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An in-depth exploration of deep learning approaches for the prediction of breast cancer subtypes

Dr. Rajesh B Mapari

Anuradha Engineering College, Chikhli, Maharashtra, India

ABSTRACT

Breast cancer stands as a contemporary health crisis, inflicting a significant toll on women globally with its high mortality rate. Early detection and accurate classification are essential for effective treatment. However, attempts to comprehend the underlying causes of this cancer using conventional machine learning techniques encounter challenges, particularly in feature extraction. Conventional machine learning models are most effective when dealing with raw data based on extracted features. In response to this limitation, innovative deep learning techniques have been introduced to diagnose breast abnormalities through diverse imaging modalities, such as Mammogram, Magnetic Resonance Imaging (MRI), and Ultrasound, achieving remarkable levels of accuracy. This comprehensive survey delves into the obstacles faced by classical machine learning models and underscores the emergence of efficient predictive models enabled by cutting-edge deep learning methods. Within this review, we provide a comparative analysis of traditional machine learning approaches and the more advanced deep learning models.

Keywords: breast cancer, naive bayes, Support Vector Machine (SVM), K-Nearest Neighbor (KNN), decision tree, Convolutional Neural Networks (CNN), alex net, Residual Network (Res Net), google net, Visual Geometry Group (VGG) net

Address for correspondence:

Dr. Rajesh B Mapari

Anuradha Engineering College, Chikhli, Maharashtra, India

E-mail: rajeshmappariaec@outlook.com

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INTRODUCTION

Breast cancer ranks as the second most perilous ailment globally, trailing only lung cancer in terms of its threat to human health, especially among women. This malignancy exerts a profound toll in terms of mortality among the female population. Extensive literature studies have revealed a sobering statistic: approximately one in every eight women, on average, is susceptible to developing breast cancer at some point in their lives. It is worth noting that a significant proportion, approximately 66%, of women worldwide encounter the specter of breast cancer after the age of 55, with the majority of cases manifesting between the ages of 35 and 54.

Breast cancer manifests in two primary forms: benign and malignant. Benign cancer, also known as non-cancerous growth, is characterized by the uncontrolled proliferation of cells that remain confined within the boundaries of the breast, without invading the neighboring tissues. In stark contrast, malignant breast cancer involves the emergence of abnormal tissue masses that evolve into invasive tumors, posing a considerable threat as they infiltrate nearby tissues. The severity of malignant breast cancer can vary significantly.

A comprehensive survey of the available literature has identified distinct types of breast cancer, including:

Invasive ductal carcinoma

This cancer originates in the milk ducts and extends into the fibrous tissues surrounding the ducts. Alarmingly, it accounts for approximately 80% of reported cases (Figure 1).

Invasive Ductal Carcinoma (IDC) itself cannot be visualized on an image because it's a microscopic abnormality within the breast tissue. However, imaging tests like mammograms can show some signs that might be indicative of IDC, such as:

- Clusters of microcalcifications (tiny deposits of calcium)
- A mass within the breast tissue
- A distorted spiculated mass (mass with finger-like projections) and
- Changes in breast density

Ductal Carcinoma *in-Situ* (DCIS)

DCIS represents a precancerous stage, often referred to as stage 0. In this stage, the cancer remains confined to the milk ducts, without spreading to the surrounding breast tissues. However, if

left untreated during this early stage, it may evolve into invasive cancer.

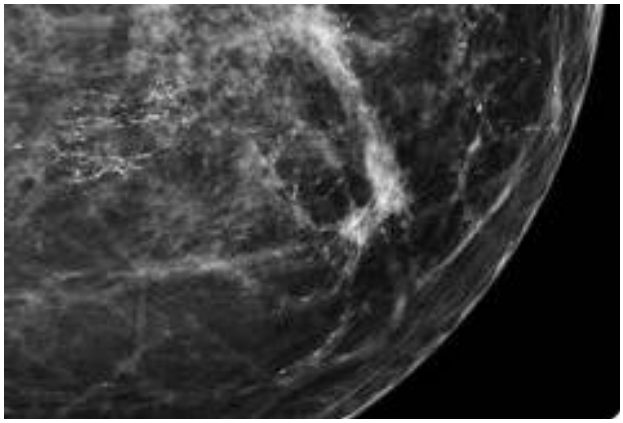

Fig. 1. Flowcharts for systematic review

Invasive lobular carcinoma

This variant commences in the breast lobules and subsequently invades adjacent cells. Research has indicated that approximately 10% to 15% of cases fall under this category. Notably, it can be challenging to detect via mammograms.

