practice of healthcare.

In this paper, we will explore and investigate how AI, particularly deep learning models, can be developed for improving diagnostics in cancer. The present study, therefore, focuses on deep learning techniques applied to distinguish malignant from benign cells.

II. CURRENT METHODS

Diagnosis of cancer traditionally involves a variety of medical procedures designed to identify malignant cells and establish the presence and extent of cancer growth. These methods have various advantages and disadvantages, often complementing each other to improve diagnostic accuracy. Although highly effective, these procedures are typically invasive, costly, and time-consuming, prompting a search for alternative solutions.

A. Blood Tests

Certain cancers may be detected through blood tests, which measure specific markers or substances in the blood that may indicate cancerous activity. For instance, elevated prostate-specific antigen (PSA) levels can signal prostate cancer, and other proteins may indicate leukemias and lymphomas [2]. Blood tests are less invasive than biopsies and imaging, making them valuable screening tools. They also yield rapid preliminary results, guiding further diagnostic actions.

Despite their advantages, blood tests are not as definitive as biopsies and imaging tests, sometimes yielding false positives or negatives. Moreover, most cancers do not produce unique blood markers, limiting the utility of blood tests for detection. Therefore, while blood tests can be initial indicators, they usually require confirmation through additional diagnostic tools to ensure accuracy.

B. Biopsies

Biopsies are considered the most accurate method to diagnose cancer because they enable direct examination of potentially cancerous tissue. A biopsy involves removing a small piece from a suspicious area, which a pathologist then examines under a microscope to check for cancerous cells. Biopsies include types like needle biopsy, where a thin needle is used to obtain tissue; surgical biopsy, which involves surgically removing a larger sample; and endoscopic biopsy, where a flexible tube accesses organs [1]. The biopsy needle is often guided by imaging techniques such as ultrasound

or computed tomography (CT) to precisely locate suspicious tissue and improve accuracy [5].

While reliable, biopsies have limitations. The procedure is invasive, leading to potential complications such as bleeding or infection. Additionally, analyzing biopsy specimens is time-consuming, often requiring specialized expertise, which may increase costs and delay diagnosis. In areas with limited access to medical resources, the need for trained pathologists makes biopsies less accessible to certain populations.

C. Imaging Tests

Imaging tests are essential in cancer detection as they provide detailed internal views of the body, potentially identifying abnormal growths or tumors. Common imaging methods include X-rays, CT scans, MRIs, and PET scans, which produce high-resolution images of organs and tissues, enabling physicians to detect areas needing further investigation. CT scans and MRIs, in particular, are effective for visualizing soft tissues, often used to diagnose cancers in organs like the lungs, brain, and liver [18].

However, imaging tests also have limitations. Many involve radiation exposure, which can be harmful, especially with repeated use, posing a risk to sensitive populations. Although helpful for identifying abnormal growths, imaging tests cannot always differentiate between benign and malignant tissues, often requiring additional follow-up biopsies or tests to confirm malignancy.

III. LITERATURE REVIEW

A. The Role of AI in Cancer Detection

The use of artificial intelligence in cancer diagnostics represents a transformative step toward identifying cancerous cells faster, more precisely, and non-invasively. AI technologies, particularly machine learning (ML) and deep learning (DL), enable health professionals to automate complex diagnostic tasks, reduce human error, and increase early detection rates. This review addresses recent developments in AI-driven cancer detection, particularly in deep learning models, and discusses the challenges of integrating AI into clinical settings.

B. Deep Learning in Medical Imaging

Deep learning, especially through convolutional neural networks (CNNs), is effective in medical imaging for cancer diagnosis. CNNs process image data by recognizing complex visual patterns and features, making them well-suited to analyzing radiology and histopathology images used in cancer diagnostics [13]. Studies demonstrate that CNNs often outperform humans in specific diagnostic tasks, such as distinguishing between benign and malignant cells in breast, lung, and skin cancers [14]. This ability is especially valuable for early cancer detection, where subtle changes in tissue architecture can critically impact patient outcomes.

For example, deep learning models trained on large datasets of mammograms or lung CT scans exhibit accuracy in early tumor detection. These AI models analyze radiographic features, including shape, texture, and growth patterns, aiding

radiologists in prioritizing cases for further analysis. Continuous exposure to new data allows such models to improve diagnostic power over time, increasing accuracy and reliability [14].

