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Artificial Intelligence Models for Breast Cancer Prediction: A Comprehensive Review

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ABSTRACT

Breast cancer (BC) caused death in the worldwide, which raises the issue of the urgent essential for accurate and primary prediction. In oncology, we are seeing the rapid integration of Artificial Intelligence (AI), inclusive machine learning and deep learning, and we view this as a transformative opportunity to improve predictive analytics. This review paper looks at the present state of artificial intelligence (AI) in the prediction of breast cancer, which is the most common of all the malignancies worldwide. We examine the synthesis and analysis of recent advances, methods, and performance results for many AI models, inclusive ML and DL models. DL architectures, in particular Convolutional Neural Networks (CNNs), have achieved the best results in image-based detection tasks. Furthermore, the paper highlights that what may be the here and now in terms of performance does not diminish the value and interpretability of traditional ML models used for structured clinical and genomic data.

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1. Introduction

BC is a predominant cause of death between women worldwide. It presents in four principal forms: kindly, normal, in situ cancer, and invasive carcinoma [1]. A benign tumor causes little to no changes in the breast tissue and is not what we term cancer. In situ cancer is contained within the milk duct or lobular tissue systems and does not affect other organs. That which is in situ is not a threat and may be treated if it is identified at an early stage. Invasive carcinoma is the most aggressive form and can spread to other organs. BC detection includes Computed Tomography (CT), Magnetic Resonance Imaging (MRI), Positron Emission Tomography (PET), ultrasound (US), X-ray mammography, and breast temperature assessment [2]. The benchmark for diagnosis is pathological analysis, performed in the lab on tissue tasters that are typically stained with Hematoxylin and Eosin (H&E). A BC diagnosis can also be done via HPI analysis or genetic testing. HPI provides a very detailed look at the breast tissue and is key in early diagnosis. As reported in [3], radiogenomics is a growing field that puts together medical imaging with gene expression data from many scales, which in turn gives both radiological and genetic information to improve diagnosis. It looks at tissue at the molecular level to better predict and detect [4]. The main issue is that imaging provides tissue-level data, whereas radiogenomics provides molecular and genetic markers, which are more accurate [5]. Also, despite its value, radiogenomics is not widely used due to high cost and heavy computing requirements, which in turn limit it to a few labs. This study examines DL models for BC detection, evaluates their performance, the datasets used, and their diagnostic and classificatory value. Although we have seen progress in medical imaging and therapy, there remains a large-scale barrier to early and accurate diagnosis. Although some of the best of today’s AI models are very accurate, they also lack in the area of transparency, which is a major issue for the medical community [6]. Seeing recent progress in what we term Explainable AI (XAI) tools, like SHAP and Grad-CAM, which are very important in trying to bridge this gap. This review examines the performance of the latest models as well as their interpretability, with an eye to their clinical application. Our main focus is that BC affects millions every year and is seeing an increase in cases across age groups. Also, what we see is that traditional diagnostic tools like mammography fall short at times, which we see in the case of dense breast tissue that leads to missed or delayed diagnoses [7]. What we see from the use of DL in medical imaging is that it is transforming the way we do accurate analysis of complex high-dimensional data. What these techniques do is to reduce human error, improve diagnostic reliability, and also enhance overall efficiency. At the same time, present screening tools do have their pros and cons. What is important is a variety of approaches to put forth the best strategies for the detection of BC in an effort to improve diagnostic quality. We see innovations like transfer learning (TL), hybrid DL models, and also XAI as key to improving diagnostic accuracy, while at the same time, we address trust and interpretability issues, which are key for clinical integration. By putting in place these advanced tech solutions in the clinic, we hope to see improved early detection rates, thus saving many lives, and in the process, transforming the way we treat BC.

2. Related Reviews

Many papers have been conducted on BC prediction using imaging or during genomics. But, to the best of our information, no studies have been led with both methods.

