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A Review on Breast Cancer Prediction Using Machine Learning and Deep Learning Techniques

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Abstract

Breast cancer is one of the most prevalent and chronic disease that affect women. To overcome this disease, effective medical treatment is required. Early detection of the disease plays an important role for suitable medication and survival of patient. To identify the breast cancer in the patients, standard imaging technique mammography is used. Due to the subtle and varied nature of cancer tissues interpreting mammogram images can be a challenge to doctors. Machine learning (ML) and Deep Learning (DL) techniques offer promising solutions that provide efficient breast cancer detection from mammograms. In this review paper a comprehensive review of ML and DL algorithms and their applications in mammogram image analysis are presented. Various supervised and unsupervised learning techniques, such as convolutional neural networks (CNNs), support vector machines (SVMs), random forests, and other popular ML and DL models are discussed in paper. The integration of these DL methods that are efficiently used in image preprocessing techniques, feature extraction, and classification strategies. The overall survey focusses on various performance metrics, datasets, and benchmarks used in existing studies. Further the strengths and limitations of different approaches used by various researchers are identified. By understating current research trends this paper aims to contribute to the ongoing development of more accurate and reliable breast cancer detection systems using advanced ML techniques.

Keywords: Breast cancer, Predictive analytics, Decision analytics, Machine learning, Deep learning.

1. Introduction

In many countries, most of the women are suffering with breast cancer. This type of cancer is the deadliest disease among women. In women highest death rate is identified by breast cancer by comparing with other type cancers [16]. Usually in the human body breast cancer cells normally move to lymph glands and becomes a source injury to lungs and other regions of human body [17]. It is essential to identify the reason for the most prevalent cause of breast cancer to an individual. There are several reasons for any person to be affected to breast cancer including family history. Beside family history there are other reasons such as life style and malfunction of the milk-producing ducts, which are often known as invasive ducts. Beyond other reasons it may also start in the breast lobules, a kind of glandular tissue, or other cells and tissues. Researchers have identified that there is a correlation between environmental, hormonal, and lifestyle factors and an elevated risk of breast cancer [18]. Due to the unequal function and massive multiplication of abnormal cells, it creates a tumor in the breast and results in death. Growth of cells can be described in two types are malignant and benign [19]. Malignant cells grow in an

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uncontrolled way and can invade nearby tissues and spread to other parts of the body through the blood and lymph system. In benign cells the growth is not considered as cancer also it does not invade nearby tissue or spread to other parts of the body. The structure of malignant cells and benign cells is shown in Figure 1. Usually a nodule (lump), mass or densities are treated as possible abnormalities. In most of the case all anomalies are not malignant. For example, a smooth bounded bulge is often benign. A starburst-shaped, irregularly bordered tumor, on the other hand, might be malignant, and to confirm the cancer biopsy is necessary [20]. Cancer causes an abnormal growth of cells and often spreads out rapidly in body tissues. It is usually named after the part of the body in which it occurs. At the early stage of development, it forms a lump or mass, often referred to as tumor. The tumor produces no significant pain at the early stage of treatment. Hence, conducting screening is crucial for early detection of the disease formation.

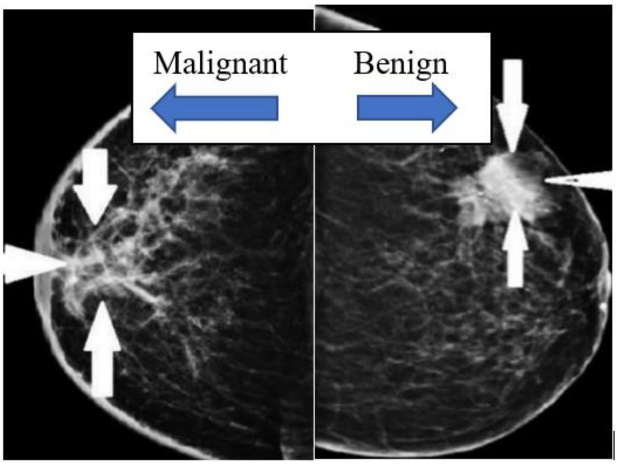

Figure 1. Images of breast cancer malignant and benign.

Mammography is an effective imaging technique utilized by radiotherapists in the detection and screening of breast cancer. It is a lower dose X-ray procedure that enables the visualization of the interior part of the breast. The Mammography is extremely precise however; it is the major clinical testing [21]. Typically, mammography would identify around 80–90% of breast cancer in females without any symptoms. Inappropriately, data recommended that initial commercial CAD system has not resulted in the major development of efficient and stagnated progress over the year. These mammography images are examined by radiologists in order to diagnose breast cancer. The accomplishment of deep in visual object detection and recognition it is significant that DL methods help radiotherapist and enhance the screening mammography accuracy. Researchers from all around the world are working on deep learning models for breast cancer screening based on medical imaging. Nevertheless, radiologists' assessments on the existence of breast cancer may vary owing to variations in their past experiences and understanding.

One of the main challenges is accurately detecting breast masses (mass and tumor are used interchangeably) from high-resolution mammography images is that the ratio of some breast masses to the overall image size is too small [22]. Furthermore, some breast masses can still be greater in size but have very low contrast which can be overlooked when examining the full-sized high-resolution mammograms. In spite of its benefit, mammography screening is related to high risk of false negative and positive result [23]. Some prior work addressed this issue by using manually annotated lesions to narrow down the potential Region of Interest (RoI) so that deep learning models can focus only on that RoI [24]. However, manually annotating RoI is laborious and ultimately restricts to having fully automated real-world applications due to the absence of such annotated RoI for in-the-wild data. Other studies attempted to train deep Convolutional Neural Networks (CNN) using the whole mammogram images. Unfortunately, due to the input size restrictions and pooling layers, even state-of-the-art object detection models miss some of the significant lesions or micro-calcifications. A Single-Shot Detector (SSD) object detection model for the whole mammogram to obtain RoIs for further tumor shape classification was utilized in existing works [25]. However, the accuracy of the classification is based on the premise that SSD is able to detect all tumors, which in general, is not true. Considering these issues, appropriate automatic RoI extraction methods

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should be exploited. Another common issue in breast cancer diagnosis is that most of the existing DL-based models classify detected tumors/abnormalities into benign and malignant categories [26].