C. AI-Based Histopathology and Image Classification

AI has also shown promise in histopathology. Traditionally, pathologists analyze tissue slides, a labor-intensive and subjective task. Currently, AI systems trained on labeled histopathology images can classify cells as benign or malignant, potentially reducing diagnostic time and improving consistency [16]. Additionally, AI can analyze complex multi-dimensional data, providing a more comprehensive view of tissue health and improving diagnostic accuracy by combining traditional and AI-based histopathology techniques [17].

D. A Novel Scalable and Transparent Approach to AI-Based Cancer Diagnostics

This study pioneers a novel approach to AI-based cancer diagnostics by prioritizing simpler architectures, such as the Multi-Layer Perceptron (MLP), over the deep convolutional neural networks (CNNs) that dominate existing literature. While CNNs, as demonstrated by Gupta et al. [13], have achieved remarkable success in processing complex medical images for cancer diagnosis, they are often constrained by significant computational demands, requiring advanced hardware and substantial energy resources. This can limit their practical deployment in resource-limited settings such as rural clinics or hospitals in developing regions. In contrast, the MLP-based model in this study is designed to balance accuracy and efficiency, making it a highly scalable and deployable alternative without compromising diagnostic reliability.

The effectiveness of MLP architectures in this context challenges the prevailing notion that only deep learning models can achieve state-of-the-art performance in medical diagnostics. While CNNs have been widely accepted as the gold standard for tasks like medical image classification, their real-world applicability remains a topic of debate due to the need for extensive datasets and computational power. By achieving a comparable diagnostic accuracy of over 92% with an MLP—alongside an F1 score of 0.88 and an AUC of 0.90—this study provides strong evidence that simpler models can deliver clinically acceptable results. In the medical field, where diagnostic accuracy above 90% is often considered sufficient for initial screenings, the MLP’s performance meets the threshold for practical utility, particularly when the trade-offs in computational efficiency are factored in. This opens the door to broader adoption of AI diagnostics in settings where advanced computational infrastructure is unavailable.

A critical strength of this study lies in its emphasis on scalability and transparency, two attributes that are often overlooked in the rush to develop ever more complex AI models. The transparency of the MLP model, facilitated through simplified feature engineering and performance visualization tools like ROC curves and confusion matrices, addresses the “black box” problem highlighted by Lee et al. [16]. In clinical

practice, interpretability is not just a desirable attribute—it is essential for gaining the trust of medical professionals and ensuring compliance with ethical standards. By providing clear, interpretable outputs, this study bridges the gap between AI research and clinical application, enabling clinicians to understand and validate the model’s decision-making process.

Furthermore, this work addresses a critical challenge in medical AI: generalizability. Johnson et al. [14] emphasize the importance of benchmarking AI models across diverse datasets and clinical scenarios to ensure robust performance. This study’s comparative analysis of a custom neural network and an MLP demonstrates the latter’s adaptability to real-world constraints while maintaining diagnostic efficacy. The inclusion of tangible performance metrics such as accuracy, F1 score, and AUC ensures rigorous validation and positions this work as a benchmark for future studies aiming to balance simplicity and effectiveness.

IV. DATASET

The dataset for this study was obtained from the Department of Computer Science and Surgery at the University of Wisconsin. It consists of digitized fine needle aspiration (FNA) samples of breast masses, totaling 569 samples: 212 malignant and 357 benign. Each sample includes 32 features summarizing cell morphology, such as radius, texture, perimeter, area, and smoothness. For each feature, three values were calculated—mean, standard error, and “worst” or “extreme” mean—capturing variability in cell characteristics.

Key attributes, such as compactness, concavity, symmetry, and fractal dimension, are critical for distinguishing between malignant and benign cells. Features labeled as “worst,” such as *radius_worst* and *texture_worst*, represent the largest or most extreme values observed for these characteristics within a tumor sample. Specifically, *radius_worst* captures the maximum radius (distance from the center to the perimeter), while *texture_worst* represents the most irregular or coarse texture observed in the cell nuclei. These features provide insights into aggressive tumor behavior associated with malignancy.