Lobular Carcinoma *in-Situ* (LCIS)

LCIS denotes a change in breast tissue where cancer cells proliferate within the milk-producing glands. It is not classified as full-fledged cancer, but it elevates the risk of developing invasive breast cancer. Thus, regular breast cancer screenings and mammograms are indispensable for early detection and effective management (Figure 2).

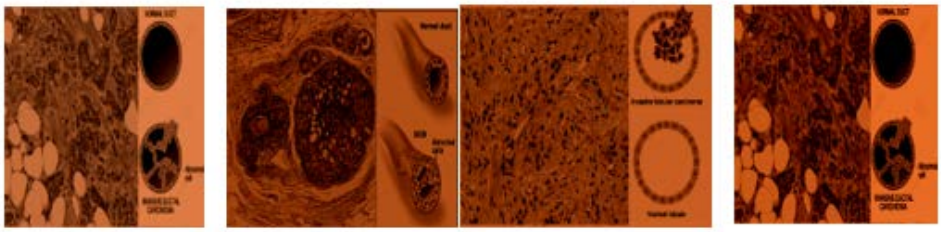

Fig. 2. Types of breast cancer

The breast is composed of diverse tissues, including ligaments, nerves, lymph nodes, blood vessels, connective tissues, and lymph vessels. Mammogram imaging serves as a crucial tool for early-stage breast cancer detection, capable of identifying tumors of minuscule dimensions. When breast cancer is diagnosed, medical professionals typically recommend additional tests to ascertain whether cancer cells are localized solely within the breast's lymph nodes or have spread beyond its confines, a key factor in determining the cancer's stage.

Various screening tests are conducted within clinical trials, including tissue sampling, thermography, and breast examinations. Detecting breast cancer is also possible through Magnetic Resonance Imaging (MRI), clinical breast exams, and ultrasound. An emerging technology known as Three-Dimensional (3-D) mammography or Digital Breast Tomosynthesis (DBT) is gaining prominence in clinics. This innovation captures breast images from multiple angles, producing a 3-D representation. Research has indicated that DBT reduces the occurrence of false-positive cases, potentially leading to a decline in breast cancer-related mortality.

The structure of this review paper is organized into six sections for clarity:

Section II delves into related research and findings. Section III provides an exploration of traditional Machine Learning techniques. Section IV is dedicated to a discussion of Deep Learning techniques. Section V undertakes a comparison of experimental results. Section VI encapsulates the study's concluding remarks and findings.

RELATED WORK

In this section, we provide an overview of the foundational work in the domains of traditional Machine Learning and Deep Learning models applied to the detection and classification of breast cancer.

Sara Alghunaim et al. introduced various machine learning models for the prediction and classification of breast cancer within extensive datasets. The authors expanded the utility of Random Forest, Support Vector Machine (SVM), and Decision Trees by employing two distinct or combined datasets Gene Expression and DNA Methylation. Their experiments demonstrated that, within the Spark environment, the Support Vector Machine classifier achieved an impressive accuracy of 99.68%, coupled with the lowest error rate, particularly when using the individual Gene Expression dataset [1].

Yadavendra et al. explored diverse machine learning and deep learning models to efficiently discern between benign and malignant tumors in minimal time. Their study revolved around a standardized dataset of Breast Histopathology images, boasting more than 200,000 color patches, each measuring 50 × 50 in size. The experiment allocated 60% for training, 20% for validation, and 20% for testing. Results revealed various performance metrics: Logistic Regression scored 0.72% precision, Random Forest achieved 0.80%, Bagging and Voting models reached 0.81%, Supervisor Call (SVC) and Ada Boost algorithms garnered 0.82%,

and the Deep Learning approach using the exception method excelled with 0.90 [2].

Yi-Ju Tseng et al. proposed the inclusion of serum human epidermal growth factor receptor as part of pathological image features to predict breast cancer metastasis. They deployed Support Vector Machines (SVM), Random Forest, and Logistic Regression in their analysis. The findings underscored that the Random Forest algorithm emerged as the optimal choice for detecting breast cancer metastasis up to three months in advance [3].

Sana Ullah Khan et al. introduced a transfer learning model utilizing Google Net, Visual Geometry Group (VGG) Net, and Res Net for breast cancer prediction and classification. Feature extraction hinged on breast cytology images using convolutional neural network models. The research outcomes exhibited classification accuracies with individual CNN models: Google Net at 93.5%, VGG Net at 94.15%, Res Net at 94.35%, and an even higher accuracy of 97.525% with transfer learning [4].