In [8] introduce a study that is used to predict and classify BC into two groups utilizing the Wisconsin Diagnostic Breast Cancer (WDBC) feature set, and to select the strong features to achieve accurate and reliable classification. This research discovers automatic BC prediction via multi-model features and ensemble ML (EML) methods. An advanced ensemble method combining boosting, stacking, voting, and bagging is used to train the classifier in the suggested EML models and to discriminate between cancerous and noncancerous cases. Where, the feature extraction phase, propose a recursive feature elimination method to determine the significant features of the WDBC that are pertinent to BC prediction and classification.

In [9], the authors planned a new architecture for BC detection. This architecture usages CNNs and image-processing. An efficient, fast CNN-based architecture, RetinaNet, has been utilized in this research. RetinaNet is an uncomplicated one-stage object detector. Two-stage TL has been applied to the selected detector to improve performance. The RetinaNet model is initially trained on the COCO dataset. The TL is then utilized to excute the RetinaNet model to the CBIS-DDSM dataset. Finally, the second TL approach is utilized to assess the RetinaNet model on the INbreast dataset.

The Wisconsin Breast Cancer Dataset (WBCD), sourced from the UCI ML source, has been utilised as a training set to assess and compare the performance of various ML models. The authors in [10] used 11 types ML classifiers, such as random forest (RF), gradient boosting (GB), K-nearest neighbours (K-NN), Decision tree (DT), support vector machine (SVM), Naïve Bayes (NB), logistic regression (LR), AdaBoost (AB), Multi-layer Perceptron (MLP), Nearest Cluster Classifier (NCC), and voting classifier (VC), for comparison and evaluating BC into cancerous and noncancerous.

The researcher in [11] introduces the Online Sequential Extreme Learning Machine (OSELM) as a method to improve BC diagnosis precision. OSELM can handle both multi-class and binary classification tasks, mitigate overfitting, and offer performance comparable to kernel-based SVMs, all within a neural network (NN) framework. The study evaluates the effectiveness of OSELM using two datasets: the WDBC and WBCD.

A study that put forth a new Computer-Aided Diagnosis (CAD) system that uses DL and computer vision techniques (CV) was introduced in [12]. It detects and classifies breast lesions, segments them, and then classifies them by pathology. They performed extensive validation of the CAD system with the Curated Breast Imaging Subset of the Digital Database for Screening Mammography (CBIS-DDSM), which they report did very well.

The researcher in [13] introduced new and advanced methods based on ML and regression techniques, the main goal of which is to robotically predict BC via the utilization of advanced methods and images. aspiration (FNA) images were gathered from WBCD, and four classifier models were utilized: one regression model and three ML models: the DT, K-NN, SVM, and NB.

A new scheme named "DXAIB" has been proposed [14], which puts together CNNs with the RF model to improve BC detection accuracy. In terms of what has been done differently in "DXAIB," note that a large focus is on making predictions easy to interpret. The RF element in "DXAIB" that performs label prediction presents an automated feature to the model, which, in turn, includes a number of convolutional layers. Furthermore, the report on the issue of AI interpretability, "DXAIB," does more than just report results; it uses the "SHAP" method to present both local and global explanations for each prediction.

The study employed diagnostic features from patients, and several ML classifiers to detect BC was introduced in [15]. Using XAI methods uncovered the key factors that inform the models' predictions, thereby increasing transparency and interpretability.

Comprehensive research aimed to develop a reliable system for BC detection using CNNs was proposed [16]. It covers steps like collect data, make a preprocessing, develop a model, and asses performance. By using the Mini-DDSM dataset, that has 1952 film mammogram images from varied populations. Preprocessing was applied to the dataset, including illumination correction, denoising, normalization, and augmentation, thereby improving data quality and variety. In model development, evaluated several CNN architectures, counting Basic CNN, FT-VGG19, FT-ResNet152, and FT-ResNet50.

An innovative CAD system named BREAST-CAD, designed to assist doctors in the identification of BC, was introduced [17]. The strategy adheres to a three-phase methodology: A thorough literature study conducted from 2000 to 2025 determined which dataset to use and which of the NB, KNN, SVM, and DT techniques to apply. We preprocessed the data and trained and tested four ML models, which found DT to perform best.

3. Methods

Our focus is on BC detection through DL and ML. We reviewed approximately 20 recent papers related to BC prediction. Some papers focused solely on DL, while others combined ML with DL. primarily used the Scopus database to identify these papers, excluding non-refereed publications.