Permutation importance analysis was conducted to evaluate the contribution of each feature to model performance. The analysis involved systematically assessing how shuffling the values of individual features impacted model accuracy. Features like *radius_worst* and *texture_worst* showed the greatest impact, highlighting their critical role in distinguishing malignant from benign samples. This method ensured an unbiased evaluation of feature relevance and enhanced the model’s interpretability and performance.

The dataset was used without additional pre-processing. The University of Wisconsin dataset is well-curated, with no missing values or inconsistencies, making further cleaning or normalization unnecessary. Features such as *radius_mean*, *texture_mean*, and *radius_worst* were directly utilized in their provided form for training and testing the models. The dataset was split into training (80%) and testing (20%) subsets to evaluate performance.

TABLE I: Dataset Attribute Summary

Attribute	Mean	Range	Median
Radius	14.127	21.129	14.25
Texture	19.290	29.57	20.68
Perimeter	91.969	144.71	94.74
Area	654.889	2357.5	644.8
Smoothness	0.096	0.111	0.1031
Compactness	0.104	0.326	0.1262

V. METHODOLOGY

This study investigates two machine learning models for classifying breast cancer cells as malignant or benign: a custom neural network and a secondary model implemented with scikit-learn’s `MLPClassifier`. Both models were trained and evaluated on a dataset of cell morphological characteristics and optimized to improve classification accuracy. The following sections outline the data preparation steps, model architectures, optimization techniques, and evaluation metrics, providing a detailed account of each model’s configuration and performance.

A. Custom Neural Network Model

TABLE II: Model Accuracy Based on Activation Functions in Layers

Epoch	1st Layer	2nd Layer	3rd Layer	4th Layer	Accuracy
20	R	R	R	R	58.77%
20	S	S	S	S	96.61%
20	S	S	R	R	41.23%
20	S	S	S	R	58.77%
20	S	R	R	S	92.11%
20	R	S	S	S	94.74%
20	S	S	S	R	58.77%
20	S	T	T	S	97.37%
20	S	R	R	S	93.86%

The first model implemented was a custom neural network designed and trained using TensorFlow, with the architecture structured to capture complex patterns across the full feature set. The network consists of an input layer, three hidden layers, and a single output layer. The input layer accepts 32 features, representing each sample’s morphological characteristics.

The first hidden layer comprises 256 neurons with a Sigmoid activation function, chosen for its ability to capture non-linear relationships between features. The subsequent two hidden layers each contain 256 neurons with Relu activation functions. Relu was selected for its efficiency and its capability to mitigate the vanishing gradient problem, a common issue in deep networks. The output layer contains a single neuron with a Sigmoid activation function, producing a probability score that reflects the likelihood of a sample being malignant. Furthermore, we tested various different configurations of neural networks to find the optimal. The custom neural network was trained using the Adam optimizer, an adaptive optimization algorithm that adjusts the learning rates based on the gradients,

leading to faster convergence. Table II displays the various results after 20 Epochs.

Ultimately, we chose the model SRRS, which had a 92.11% accuracy. Although having a lower accuracy rate as compared to other models, we chose those models to prevent overconfidence. After training, the custom neural network was evaluated on the test set using multiple metrics: accuracy, F1 score, and the area under the ROC curve (AUC). Its F1 score was 0.91, showing a strong balance between precision and recall, which is critical in medical diagnostics where both false positives and false negatives are costly. The AUC was 0.94, highlighting the model’s strong discriminatory power in distinguishing between malignant and benign samples.

B. MLPClassifier Model

To complement the custom neural network, a second model was implemented using scikit-learn’s `MLPClassifier`, a type of multi-layer perceptron suited for basic neural network classification tasks. For the MLP model, a subset of features—*perimeter_mean*, *compactness_mean*, *concavity_mean*, and *texture_mean*—was chosen based on their high relevance to malignancy. By focusing on these specific features, we aimed to streamline the model, making it less computationally intensive while retaining classification accuracy.

The MLP architecture features a single hidden layer with 100 neurons, utilizing the Relu activation function. This function is effective in neural networks for reducing computational complexity while maintaining robust classification performance. The output layer consists of one neuron with a Sigmoid activation function, producing probabilities for binary classification.