M. Arfan Jaffar et al. proposed a Computer-Aided Diagnosis (CAD) framework, a novel amalgamation of Deep Convolutional Neural Networks (CNN) and SVM. Their experiments leveraged standard mammogram datasets Mammographic Image Analysis Society (MIAS) and DDAS, yielding a notable accuracy of 93.35% and a sensitivity rate of 93% [5].

Jing Zheng et al. introduced an ensemble model, incorporating CNN-based transfer learning for the classification of breast masses using Mammography, Tomosynthesis, MRI, and Ultrasound. The results demonstrated impressive accuracy, with 97.2%, a sensitivity of 98.3%, and a specificity of 96.5% [6].

Umit Budak et al. presented a framework employing Fully Convolutional Networks (FCN) and Bi-LSTM for histopathological images. Their research was based on the publicly available Break His dataset, utilizing images as input to FCN to extract high-level features. This novel framework achieved an accuracy of 95.69%, a sensitivity of 98.10%, and a specificity of 90.40% [7].

Zhongyi Han et al. introduced an ensemble approach, CS-DCNN, for the multi-classification of histopathological images, distinguishing Ductal carcinoma, Lobular carcinoma, and Benign cancer. Their model, when evaluated on the Break His dataset with augmentation, attained an accuracy of 93.2% [8].

Duc My Vo et al. proposed an ensemble deep CNN model designed to select vital features from histopathological images. This incremental boosting convolution network classified multi-scale images into normal, benign, in situ, and invasive stages. The model showcased a remarkable accuracy of 95.1%, outperforming other inception models in detecting various stages of breast cancer [9].

Zhiqiong Wang et al. introduced a Computer-Aided Diagnosis (CAD) system. This research incorporated CNN features and unsupervised learning to classify benign and malignant masses. It fused traditional subjective and objective features with essential mammogram attributes for classification [10].

Erkan Deniz et al. introduced a transfer learning approach involving deep feature extraction methods applied to histopathological images. Their methodology encompassed feature extraction through Alex Net, fine-tuning of features using VGG 16 models, and subsequent classification utilizing Support Vector Machine (SVM). The outcome yielded an impressive accuracy rate of 90.96%. There exists the potential for the implementation of alternative CNN models to further enhance accuracy [11].

Venketkumar Hariraj et al. put forth an efficient Fuzzy Multi-Layer SVM framework designed for the classification of normal, benign, and malignant masses utilizing Mammograms. Their experiment was carried out with a mini MIAS dataset, extracting features based on texture and morphology. Notably, the framework attained a remarkable accuracy of approximately 98%, surpassing the performance of KNN, SVM, and MLP methods [12].

Sami Ekici et al. implemented optimized Convolutional Neural Networks (CNNs) in the context of breast thermographs. This approach involved the extraction of features from patient biodata and thermograph images to classify normal and abnormal images. The model achieved an impressive accuracy rate of 98.95% when applied to a dataset comprising 140 patient thermal images, of which 98 were healthy and 42 were deemed unhealthy [13].

D. Selvathi et al. undertook the implementation of three distinct deep learning models, namely Convolutional Neural Networks, Sparse Autoencoder, and Stacked Sparse Autoencoder, for the prediction of breast cancer using mammogram images. These techniques demonstrated the ability to accurately identify minute masses and classify cells as benign or malignant. The proposed CNN model achieved an accuracy rate of 97%, while the Sparse Autoencoder reached 98.5%, and the Stacked Sparse Autoencoder excelled at 98.9% accuracy [14].

Ahmet Hasim Yurttakal et al. introduced a multi-layer deep convolution neural network framework augmented with data to classify benign and malignant tumors through MRI images. This model harnessed the capability to automatically extract visual features from MRI images. The experiment yielded an impressive accuracy of 98.3% with a minuscule error rate of 0.0167% [15].

Traditional machine learning models

Several conventional machine learning models are employed for the diagnosis and categorization of both benign and malignant cancers. This study encompasses the utilization of classifiers such as Naive Bayes, Support Vector Machine (SVM), K-Nearest Neighbours (KNN), and Decision Trees.

Naive bayes classifier

The Naive Bayes model operates based on Bayes' theorem, serving as a combination of multiple algorithms that adhere to a common principle. It classifies each pair of features independently. The dataset is typically partitioned into a feature matrix, encompassing all the dependent features, and a response vector, which contains the predictive values for each entry in the feature matrix. When applied to a specific dataset, the Naive Bayes model effectively categorizes it into cancerous and non-cancerous classes, achieving an accuracy rate of 93% [16].