Start by limiting the selection to 20 studies that used genetic expression and imaging and focused solely on journal and conference articles. Evaluated the imagery sense modality of US, mammography, radiography, CT, and MRI, alongside various gene expression and sequencing methods. This examination focused on studies that use AI methods for BC detection, as well as those that forecast BC by combining genetic and imaging data. Implemented the following eligibility standards for separately paper: the language is English, and the subject is BC screening and therapy. The manuscript examines hybrid models of ML and DL; The manuscript exclusively addresses DL; The manuscript investigates imaging data; the manuscript analyzes genetic expression data; only conference publications and journals are preserved; Only biomedical engineering or medical publications pertinent to the topic are retained. It is important to highlight that non-refereed publications were omitted from the study.

Initially, document the essential details, including the paper title, year of publication, author list, and publisher. Subsequently, pertinent information was incorporated into the review, including the algorithm used, the research focus on DL or a blend of DL and ML, recorded accuracy, the dataset, features, and various other categories. addressed our research enquiries utilizing these criteria.

4. Discussion and Analysis

The initial search for this investigation yielded 200 journal and conference articles. We kept 20 papers applicable to both machine learning and deep learning after removing duplicate articles and research focused solely on medicine or cancer in general. This review focuses only on DL-ML hybrid models or DL methods; only articles connected to DL were selected as listen in Table 1 which describe the comparative review studies for breast cancer prediction based on DL-ML Models.

Table (1): A comparative review of studies for breast cancer prediction based on DL-ML Models.

Authors	Techniques	Dataset	Accuracy (%)
Zuo D. et al. [18]	ML + XAI	Collect dataset	98.1
Atrey K. et al. [19]	ML + LSTM (DL)	BreaKHis	99.85
Ebrahim M. et al. [20]	ML + DL	Obtained from the National Cancer Institute	98.7
Garg V. et al. [21]	ANN	BCW	97.36
Al Fryan L. et al. [22]	CNNs	METABRIC+ TCGA	94.50
Zakareya S. et al. [23]	DL (DNN R3_R5_R35)	Cairo University ultrasound images	93 & 95
Rafiq A. et al. [24]	CNN-based fusion model	PatchCamelyon benchmark	98
Hanon W. et al. [25]	PCA + KNN	BCW	99.12
Devi S. et al. [26]	ML + DL	WDBC	96.49
Sahoo G. et al. [27]	ensemble learning (EL)	UMCIO + WPBC	96.31 & 95.81
Shinde M. et al. [28]	TL	PatchCamelyon benchmark	94.46
AL-NAWASHI M. et al. [29]	DL + adaptive histogram equalization + ML	Collect dataset	98.70
Hamedi S. et al. [30]	DNN + ML	Collect dataset (2 different datasets)	85.56
Almarri B. et al. [31]	DL + ML, (BCPM)	WDBC	92.63 & 91.84
Gurcan F. et al. [32]	DL + ML + EL	BCW	97.72

Kumari D. et al. [33]	DL + ML	WDBC and WPBC	97 & 92
Rhagini A. et al. [34]	CNNs + ML + XAI	BCW	99.5
Lilhore U. et al. [35]	CNNs + TL + LSTM	CBIS-DDSM	99.2
Güler M. et al. [36]	DL + EL	Breast Histology Images	89.4
Zhu J. et al. [37]	DL + Select features + ML + XAI	WDBC	99

Zuo D. et al. [12] presented research analyzing various ML algorithms to identify the most effective for forecasting BC recurrence. They used 11 different ML algorithms to build a model that would make the prediction. These were LR, RF, linear discriminant analysis (LDA), SVM, XGBoost, GBDT, DT, MLP, adaptive boosting (AdaBoost), GaussianNB, and LightGBM. They selected the best ML model based on performance and used Shapley Additive Explanations (SHAP) values to rank the importance of any feature. AdaBoost was the most accurate of the 10 algorithms tested at predicting BC recurrence, so it was chosen to build the classification model. Also, CA125, CEA, Fbg, and tumour diameter were the best predictors of breast cancer recurrence in our dataset.