Many machine learning [27], deep learning [28], and bio-inspired computer approaches [29] have been applied to different medical diagnoses in recent years. Despite the fact that several modalities have been demonstrated, none of them can produce an accurate and reliable outcome. Physicians performing mammography should read a large amount of imaging data, which lowers accuracy in predicting the breast cancer. This manual process of understanding the images takes a long time, and in many cases, it may identify the stage of the illness incorrectly. In order to identify the disease from the input features, several machine learning algorithms, Deep Learning and Artificial Intelligence are used by several researchers.

1.1 Machine Learning

Machine Learning (ML) is a branch of artificial intelligence and computer science that focuses on the using of data and algorithms to enable Artificial Intelligence to imitate the way that humans learn, gradually improving its accuracy. Machine learning work flow is given as;

Decision Process: In general, machine learning algorithms are used to make a prediction or classification. Based on some input data, which can be labeled or unlabeled, ML algorithm will produce an estimate about a pattern in the data.

Error Function: An error function evaluates the prediction of the model. Based on the known examples, an error function can make a comparison to assess the accuracy of the model.

Model Optimization Process: If the model can fit better to the data points in the training set, then weights are adjusted to reduce the discrepancy between the known example and the model estimate. The algorithm will repeat this iterative “evaluate and optimize” process, updating weights autonomously until a threshold of accuracy has been met.

1.2 Deep Learning

Deep learning is a subset of machine learning that uses multilayered neural networks, called deep neural networks, to simulate the complex decision-making power of the human brain. Deep learning can be defined as the method of machine learning and artificial intelligence that is intended to intimidate humans and their actions based on certain human brain functions to make effective decisions. Deep learning algorithms play a crucial role in determining the features and can handle the large number of processes for the data that might be structured or unstructured. Although, deep learning algorithms can overkill some tasks that might involve complex problems because they need access to huge amounts of data so that they can function effectively.

Artificial intelligence: Artificial intelligence [30], or AI, is technology that enables computers and machines to simulate human intelligence and problem-solving capabilities. As a field of computer science, artificial intelligence is often mentioned together with machine learning and deep learning. These disciplines involve the development of AI algorithms, modelled after the decision-making processes of the human brain, that can ‘learn’ from available data and make increasingly more accurate classifications or predictions over time.

Hybridisation of algorithms: The machine-learning and deep learning models are combined with an empirical relationship developed using the same training datasets to generate corresponding hybrid models [31]. Hybrid machine learning models and algorithms learn structured representations from empirical data. These representations are transformed views of the data which make it more interpretable or more usable for downstream modelling and prediction.

2. Literature Survey

A systematic literature review [32] strategy is an exacting and comprehensive method of reviewing books, articles, and other publications related to a particular field of study or subject. Providing a comprehensive synthesis and evaluation of all pertinent, high-quality data is the main objective of this technique. This type review helps to address research issues and make direct decisions regarding policy or practice. The procedure, which is composed

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of numerous clearly specified procedures, guarantees the observability, repeatability, and objectivity of the review. A detailed study performed using available articles in google scholar on various machine learning algorithms for prediction of breast cancer using is shown in figure-2. The papers are referred on supervised machine learning techniques named Naïve Bayes, Support Vector Machine (SVM), Decision Tree, random forests and Artificial Neural Networks (ANNs).

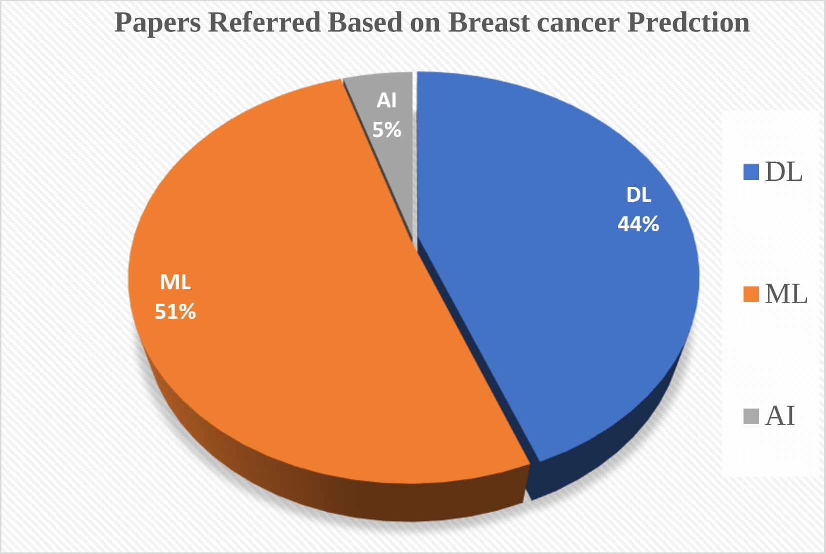

Figure 2. Papers based on breast cancer prediction using ML techniques available in google scholar.

2.1 Support Vector Machine (SVM)

A supervised ML-based technique, SVM selects the moderate number of samples called support vectors and builds a linear discriminant function. SVM solved the restriction of linear limits [33]. SVM can be considered a two-class data set that can be partitioned linearly to show a maximum hyperplane margin. The new samples are linearly fit or appear linearly separable in the high-level plane following the selection of the appropriate mapping. The SVM tries to find the most advantageous hyperplane that minimizes the distance between two groups.

Wu and Moon [1] conducted study to classify the cancer data. The study evaluated 210 ultrasound breast tumor images, including 120 benign tumors and 90 malignant tumors. The breast tumors were segmented automatically by the level set method. The autocovariance texture features and solidity morphologic feature were extracted, and a support vector machine was used to identify the tumor as benign or malignant. The accuracy of their proposed diagnostic system for classifying breast tumors was 92.86%, the sensitivity was 94.44%, the specificity was 91.67%, the positive predictive value was 89.47%, and the negative predictive value was 95.65%. Further their proposed system reduced the training time compared to systems based only on the morphologic analysis.