This model use Bayes Theorem which is showcased in following steps:

$$P(Q/R) = \frac{P(R/Q)P(Q)}{P(R)} \quad (1)$$

$$P(R) = \sum\nolimits_{N} P(R|Q)P(Q) \quad (2)$$

Where P(Q|R) is posteriori probability, P(Q) is priori probability, P(Q|R) is likelihood and (R) is normalizing constant as the dataset is having two classes benign and malignant with class label of X, P (X|C Benign)P (C Benign) is computed for each class C Benign. Classifier predicts that X is the class C Benign only if P (X|C Benign) P (C Benign) >P (X|C Malignant)P(C Malignant) for 1 ≤ malignant ≤ n, malignant ≠ Benign.

Algorithm 1: Diagnostic classification of Breast cancer by Naïve Bayes Classifier

Input

Data set P = (p1, p2.....,pn)

Output

Classification of benign and malignant cells

Algorithm

- Input the dataset, denoted as P.
- Compute the mean and standard deviation, along with the overall mean for all data points.
- Evaluate the likelihood for each class.
- Determine the maximum likelihood.
- Categorize cells as either benign or malignant, based on the maximum likelihood assessment

Support Vector Machine (SVM)

The Support Vector Machine (SVM) model employs optimal hyperplanes to segregate datasets into different classes within a multi-dimensional space. Support vectors are integral in this process, representing distinct data points that define the margin and position of these hyperplanes. Kernels play a crucial role in classifying patterns from the dataset, particularly in the transformation of non-linear data into a linear format. The kernel trick is utilized to reshape the datasets and establish the most effective decision boundary. Remarkable accuracy levels were attained when dealing with linearly separable data. In a practical application, the Support Vector Machine was implemented on the Wisconsin Prognostic Breast Cancer (WPBC) dataset, achieving an impressive accuracy rate of 96.91% [17].

Linear kernel function

$$f(y) = w^{T} * y + a \tag{3}$$

Where y input data set, w is the minimized weight vectors, a is the linear coefficient.

Polynomial kernel function

$$f(y1, y2) = (p + y1T + y2)q \tag{4}$$

f(y1,y2) represents decision boundary, y1,y2 is input data (Figure 3).

RBF kernel function

$$f(a,b) = \exp\left(-\frac{\|a-b\|^2}{2\sigma^2}\right) \tag{5}$$

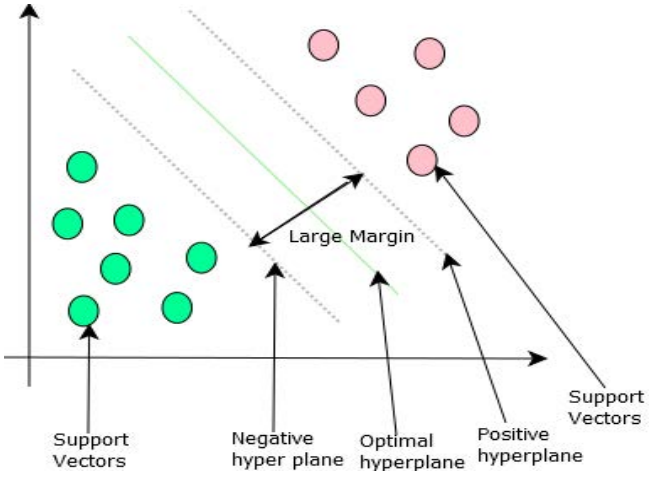

Fig. 3. Support vector machine

K-Nearest Neighbor (KNN)

KNN, which stands for K-Nearest Neighbours, is a machine learning algorithm that doesn't learn from a training dataset but relies on previously loaded data. It assigns new features to the group with the maximum number of neighbouring data points. This is accomplished by calculating the Euclidean distance, a distance metric, to measure the proximity between features, and subsequently assigns each feature to the category with the shortest distance. In practice, the K-Nearest Neighbour model has been applied to Wisconsin's breast cancer dataset, consisting of 569 samples. Out of these, 212 samples were categorized as malignant, and 357 were labelled as benign, achieving an impressive accuracy rate of 94.35% [18] (Figure 4).

Algorithm 2: Classification of Breast cancer by KNN

- Select the K number of neighbours.
- Calculate the Euclidean distance between data. points in an n-dimensional space.
- Euclidean distance (a,b) = $\sqrt{\sum_{j=1}^{m}(a_j - b_j)^2}$
- Group the K-nearest neighbours as benign and malignant class.
- Count the number of features in each group.
- The new feature can be assigned to the benign or malignant category which is having maximum number of data

points.