Atrey K. et al. [19] presented a multifaceted classification method for danger lamination of BC in HPI, via ML techniques and an LSTM-based DL method. Experiments achieved on a widely accessible HI database extract 658 picture characteristics, which are then reduced to 192 relevant features by a genetic approach. The LSTM method achieves 99.85% accuracy on these 192 features using a 5-fold cross-validation strategy.

Ebrahim M. et al. [20] introduce a study that utilized both ML and DL methods to evaluate accuracy. The study used classical DT, LDA, LR, SVM, and EL, and also examined probabilistic NNs (PNNs), recurrent NNs (RNNs), and deep NNs (DNNs) for a different perspective. Also, examine the role of feature selection in accuracy. What was found is that DT and ensemble methods performed very well, achieving a result accuracy of 98.7%.

Garg V. et al. [21]proposed a binary classification model based on NN. They gathered the dataset, cleaned it up, and utilized it to train the NN model. The model they report achieving 97.36% accuracy on the test data, which in turn is the ratio of truthful predictions. That said, the increase in accuracy suggests that the NN does a good job at classifying BC.

Al Fryan L. et al. [22] introduced in a study using CNNs to present an automated solution for the classification of BC through histology, which in turn reports on improved accuracy and consistency, and at the same time, a reduction in subjectivity and bias was observed. They selected regions of interest (ROIs) for their analysis, excluded images that lacked sufficient illustration of tumor cells, and trained a CNN to perform the classification.

Zakareya S. et al. [23] proposed a new DL algorithm that was used for grouping BC. It features granular computing, shortcut connections, two learnable activation functions in place of standard ones, and an attention mechanism, which we put forward to improve diagnostic accuracy and make doctors' tasks easier. In this model, granular computing uses highly specific information from cancer images, which in turn improves accuracy. That observed that the model achieves 93% accurate on ultrasound and 95% on breast HPI.

Rafiq A. et al. [24] proposed three types of CNN architectures: a simple CNN (1-CNN), a fusion CNN (2-CNN), and a triple CNN (3-CNN). The results showed that the 3-CNN algorithm performed best, achieving 90.10% accuracy.

Hanon W. et al. [25] they developed a method of dimensionality reduction, which uses PCA and KNN to identify early signs of BC. The DPBC model, used to detect and predict BC, reduces data volume by selecting the most important attributes that capture most of the data's variability. It was 99.12% accurate, which is very high.

Devi S. et al. [26] compare conventional ML classification methods with cutting-edge DL techniques. They employ a combination of traditional models, such as k-NN, SVM, NN, GB, the CN2 rule inducer, NB, SGD, and DT, as well as DL models, including Neural Decision Forest and MLP. With an accuracy rate of 96.49%, the MLP model effectively distinguishes between positive and negative classes.

Sahoo G. et al. [27] conducted a study to assess how well DNNs, ANNs, and ML approaches such as bagging, averaging, and voting could enhance the diagnosis of BC recurrence using two datasets. The findings indicate that the EL techniques enhanced accuracy to 96.31% and 95.81%.

Almarri B. et al. report in [28] on the introduction of the BC Prediction and Diagnosis Model (BCPM), which they put together to improve the accuracy of BC diagnosis and forecasting. BCPM, which they developed gathers reliable information from public databases, clinical trials, and electronic medical records. They did extensive pre-processing, which corrected errors and filled in for missing values. Also, they applied feature scaling to put all data on the same scale, which in turn makes for fair comparison of features and see to it that some do not dominance the others. Also, they used feature selection methods that help to zero in on the important features for BC prediction and diagnosis, thereby improving model performance. The BCPM they put forth is a mix of many machine learning methods LR, RF, DT, SVMs, and NN, they use to develop very reliable models.

Shinde M. et al. introduced a model which is based on the EfficientNetB0 architecture that they pre trained on ImageNet and out of which they removed the classification head to enable fine tuning for cancer diagnosis. They used the Breast HPI from Kaggle for the training and testing. We report that the model's performance was very good which had training and test accuracy of 94.49% and 94.46% respectively and corresponding losses of 0.13 and 0.16. Also it did very well on the test set which saw an accuracy of 94.0% [28].