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Table1. Analysis of few papers on prediction of breast cancer using SVM

Authors	Algorithm	Data set	Characteristics	Results
Wu and Moon (2008)	SVM, 5-fold-crossvalidation, kernel: nonlinear Gaussian basis.	210 sonograms, 100 malignant and 120 benign tumors.	Autocovariance texture features and solidity morphologic features	Acc: 92.86%; Sens: 94.44%; Spec: 91.67%; Maximum AUC: 0.949.
Renjie et al. (2011)	SVM, kernels: linear, polynomial, Gaussian radial basis function and sigmoid function.	210 sonograms	Sonographic features; Texture features based on SGLD matrix	Acc: 86.92%; Sens: 75.18%; Spec: 96.11%
Ebrahim Edriss Ali (2016)	SVM and ANN	UCI repository	Mammogram images	Acc: 84.9%
Elsayed Badr (2022)	GWO (Grey wolf optimizer)-SVM	Wisconsin diagnosis breast cancer (WDBC) dataset and Electronic Health Records (HER)	569 instances divided into two classes. Malignant 357 benign 212 cases respectively	Acc: 93.26%

Renjie et al. (2011) [2] used new set of features for differentiating benign from malignant breast lesions using ultrasound (US) images. Two types of features (sonographic and textural features) are considered. Among them, three sonographic features are novel. Sonograms of 321 pathologically proven breast cases are analyzed and classified into benign and malignant categories. The discrimination capability of the extracted features was evaluated using the support vector machines (SVM) in comparison with the results obtained from artificial neural networks (ANN) and K-nearest neighbor (KNN) classifier. The model exhibited the accuracy of 86.92%.

Ebrahim Edriss Ali (2016) [3] conducted experiments using Wisconsin Diagnosis Breast Cancer database to classify the breast cancer as either benign or malignant. Supervised learning algorithm -Support Vector Machine (SVM) with kernels like Linear, and Neural Network (NN) are used for comparison to achieve these tasks. The performances of the models are analyzed where Neural Network approach provided more ‘accuracy’ and ‘precision’ as compared to Support Vector Machine in the classification of breast cancer. The resulted accuracy was 84.9%.

Elsayed Badr (2022) [4] proposed sequential model that is applied on two different datasets, Wisconsin diagnosis breast cancer (WDBC) dataset and Electronic Health Records (EHR). Experimental results of WDBC show that the proposed hybrid GWO-SVM model achieves 98.60% with normalization scaling. Also, using the proposed scaling techniques with the proposed GWO-SVM model gives a fast convergence and achieves accuracy rate by 99.30%. The parallel version of the proposed model achieves a speedup by 3.9 on four CPU cores. On the other hand, Experimental results of EHR show that the proposed hybrid GWO-SVM model achieves 93.26% with normalization scaling against 82.05 for SVM.

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2.2 Random Forest

Random Forest algorithm [34] is a powerful tree learning technique in machine learning. It works by creating a number of decision trees during the training phase. Each tree is constructed using a random subset of the data set to measure a random subset of features in each partition. This randomness introduces variability among individual trees, reducing the risk of overfitting and improving overall prediction performance.

In prediction, the algorithm aggregates the results of all trees, either by voting (for classification tasks) or by averaging (for regression tasks). This collaborative decision-making process, supported by multiple trees with their insights, provides an example stable and precise results. Random forests are widely used for classification and regression functions, which are known for their ability to handle complex data, reduce overfitting, and provide reliable forecasts in different environments.

Table 2. Analysis of few papers on prediction of breast cancer using Random Forest.

Authors	Algorithm	Data set	Characteristics	Results
T. L. Octaviani, Z. Rustam [2019]	Random forest	Breast Cancer Wisconsin Data	Mammogram image classification for malignant	80.8%
Cuong Nguyen [2013]	Random forest classifier combined with feature selection	Wisconsin Breast Cancer Prognostic Dataset	n-fold cross validation to training learning algorithm	91.6%
Wang, Sutong, et al [2020]	Random Forest (RF)-based rule extraction (IRFRE) method	wisconsin Diagnostic Breast Cancer (WDBC) dataset, Wisconsin Original Breast Cancer (WOBC) dataset, and Surveillance, Epidemiology and End Results (SEER) breast cancer dataset	interpretable classification rules from a decision tree ensemble for breast cancer diagnosis	93.4%
Madeeh Nayer Elgedawy [2017]	Random forest algorithm	Wisconsin Breast Cancer Database	patients' trauma are benign or malignant	96.4%

T. L. Octaviani, Z. Rustam [5] classified breast cancer using random forest method. The result was more than 80 %. when 70% of the data was used for training. Cuong Nguyen [6] study aims at diagnosing and prognosticating breast cancer with a machine learning method based on random forest classifier and feature selection technique. By weighting, keeping useful features and removing redundant features in datasets, the method was obtained to solve diagnosis problems via classifying Wisconsin breast cancer diagnosis dataset and to solve prognosis problem via classifying Wisconsin breast cancer prognostic dataset. On these datasets we obtained classification accuracy of 100% in the best case and of around 99.8% on average.

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Wang, Sutong, et al [7] used rule extraction method named improved Random Forest (RF)-based rule extraction (IRFRE) method. This is developed to derive accurate and interpretable classification rules from a decision tree ensemble for breast cancer diagnosis. Firstly, numbers of decision tree models are constructed using Random Forest to generate abundant decision rules available. And then a rule extraction approach is devised to detach decision rules from the trained trees. Finally, an improved multi-objective evolutionary algorithm (MOEA) is employed to seek for an optimal rule predictor where the constituent rule set is the best trade-off between accuracy and interpretability. The overall accuracy obtained through this method was 93.4%.

Madeeh Nayer Elgedawy [8] three machine learning techniques: Naïve Bayes, SVM and Random Forest to Wisconsin Breast Cancer Database. The three developed models predict whether the patients’ trauma is benign or malignant. The paper aims at comparing the performance of these three algorithms through accuracy, precision, recall and f-measure. Results show that Random Forest yields the best accuracy of 99.42%.

2.3 Naive Bayes (NB)

Naive Bayes [35] is a statistical classification technique based on Bayes Theorem. It is one of the simplest supervised learning algorithms. Naive Bayes classifier is the fast, accurate and reliable algorithm. Naive Bayes classifiers have high accuracy and speed on large datasets. Naive Bayes classifier assumes that the effect of a particular feature in a class is independent of other features. Even if these features are interdependent, these features are still considered independently. This assumption simplifies computation, and that's why it is considered as naive. This assumption is called class conditional independence.