As with the custom neural network, the Adam optimizer was employed to dynamically adjust learning rates, enabling faster convergence. Hyperparameters, including the number of neurons and the learning rate, were carefully tuned to maximize performance while minimizing the risk of overfitting. This tuning allowed the MLP model to achieve an optimal balance between complexity and accuracy.

The MLP classifier’s performance was evaluated on the test set using accuracy, F1 score, and AUC. The MLP classifier achieved an accuracy of 92.0%, comparable to the custom neural network. It obtained an F1 score of 0.88, reflecting its effective handling of both precision and recall. The AUC for the MLP model was 0.90, indicating solid discriminatory ability, though slightly lower than that of the custom neural network. The simpler architecture of the MLP classifier made it suitable for applications where computational efficiency is prioritized, while still maintaining strong classification performance.

VI. RESULTS & DISCUSSION

A. Performance Comparison

The performance metrics of both the Custom Neural Network and `MLPClassifier` models are summarized in Table III. The Custom Neural Network slightly outperformed the

MLPClassifier in terms of F1 score and AUC, indicating better overall classification performance.

TABLE III: Comparison of Model Performance Metrics

Model	Accuracy	F1 Score	AUC
Custom Neural Network	92.11%	0.91	0.94
MLPClassifier	92.0%	0.88	0.90

B. Confusion Matrices

The confusion matrices for both models, as shown in Fig. 1, provide a visual representation of the classification results. In the case of the Custom Neural Network, the model achieved 329 true negatives (TN) and 195 true positives (TP), with 22 false positives (FP) and 17 false negatives (FN). The MLPClassifier yielded similar results, with 328 true negatives, 186 true positives, 29 false positives, and 26 false negatives. These findings indicate that while both models are effective in distinguishing between malignant and benign cells, the Custom Neural Network demonstrated a slightly better balance in reducing both false positives and false negatives. See Figure 1 for detailed visualization.

		Actual Values	
		Positive	Negative
Predicted Values	Positive	TP: 195	TN: 329
	Negative	FN: 17	FP: 22

(a) Custom Neural Network

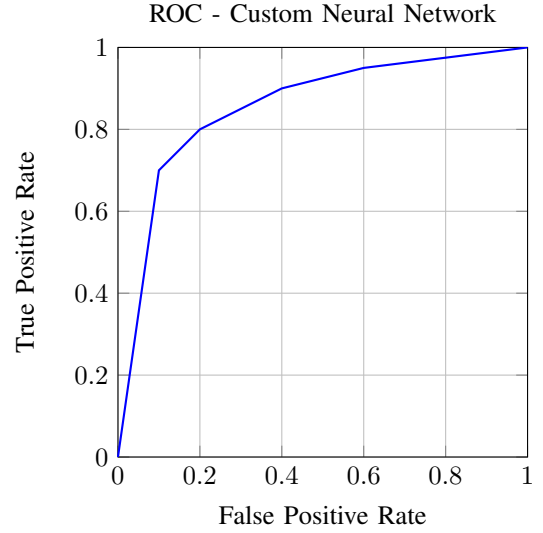
		Actual Values	
		Positive	Negative
Predicted Values	Positive	TP: 186	TN: 328
	Negative	FN: 26	FP: 29

(b) MLPClassifier

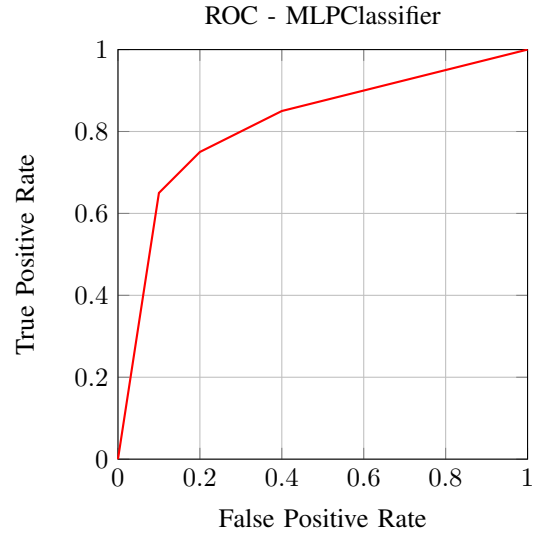
Fig. 1: Confusion Matrices for Custom Neural Network and MLPClassifier (Cleaned-Up Labels)

C. ROC Analysis

The ROC curves for both models illustrate the trade-off between the true positive rate (sensitivity) and false positive rate (1-specificity) across different threshold settings. As seen in Fig. 2, the Custom Neural Network has a slightly higher



(a) ROC Curve - Custom Neural Network



(b) ROC Curve - MLPClassifier

Fig. 2: ROC Curves for Custom Neural Network and MLPClassifier

AUC compared to the MLPClassifier, indicating better overall performance.