AL-NAWASHI M. et al. [29] introduce an automated technique for BC detection via an ML model. used CNNs to extract features and Contrast Limited Adaptive Histogram Equalisation (CLAHE) to reduce noise. The research also analyzes five algorithms: K-NN, NB, RF, SVM, and LR. It tested the models on a set of 3002 merged photos, that we had compiled for this purpose. The collection included data from 1,400 patients who had digital mammograms between 2007 and 2015.

Hamedi S. et al., [30] introduce a multi-method approach they used to predict 5-year survival in women with breast cancer, which also includes a DNN and 11 other traditional ML models. Also of note is that they used data from two locations, totaling 2,644 records, and included external validation. They conducted a literature survey and examined public variables across together datasets, identifying 34 characteristics. They set a p-value threshold of 0.05 and got input from oncologists in selecting the relevant features. In total, they trained 108 models. As per external validation, the DNN model, trained on the Shiraz data with all features, performed very well at 85.56%. While the DNN performed very well in external validation, its overall performance wasn't the best across all tests.

Almarri B. et al. introduce in [31] the BC Prediction and Diagnosis Model (BCPM), which they put together, uses ML to improve the accuracy of BC diagnosis and forecasting. BCPM, which they developed to gather reliable information from public databases, clinical trials, and electronic medical records. They did extensive pre-processing, which corrected errors and imputed missing values. Also, they applied feature scaling to put all data on the same scale, which in turn makes for a fair comparison of features and ensures that none dominate the others. Also used feature selection methods to identify the most informative features for BC prediction and diagnosis, which in thereby improving model performance. The BCPM they put forth is a mix of many machine learning methods, LR, RF, DT, SVMs, and NN, which they use to develop highly reliable models.

Gurcan F. et al. [32] suggested a study that examined the integration of ensemble models with DL using stacked ensembles, which was applied to the BCW dataset to improve BC detection. Evaluated several ensemble procedures, including RF, GradientBoosting, XGBoost, ExtraTrees, HistGradientBoosting, LightGBM, AdaBoost, and CatBoost, to assess their performance in BC diagnostic models. looked at the use of DL models such as CNNs, RNNs, GRUs, BiLSTMs, and LSTMs as meta-predictors in association with ensemble techniques, which performed very well in real-time diagnosis due to their high accuracy and rapid training. The result found that using basic predictors like ExtraTrees, LGBM, and CatBoost with a DL-based meta-predictor, a CNN, and using it in a stacking ensemble setting improved the accuracy of BC prediction.

Kumari D. et al. [33] present the BCR-HDL framework, which performs an excellent, well-defined job at predicting BC recurrence. The study evaluates the performance of a variety of DL architectures, such as MLP, VGG, ResNet, and Xception, in combination with traditional ML models, including SVM, DT, RF, and LR, on the WDBC and WPBC datasets. A total of 16 very robust models were put forth, which also perform well on issues such as working with small datasets, handling imbalanced classes, and pre-processing data. Also, what stands out about the BCR-HDL framework is that it provides a comprehensive picture of the fight against BC through diagnostic outcome prediction, identification of prognostic factors, and the determination of recurrence time.

Rhagini A. et al. [34] introduce research that presents a comprehensive BC diagnostic methodology that amalgamates ML, DL, and XAI techniques with the BCW data set. They compare DL techniques with more traditional ML methods such as RF, SVM, and LR. ML models help us identify what's wrong, but deep learning models might be better when the data is very large and complex. offer a new Hybrid Explainable Attention Mechanism (HEAM) for DL models that leverage kindness mechanisms to address these problems.

Lilhore U. et al. [35] suggest a new hybrid model that uses EfficientNet-B0, which is a pre-trained architecture, as well as CNNs and Bi-LSTM networks. By using EfficientNet-B0, which was trained on the big and varied ImageNet dataset. It uses TL to extract better features from mammograms than traditional methods that require training CNNs from scratch. Bi-LSTM improves the model's performance by allowing it to see how the data changes over time. This is important for finding complicated patterns in pictures of BC. We used the Adam optimizer to enhance the model's routine. It was much more accurate and faster at processing. A comprehensive analysis of reliable datasets, including CBIS-DDSM and MIAS, achieved an exceptional 99.2% accuracy in differentiating between benign and malignant tumors.