Table 3. Analysis of few papers on prediction of breast cancer using Naive Bayes.

Authors	Algorithm	Data set	Characteristics	Results
Megha Rathi [2018]	Naïve Bayes	From UCI repository	to identify malignant and benign	94.2%
Murat Karabatak [2015]	Naïve Bayes	Wisconsin breast cancer database	weighted NB classifier was proposed for classification of the breast cancer	98.2%
Ceren Güze (2019)	Naïve bayes	Wisconsin breast cancer database	Impute missing values for classification	97.6%

Megha Rathi [9] predictive model to identify the type of breast cancer as benign or malignant. For this purpose, naïve bayes classifier was used which helps oncologist in diagnosing the cancer type with in no time and then helps oncologist in decision making in treatment method for the same purpose. The dataset is taken from UCI ML repository which consists of 699 valid instances and 10 attributes on the basis of which we will find out the type of cancer one is suffering from. The overall accuracy obtained 94.762%.

Murat Karabatak [11] Wisconsin breast cancer database with 9 attributes and 699 records was used in the experimental works. It is worth to mention that 16 records were discarded because of missing values. Moreover, 5-fold cross validation test was applied and average values were calculated for performance measurements. When 5-fold cross validation test was applied, the first 3 folds contained 546 samples for the training dataset and the retained 137 samples that were used in the test set. The overall accuracy obtained was 98.2%.

Ceren Güze [12] developed an approach to impute missing values with k Nearest Neighbor algorithm (kNN) and Naïve Bayes. The performance of the system is evaluated by kNN and Naïve Bayes classifier to detect breast cancer. They measured by performance criteria such as accuracy, sensitivity, specificity and ROC analysis. With this approach, 95 out of 131 missing data which is 9.89% of all data are filled. The experimental results on

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Mammographic Mass database demonstrate the effectiveness of our proposal with 82.49% accuracy while 81.69% accuracy is obtained without any imputation using same training and testing dataset.

2.4 Artificial Neural Network (ANN)

In the past decades, ANNs have been utilized by researchers, thus making them a relevant research area. Greatly, the network has enabled great success, especially in Breast Cancer classification and early-stage prognosis. ANN models [36] usually have three layers: input, hidden, and output. The layers comprise interconnected neurons with nonlinear switching activation functions to enhance nonlinear capacity. First, the input layer gets the data, then passes it to a hidden layer for analysis and returns the results to the output layer. Results shows are now displayed through the output layer. However, given the constraints, training and ANN will likely require long informal chains of computing processes. There are three dense layers and two dropout levels in the ANN structure used in this study. The DNN, on the other hand, is made up of five dense layers and three dropout layers.

Many researchers worked used machine learning algorithms to develop successful prediction model to classify or to identify the seriousness of the breast cancer by using mammogram data and other clinical data. But these algorithms exhibit poor performance when dealt with large data. In most of the cases overfitting problem is also encountered by using machine learning models. The accuracy and reliability of machine learning models heavily depend on input data quality. If the data is complete, balanced, and updated, it can lead to accurate predictions and decisions. Maintaining high-quality data requires ongoing efforts, including data cleansing, validation, and monitoring. The below table 4 show that researchers used different ML algorithms along with ANN to find the breast cancer. Many of them could able to produce satisfactory results.

Table 4. Analysis of few papers on prediction of breast cancer using machine learning algorithms

Authors	**Algorithm**	**Data set**	**Characteristics**	**Results**
Chokri, Ferkous (2017) [61]	Multilayer perceptron	DDSM/480	Finding Malignant or Benign RDM, SGLDM	88.02%
Chisako Muramatsu (2016) [60]	ANN Random Forest SVM	Private Data Collected	Finding Malignant or Benign RLTP, GLCMs	Not available
Li et al. [62]	ANN, SVM, KNN	DDSM/323	Intensity, shape and texture	99.66%
Beura et al. (2015) [63]	BPNN	MIAS, DDSM	Multisolution analysis to Malignant or Benign	97.4%
Rahimeh et al. (2016)	MLP	MIAS	Statistical	90.9%

Chokri, Ferkous [61] discussed about computer-aided diagnosis system to differentiate between four breast imaging reporting and data system (Bi-RADS) classes in digitised mammograms. This system is inspired by the approach of the doctor during the radiologic examination as it was agreed in BI-RADS, where masses are described by their form, their boundary and their density. The segmentation of masses in the authors' approach is manual because it is supposed that the detection is already made. When the segmented region is available, the features extraction process can be carried out. 22 visual characteristics are automatically computed from shape, edge and textural properties; only one human feature is used in this study, which is the patient's age. Classification is finally done using a multi-layer perceptron according to two separate schemes; the first one consists of classify

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masses to distinguish between the four BI-RADS classes (2, 3, 4 and 5). In the second one the authors classify abnormalities on two classes (benign and malign). The proposed approach has been evaluated on 480 mammographic masses extracted from the digital database for screening mammography, and the obtained satisfactory results.

Chisako Muramatsu [60] used image retrieval method for breast masses on mammograms has been investigated in our previous study, and the result indicated the potential advantage of a machine learning technique using sample cases with experts subjective similarity data. In this study, the effect of presenting reference images to observers ability to distinguish between benign and malignant masses was investigated. Eleven physicians and 11 radiological technologists evaluated 98 masses and recorded their confidence of a lesion being malignant without and with reference images. The areas under the receiver operating characteristic curves improved from 0.926 to 0.938 (p=0.17) and from 0.895 to 0.928 (p=0.004) for the physician and technologist groups, respectively. The results indicate that reference images may be useful for diagnosis of breast masses

Rahimeh et al. [64] authors developed an enhanced mammography CADx system with an emphasis on the segmentation step. In particular, we present two hybrid algorithms based upon region-based, contour-based and clustering segmentation techniques to recognize benign and malignant breast tumors. In the first algorithm, in order to obtain the most accurate final segmented tumor, the initial segmented image, that is required for the level set, is provided by one of spatial fuzzy clustering (SFC), improved region growing (RG), or cellular neural network (CNN). In the second algorithm, all of the parameters which control the level set are obtained from a dynamic training procedure by the combination of both genetic algorithms (GA) and artificial neural network (ANN) or memetic algorithm (MA) and ANN. After segmenting tumors using one of the hybrids proposed methods, intensity, shape and texture features are extracted from tumors, and the appropriate features are then selected by another GA algorithm. Finally, to classify tumors as benign or malignant, different classifiers such as ANN, random forest, naïve Bayes, support vector machine (SVM), and K-nearest neighbor (KNN) [13] are used. Experimental results confirm the efficiency of the proposed methods in terms of sensitivity, specificity, accuracy and area under ROC curve (AUC) for the classification of breast tumors. It was concluded that RG and GA in adaptive RG-LS method produce more accurate primary boundary of tumors and appropriate parameters for the level set technique in segmentation and subsequently in classification.