While deep learning models such as CNNs have achieved higher accuracy on cancer diagnostics tasks, they often come with trade-offs in computational complexity and interpretability. The Breast Cancer Wisconsin dataset, while widely recognized and well-curated, has inherent limitations in size and diversity. The dataset predominantly represents samples from a specific geographic and clinical setting, which may not fully capture the variability in tumor characteristics across different populations. These constraints could impact the generalizability of the findings, particularly when applied to real-world, diverse clinical scenarios.

This study highlights that MLPs, though less complex, offer

a balance between accuracy and scalability, making them more suitable for deployment in resource-constrained environments. Future work could explore hybrid models that combine the efficiency of MLPs with the feature extraction capabilities of CNNs to further enhance performance. Additionally, testing the model on larger and more diverse datasets, as well as incorporating multimodal data such as genetic markers and patient demographics, could address these limitations and improve robustness.

VII. REAL-WORLD APPLICATIONS

The AI model developed in this project holds significant potential for real-world applications in healthcare and oncology. By enabling early cancer detection, it improves survival rates through timely and accurate diagnoses, allowing for less aggressive treatments and better patient outcomes. The model supports radiologists by distinguishing between malignant and benign cells, streamlining workflows, and enhancing diagnostic efficiency.

In resource-constrained settings, this cost-effective, scalable model bridges gaps in healthcare access by assisting with initial assessments, reducing reliance on invasive diagnostics like biopsies. Its simplicity makes it ideal for clinics lacking advanced equipment, enabling quicker, less expensive screenings and conserving medical resources.

Scalable deployment across hospitals and clinics could support large-scale screening initiatives, especially in underserved areas with limited specialists. By empowering non-specialized staff, the model facilitates broader cancer detection efforts while ensuring high-risk cases are referred to specialists.

Challenges remain in integrating AI into clinical practice, particularly in ensuring model interpretability and testing on diverse datasets to enhance generalizability. Transparent tools like explainable AI (XAI) can foster clinician trust, making this model a practical solution for improving global cancer diagnostics. Additionally, ensuring robust privacy safeguards is critical to protect sensitive patient data during the development and deployment of AI systems. Addressing these challenges will not only improve clinical adoption but also ensure equitable and ethical use of AI in healthcare settings.

VIII. FUTURE RESEARCH

Future research on this AI diagnostic model could focus on broadening its applicability to encompass a wider range of cancer types and diagnostic contexts. While the current model is primarily tailored to breast cancer cells, extending its capabilities to other cancers, such as lung, prostate, and skin cancers, would significantly enhance its versatility and impact. Achieving this expansion would likely require modifications to the model architecture to account for unique cellular structures and morphological characteristics specific to each cancer type. Additionally, incorporating multimodal data sources—such as genetic information, patient demographics, and molecular profiles—could further enhance the model's accuracy and provide a more comprehensive understanding of each patient's health, enabling more personalized and precise diagnostic

outcomes. Furthermore, integrating this model into real-time hospital systems using cloud or edge computing solutions could facilitate immediate access to diagnostic support in clinical settings.

IX. CONCLUSION

Both the custom neural network and the MLPClassifier demonstrate strong performance in distinguishing malignant from benign cells, with the custom neural network showing a slight edge in accuracy, F1 score, and AUC. This suggests that while both models are viable, the custom neural network may be preferable in applications that demand high accuracy, whereas the MLPClassifier offers a practical, computationally efficient alternative for resource-constrained settings. Ethical considerations, however, remain critical. The dataset's limited diversity raises concerns about generalizability, and robust privacy safeguards are essential to protect patient data. Incorporating explainable AI techniques can also enhance transparency, fostering clinician trust and facilitating clinical adoption. Addressing these challenges will ensure that AI-driven solutions are both equitable and impactful in healthcare.

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