Güler M. et al. [36] utilized 11 distinct DL models (Vanilla, DenseNet152, DenseNet201, ResNet152, ResNet50, VGG16, EfficientB1, MobileNetv2, NasNet, ensemble, and Tuned Model) to predict breast cancer. We used pathological samples from breast biopsies that had been divided into benign and malignant groups for classification analysis. DenseNet201 records the highest accuracy of 89.4%.

Zhu J. et al. [37] displayed a novel method for select features that utilizes Shapley additive explanation (SHAP) values as the foundation for Recursive Feature Elimination (RFE) and incorporates an RF algorithm into the RFE framework. To address data imbalance, they used Borderline-SMOTE1. We used five machine learning models, KNN, RF, LR, LGBM, and SVM, to evaluate the proposed method on the WBCD datasets. Via the Particle Swarm Optimization (PSO) technique to make the hyperparameters of five models better.

Hybrid pipelines and ensembles always work well. A lot of research shows that ensemble techniques similar AdaBoost, stacking ensembles, and gradient-boosting families, or hybrid pipelines that mix DL feature extraction with machine learning classifiers, work better. DL is great for working with images, but classical ML remains effective for handling tables and clinical data. When CNNs, EfficientNet, or LSTMs are used on image features, the results are usually very accurate (over 90% of the time). However, tree-based ensembles or DT, EL methods are usually better suited to tabular clinical datasets. Choosing the right features and understanding them are both important. Numerous studies employ SHAP, Grad-Cam, genetic selection, or variants of RFE to diminish dimensionality and pinpoint clinically significant predictors (e.g., CA125, CEA, Fbg, tumor diameter). Explainability methods help with feature selection and build trust. TL and pretraining make it easier to work with small photo datasets. Research indicates that enhancing ImageNet-pretrained architectures such as EfficientNet, VGG, and ResNet can be effective, even with limited medical image datasets.

Commonly cited or suggested limitations in research studies:

- Dataset diversity and size: Many high accuracies come from just one dataset or a carefully chosen subset (like Breast HPI, CBIS-DDSM, and WBCD). External assessment is rare; when it occurs, performance may decline (Hamedi et al.).
- Class imbalance and the risk of overfitting: Numerous studies recommend using techniques such as SMOTE variants and cross-validation. But the fact that the reported accuracies are so high (close to 99%) makes me think that overfitting or overly positive evaluations without enough external test sets could be an issue.
- Details on reproducibility: It's hard to compare hyperparameter tuning techniques, exact train/test splits, and preprocessing phases directly because they aren't always fully explained.

5. Conclusions

The published papers show that there isn’t a one-size-fits-all method to tasks, and the best approach is usually a hybrid DL+ML pipeline. Also, in terms of what makes a great model versus a clinical-grade one, we see that the level of explainability and rigour in validation is key. In a review study, highlight (a) that performance by modality is an issue, (b) the very large need for feature selection and XAI, and (c) that we have to have external validation with which we can trust before we see true clinical value.

Conflict of Interest: The authors declare that there are no conflicts of interest associated with this research project. We have no financial or personal relationships that could potentially bias our work or influence the interpretation of the results.

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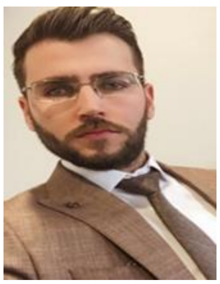	Humam Khalid Jameel holds a Master of Science in Computer Science from the Department of Computer Science, College of Science, Al-Nahrain University, Baghdad, Iraq, in 2021. He received his B.Sc. in Computer Science from the College of Computer Science- Al Anbar University, Anbar, Iraq, in 2016. He is currently a assistant lecturer at the Department of Computer Science, College of Science, Al-Nahrain University, Jadriya, Baghdad, Iraq. His research interests include computer science, Multimedia, AI, and related fields. He can be contacted at the email address: humam.khalid@nahrainuniv.edu.iq.
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