The below figure-3 depicts papers referred that have used machine learning algorithm. Though machine learning algorithms are good in classification.

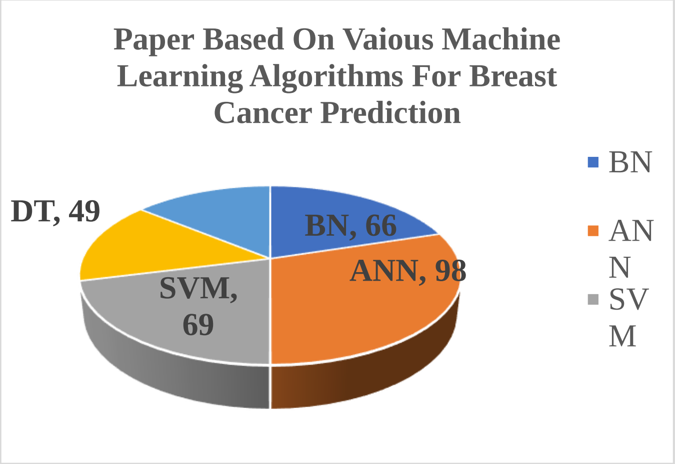

Figure 3. Papers referred on breast cancer classification using machine learning algorithms

3. Deep Learning algorithms used in Breast cancer

Deep learning [37] uses artificial neural networks to perform sophisticated computations on large amounts of data. It is a type of machine learning that works based on the structure and function of the human brain. Deep learning

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algorithms train machines by learning from examples. Industries [38] such as health care, eCommerce, entertainment, and advertising usually make use deep learning for best analysis. Deep learning algorithms feature self-learning representations, they depend upon ANNs that mirror how the human brain computes any information. During the training process, algorithms use unknown elements in the input distribution to extract features, group objects, and discover useful data patterns. Much like training machines for self-learning, this occurs at multiple levels, using the algorithms to build the models.

Deep learning models make use of several algorithms. Based on the nature of the problem some algorithms are better suited to perform specific tasks. To choose the right algorithm it is needed to gain a complete understanding of all primary algorithms

3.1 Convolutional Neural Networks (CNNs)

CNNs [39] are a deep learning algorithm that processes structured grid data like images. They are very much successful in image classification, object detection, and face recognition tasks. CNN have different layers where the data can be processed.

Convolutional Layer: This layer applies a set of filters (kernels) to the input image, where each filter slides (convolves) across the image to produce a feature map. This helps detect various features such as edges, textures, and patterns.

Pooling Layer: This layer reduces the dimensionality of the feature maps while retaining the most essential information. Common types include max pooling and average pooling.

Fully Connected Layer: After several convolutional and pooling layers, the output is flattened and fed into one or more fully connected (dense) layers, culminating in the output layer that makes the final classification or prediction.

3.2 Recurrent Neural Networks (RNNs)

RNNs [40] are designed to recognize patterns in data sequences, such as time series or natural language. They maintain a hidden state that captures information about previous inputs.

Hidden State: At each time step, the hidden state is updated based on the current input and the previous hidden state. This allows the network to maintain a memory of past inputs.

Output: The hidden state generates an output at each time step. The network is trained using backpropagation through time (BPTT) to minimize prediction error.

3.3 Long Short-Term Memory Networks (LSTMs)

LSTMs [41] are a special kind of RNN capable of learning long-term dependencies. They are designed to avoid the long-term dependency problem, making them more effective for tasks like speech recognition and time series prediction.

Cell State: LSTMs have a cell state that runs through the entire sequence and can carry information across many steps.

Gates: Three gates (input, forget, and output) control the flow of information.

Input Gate: Determines which information from the current input should be updated in the cell state.

Forget Gate: Decides what information should be discarded from the cell state.

Output Gate: Controls the information that should be outputted based on the cell state.

3.3 Generative Adversarial Networks (GANs)

GANs [42] generate realistic data by training two neural networks in a competitive setting. They have been used to create realistic images, videos, and audio.

Generator Network: Creates fake data from random noise.

Discriminator Network: Evaluates the authenticity of the data, distinguishing between real and fake data.

Training Process: The generator and discriminator are trained simultaneously. The generator tries to fool the discriminator by producing better fake data, while the discriminator tries to get better at detecting counterfeit data. This adversarial process leads to the generator producing increasingly realistic data.

Transformer Networks

Transformers [43] are the backbone of many modern NLP models. They process input data using self-attention, allowing for parallelization and improved handling of long-range dependencies.

Self-Attention Mechanism: This mechanism computes the importance of each part of the input relative to every other part, enabling the model to weigh the significance of different words in a sentence differently.

Positional Encoding: Adds information about the position of words in the sequence since self-attention doesn't inherently capture sequence order.

Encoder-Decoder Architecture: Consists of an encoder that processes the input sequence and a decoder that generates the output sequence. Each consists of multiple layers of self-attention and feed-forward networks.

3.5 Autoencoders

Autoencoders [44] are unsupervised learning models for tasks like data compression, denoising, and feature learning. They learn to encode data into a lower-dimensional representation and then decode it back to the original data.

Encoder: Maps the input data to a lower-dimensional latent space representation.

Latent Space: Represents the compressed version of the input data.

Decoder: Reconstructs the input data from the latent representation.

Training: The network minimizes the difference between the input and the reconstructed output.

3.6 Deep Belief Networks (DBNs)

DBNs [45] are generative models composed of multiple layers of stochastic, latent variables. The working mechanism of DBN is given below.

Layer-by-Layer Training: DBNs are trained in a greedy, layer-by-layer fashion. Each layer is trained as a Restricted Boltzmann Machine (RBM), which learns to reconstruct its input.

Fine-Tuning: After pretraining the layers, the entire network can be fine-tuned using backpropagation for specific tasks.

3.7 Deep Q-Networks (DQNs)

DQNs [46] combine deep learning with Q-learning. This is a reinforcement learning algorithm, to handle environments with high-dimensional state spaces. They have been successfully applied to tasks such as playing video games and controlling robots.

Q-Learning: Uses a Q-table to represent the value of taking an action in a given state.

Deep Neural Network: Replaces the Q-table with a neural network that approximates the Q-values for different actions given a state.

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Experience Replay: Stores past experiences in a replay buffer and samples from it to break the correlation between consecutive experiences, improving training stability.

Target Network: A separate network with delayed updates to stabilize training.

3.8 Variational Autoencoders (VAEs)

VAEs [47] are generative models that use variational inference to generate new data points similar to the training data. They are used for generative tasks and anomaly detection.

Encoder: Maps input data to a probability distribution in the latent space.

Latent Space Sampling: Samples from the latent space distribution to introduce variability in the generated data.

Decoder: Generates data from the sampled latent representation.

Training: This method combines reconstruction loss and a regularization term to encourage the latent space to follow a standard normal distribution.

3.9 Graph Neural Networks (GNNs)

GNNs [48] generalize neural networks to graph-structured data. They are used for social network analysis, molecular structure analysis, and recommendation systems.

Graph Representation: Nodes represent entities, and edges represent relationships between entities.

Message Passing: Nodes aggregate information from their neighbors to update their representations. This process can be repeated for several iterations.

Readout Function: After message passing, a readout function aggregates node representations to produce a graph-level representation for tasks like classification or regression.

The following figure 4. Represents the papers referred on breast cancer classification using deep learning algorithms from google scholar. In addition, a brief review is also given by discussing briefly about the paper which have done extensive work in breast cancer prediction by using deep learning models.

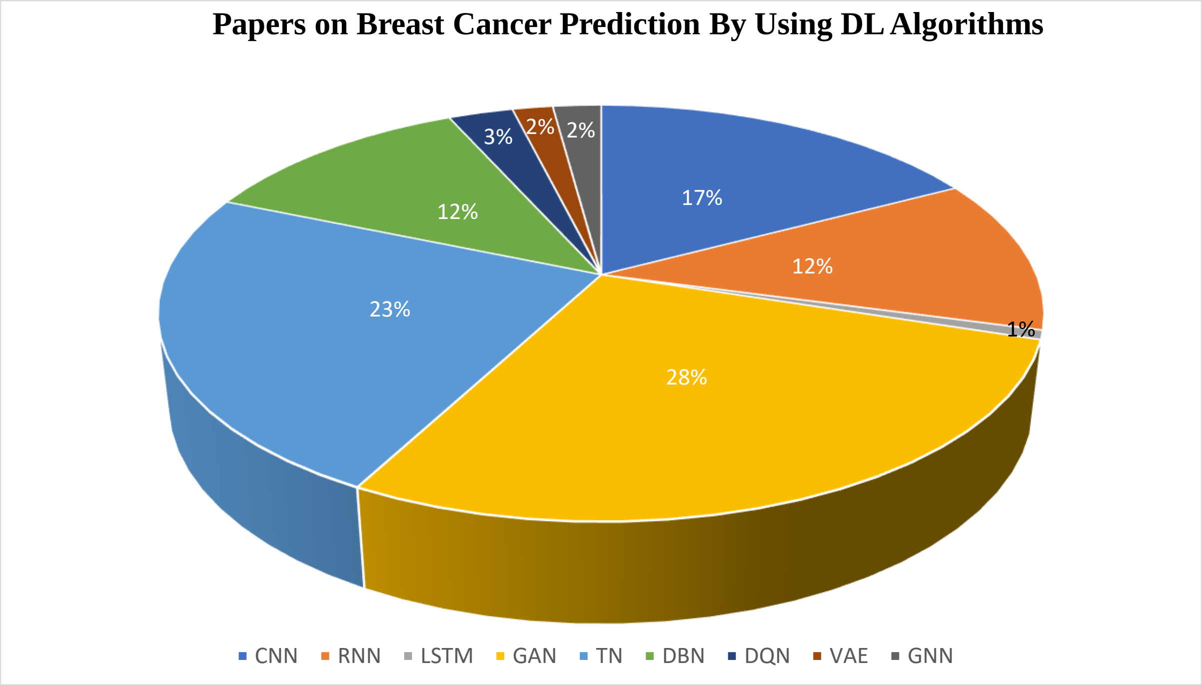

Figure 4. Papers referred on breast cancer classification using Deep learning algorithms

In 2023, Ghuge and Saravanan [49] have implemented the latest image segmentation for mammogram images and the identification architecture for the identification of breast cancers, most importantly for the women. The wanted mammogram pictures were collected from traditional global databases. The gathered pictures were fed into the segmentation process, where the images were segmented employing Swin ResUnet3+. Thus, the mammogram segmented pictures were forwarded to the identification stage, where Adaptive Multi-scale Attention-based Densenet with Extreme Learning Machine (AMAD-ELM) model was implemented to identify the breast tumor effectively from the mammogram pictures. The parameters from AMAD-ELM were optimized through the suggested Position-based Improved invasive Weed and Crisscross Optimization (PIWCO). The effectiveness of the recommended breast tumor identification system with the help of deep learning was analyzed through various existing models to show its effectiveness.

In 2023, Chakravarthy *et al.* [50] have proposed a robust framework that incorporated the concept of ELM and Deep Transfer Learning and the performance of ELM was improved using an Iterative Flight-Length-Based Crow-Search Algorithm (iFLCSA) in this research work. Performance of ELM heavily depends on its parameters and to provide enhanced performance, the optimum parameters of ELM were found through the iFLCSA. When compared to the existing Crow Search Algorithm (CSA), the flight length parameter will be updated iteratively using an appropriate equation in iFLCSA to provide better balance between exploration and exploitation. Digital & full-field digital mammograms from the Mammographic Image Analysis Society (MIAS) and INbreast datasets were used for evaluation. The results obtained were then compared with the existing Support Vector Machine, ELM, Particle Swarm Optimization and CSA optimized ELM algorithms. The proposed iFLCSA-ELM provides maximum classification accuracy for MIAS & INbreast datasets respectively.

In 2022, Kavitha *et al.* [51] have presented a new Optimal Multi-Level Thresholding-based Segmentation with DL enabled Capsule Network (OMLTS-DLCN) breast cancer diagnosis model utilizing digital mammograms. The OMLTS-DLCN model involved an Adaptive Fuzzy based median Filtering (AFF) technique as a pre-processing step to eradicate the noise that exists in the mammogram images. Besides, Optimal Kapur's based Multilevel Thresholding with Shell Game Optimization (SGO) algorithm (OKMT-SGO) was applied for breast cancer segmentation. In addition, the proposed model involves a CapsNet based feature extractor and Back-Propagation Neural Network (BPNN) classification model was employed to detect the existence of breast cancer. The diagnostic outcomes of the presented OMLTS-DLCN technique was examined by means of benchmark Mini-MIAS dataset and DDSM dataset. The experimental values obtained highlight the superior performance of the OMLTS-DLCN model with a higher accuracy on the Mini-MIAS dataset and DDSM dataset, respectively.

In 2023, Sarra *et al.* [52] have proposed an effective mammography pre-processing strategy that has been proven through a classification stage to evaluate its effectiveness. Hence, proposed an accurate breast tumor detection model as the first step toward cancer detection. Several filters were used in the first stage, which was the pre-processing. In the second phase, which was tumor detection, various deep learning techniques were employed, including transfer learning, data augmentation, and global pooling techniques. To achieve that, they proposed CNN architecture for mammogram scan classification, where for the feature extraction phase we used transfer learning techniques, in which six pre-trained CNN models were used for feature extraction: InceptionResNetV2, EfficientNetB7, DenseNet201, MobileNetV2, ResNet152V2, and VGG16. Meanwhile, for the classification phase, instead of using traditional ML algorithms or fully connected layers, we used global pooling techniques. The obtained results were satisfying, putting InceptionResNetV2 and VGG16 trials ahead of the other feature extractors with high accuracy, followed by the MobileNetV2 trial. That was due to the well-chosen pre-processing filters. Meanwhile, the other models established good results as well regarding the previous studies. As for the classification phase influence, using global average pooling was more suitable for the majority of the models, except for InceptionResNetV2 and MobileNetV2 feature extractors where global max pooling achieved better results. Additionally, they were able to determine the best parameters for each model, as well as the influencing criteria.

In 2022, Kumari and Jagadesh [53] have utilized mammogram images are for breast cancer screening. The main objective was to select the better features to increase the classification performance. To achieve this, we used a 4-step process: 1. preprocessing 2. Feature extraction, 3. Feature selection, 4. Classification. Initially, the medical images were acquired and preprocessed using Contrast-Limited Histogram Equalization (CLAHE) and the features were retrieved using Advanced Gray-Level Co-occurrence Matrix (AGLCM) which extracts texture,

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shape and intensity-based features. Then feature selection was applied to obtain the better features. To achieve this, they proposed a new feature selection technique called Weighted Adaptive Binary Teaching Learning Based Optimization (WA-BTLBO) and fitness function used was the classification accuracy. The selected features were trained and tested using XGBoost classifier and the results were compared with other classifiers namely K-Nearest Neighbor (KNN), Random Forest (RF), Artificial Neural Networks (ANN), and Support Vector Machines (SVM). The experiments were done using publicly available mammogram medical images namely Mammographic Image Analysis Society (MIAS). The results showed that WA-BTLBO with XGBoost classifier was superior to other feature selection techniques namely Particle Swarm Optimization (PSO) and Binary TLBO (BTLBO) and other state-of-art methods in classifying MIAS mammogram images into normal or abnormal. This paper helped the physiologists and radiologists to detect the breast cancer in women so that life span of the patient could be increased. In future, they extend their work to use other metaheuristic methods like firefly algorithm, biogeography-based optimization and other algorithms to select the optimal features and also to apply on large databases and on other types of diseases.

In 2019, Kaur *et al.* [54] have suggested a new approach, applied on the Mini-MIAS dataset of 322 images, involving a pre-processing method and inbuilt feature extraction using K-mean clustering for Speed-Up Robust Features (SURF) selection. A new layer was added at the classification level, which carries out a ratio of 70% training to 30% testing of the deep neural network and Multiclass Support Vector Machine (MSVM). The outcome described here demonstrates that the accuracy rate of the proposed automated DL method using K-mean clustering with MSVM was better than using a decision tree model. Experimental results show that the Average Accuracy (ACC) rates of the three classes, i.e., normal, benign and malignant cancer. A 10-fold cross validation was used, and the obtained results for the Support Vector Machine (SVM), K-nearest Neighbour (KNN), Linear Discriminant Analysis (LDA) was higher than existing models.

In 2022, Altameem *et al.* [55] have used four mammography imaging datasets with a similar number of 1145 normal, benign, and malignant pictures using various deep CNN (Inception V4, ResNet-164, VGG-11, and DenseNet121) models as base classifiers. The proposed technique employed an ensemble approach in which the Gompertz function was used to build fuzzy rankings of the base classification techniques, and the decision scores of the base models were adaptively combined to construct final predictions. The proposed fuzzy ensemble techniques outperformed each individual transfer learning methodology as well as multiple advanced ensemble strategies (Weighted Average, Sugeno Integral) with reference to prediction and accuracy. The suggested Inception V4 ensemble model with fuzzy rank based Gompertz function has obtained better accuracy rate. They believed that the suggested approach has a tremendous value to healthcare practitioners in identifying breast cancer patients early on, perhaps leading to an immediate diagnosis.

In 2020, Omonigho *et al.* [56] have developed augmentation techniques to improve system classification accuracy on a large number of datasets. A popular Deep Convolutional Neural Network (DCNN) architecture known as AlexNet was modified and used to categorize mammography images into two classes of benign (normal) and malignant (abnormal) tumors. The results demonstrated better accuracy. It indicates an improved performance over traditional approaches in breast cancer diagnosis.

Table 5: Features and challenges of prior breast cancer detection methods in mammogram images using deep learning.

Author	**Methodology**	**Features**	**Challenges**
Ghuge and Saravanan (2024)	Swin ResUnet3+	It effectively segments the abnormal regions. It performs better in image restoration and edge detection tasks.	Training the model consumes more time.
Chakravarthy *et al.* (2023)	ELM	It learns the data very faster. The generalization performance and the robustness of the model are high.	Due to the presence of hidden layer, the complexity of the model is high.
Kavitha *et al.* (2022)	Capsule Neural Network	It has the ability to remove noise in the images.	The complexity of the model is high.

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		The infected breast region is segmented effectively.	It is not suitable for large datasets.
Sarrawe *et al.* (2023)	CNN	The features from mammogram images are retrieved automatically. Overfitting is eliminated by employing global pooling method.	Need of labelled data is high. Time taken for training the model is high.
Kumari and Jagadesh (2022)	XGBoost	The intensity, shape and texture-based features are retrieved for effective classification process.	Overfitting issues occur while training small datasets. Tuning hyperparameters is difficult.
Kaur *et al.* (2019)	multi-class SVM	It is suitable for resizing and noise handling operations. Even in high dimensional spaces, it performs effectively.	It does not rectify the overlapping issues. It does not provide stable results if the training samples are large.
Altameem *et al.* (2022)	CNN and Fuzzy	It provides correct decision scores from the input images.	It is not useful for localization of brain tissues.
Omonigho *et al.* (2020)	DCNN	It helps to learn and retrieve features automatically. It attains high classification accuracy.	It needs more number of parameters. Time consumption is high.

4. Artificial Intelligence

Artificial Intelligence (AI) has shown its capability and prevailed in many science and engineering fields including computational systems biology. Conventionally, computational biology works on problems of biology systems at all levels, which involve individual organisms, internal biological subsystems, cells, membranes, DNAs and relevant external ecosystems, with mathematical modelling and statistical analysis. Bioinformatics and Genomics are two very related areas of computational systems biology, in which AI can exercise its full potential. Compared to conventional computational approaches, AI offers an advanced toolbox that better facilitates problem-solving in the fields. The current trend in AI methods in bioinformatics and genomics is machine learning methods, i.e., creating more efficient, reliable and accurate neural networks and deep learning models. Nevertheless, AI methods are not limited to those. In practice, Artificial Intelligence can be used to examine molecular structures and classify biological data. Research work using AI has been also found in function-structure analysis, biological/gene sequence matching, protein-protein interaction and many more.

Bioinformatics and genomics usually possess and produce a vast amount of data, deal with numerous business-critical tasks and bear high social-economical values to society. The Research Topic aims to receive studies that reflect and address the latest advancements in AI methods that focus on the challenges in bioinformatics and genomics. Particular emphasis is placed on novel and intelligent methods tackling the practical issues in the area.

Table 4. Analysis of few papers on prediction of breast cancer using Artificial Intelligence techniques.

Authors	**Algorithm**	**Data set**	**Characteristics**	**Results**
Jong Seok Ahn [2023]	AI &CAD	CAMELYON17 dataset	Finding malignant or benign	94.2
Ali Bou Nassif [2022]	AI and Deep Learning	Real time & Wisconsin breast cancer database	Finding the stage of cancer	97.4
Said Pertuz1 [2023]	Grad-CAM & other AI algorithms	NYU Breast Cancer Screening dataset	Saliency analysis & cancer region detection	94.7%

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Jong Seok Ahn [58] comprehensively explored the diverse applications of AI in breast cancer care, underlining its transformative promise and existing impediments. In radiology, we specifically address AI in mammography, tomosynthesis, risk prediction models, and supplementary imaging methods, including magnetic resonance imaging and ultrasound. In pathology, our focus is on AI applications for pathologic diagnosis, evaluation of biomarkers, and predictions related to genetic alterations, treatment response, and prognosis in the context of breast cancer diagnosis and treatment.

Ali Bou Nassif [14] proposed that Artificial intelligence and machine learning have been used effectively in detection and treatment of several dangerous diseases, helping in early diagnosis and treatment, and thus increasing the patient's chance of survival. Deep learning has been designed to analyze the most important features affecting detection and treatment of serious diseases. For example, breast cancer can be detected using genes or histopathological imaging. Analysis at the genetic level is very expensive, so histopathological imaging is the most common approach used to detect breast cancer.

5. Problem Definition

The existing methods for breast cancer detection are not effective in visual examination to identify the lumps and irregularities. Better imaging techniques should be used for recognizing bi-lateral asymmetry and structural distortion. The breast cancer detection approaches should be robust to determine the absence or presence of malignant tissues. Some of the features and challenges of existing breast cancer detection method is given in Table 1. Swin ResUnet3+ [49] effectively segments the abnormal regions and it performs better in image restoration and edge detection tasks. But, training the model consumes more time. ELM [50] learns the data very faster. Also, the generalization performance and the robustness of the model are high. Yet, due to the presence of hidden layer, the complexity of the model is high. Capsule Neural Network [51] has the ability to remove noise in the images. The infected breast region is segmented effectively. The complexity of the model is high and it is not suitable for large datasets. CNN [52] retrieved features from mammogram images automatically. Overfitting is eliminated by employing global pooling method. However, Need of labelled data is high and the time taken for training the model is high. XGBoost [53] retrieves the intensity, shape and texture-based features are for effective classification process. However, overfitting issues occur while training small datasets and tuning the hyperparameters is difficult. multi-class SVM [54] is suitable for resizing and noise handling operations. Even in high dimensional spaces, it performs effectively. But it does not rectify the overlapping issues and it does not provide stable results if the training samples are large. CNN and Fuzzy [55] provide correct decision scores from the input images. Still, it is not useful for localization of brain tissues. DCNN [56] helps to learn and retrieve features automatically and it attains high classification accuracy. But it needs more number of parameters and the time consumption is high. Thus, an advanced breast cancer segmentation and classification approach is proposed.

6. Conclusion

Breast cancer prediction using deep learning techniques highlights significant advancements in the field, showcasing the potential of these methods to enhance diagnostic accuracy and early detection. Despite the progress, there remains substantial scope for further improvement. Continued research and development are essential to refine these models, addressing challenges such as data heterogeneity, interpretability, and computational efficiency. With ongoing innovation and interdisciplinary collaboration, deep learning techniques hold promise for even greater impact in breast cancer prediction, ultimately improving patient outcomes and advancing the field of medical diagnostics.

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