Decision tree

A Decision Tree is visually represented as a tree structure in which the intermediate nodes represent features within the dataset, the branches symbolize decision rules, and the leaf nodes yield the output of the decision tree. The decision-making process commences from the root node and progresses based on the various features. At each node, decisions are made (yes or no), leading to the further division of the tree into subtrees.

In the specific context of applying the pruned J48 tree to different features within the dataset, a significant observation is made: when the clump thickness exceeds two, cancerous cells are distributed across multiple layers, consequently classifying the tumor as malignant. Conversely, if the clump thickness is less than two, benign cells tend to appear in a single layer.

This dataset comprises 699 instances, and it's noteworthy that the accuracy rate for correctly classified instances stands at 92.8571%, while the rate of incorrectly classified instances is 7.1429% [19] (Figure 5).

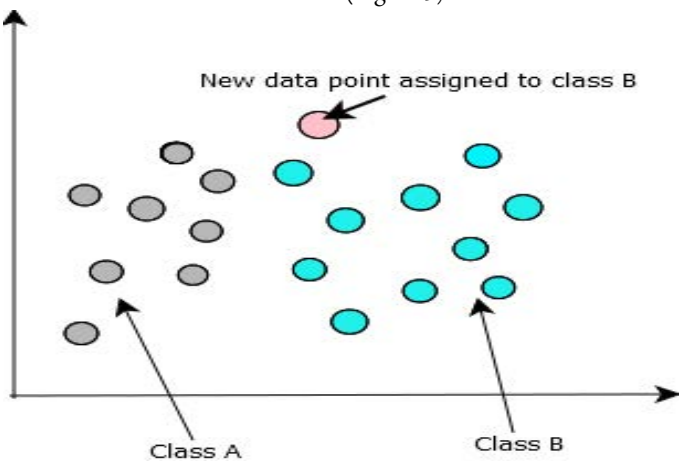

Fig. 4. K-Nearest neighbor

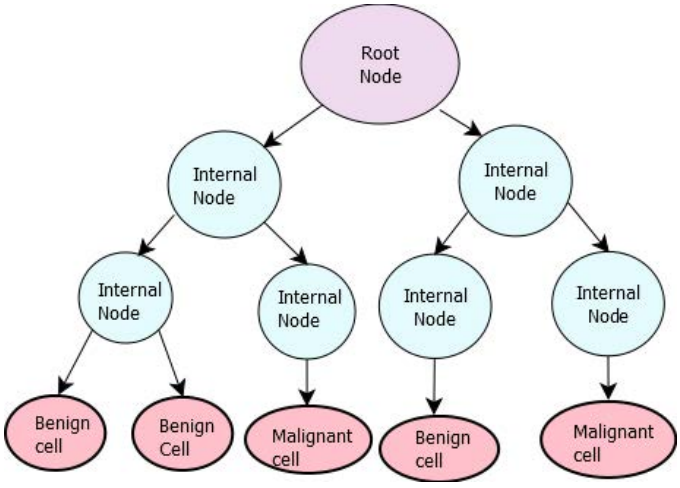

Fig. 5. Decision tree

Algorithm 3: Breast cancer classification using Decision Tree

Data Collection:

- Collect the breast cancer dataset. The dataset should include features such as tumor size, texture, perimeter, smoothness, etc., and the target variable (benign or malignant).

Data Pre-processing:

- Handle missing values: Fill or remove any missing data points.
- Encode categorical variables: Convert any categorical variables into numerical format if necessary.
- Split the dataset into training and testing sets: Typically, a split of 70-80% for training and 20%-30% for testing.

Feature selection:

- Identify and select the relevant features that contribute to the classification. This can be done using correlation analysis or feature importance techniques.

Model training:

- Initialize the Decision Tree classifier.
- Train the Decision Tree on the training dataset. This involves:
- Selecting the best feature to split the data at each node.
- Recursively splitting the data until the stopping criteria are met (e.g., maximum depth, minimum samples per leaf).

Model evaluation:

- Evaluate the model on the testing dataset using metrics

such as accuracy, precision, recall, F1-score, and confusion matrix.

Deep learning techniques

Deep Learning represents a subset within the realm of machine learning, notable for its self-learning capabilities. Novel deep learning models exhibit proficiency in classifying diverse data types, including images, audio, and text. Within this framework, deep learning architectures demonstrate a remarkable capacity to predict and classify breast cancer through the analysis of mammogram images. In particular, the Convolutional Neural Network architecture surpasses the performance of previous machine learning models.

Mammogram screening plays a pivotal role in reducing mortality among women, yet it is not without its limitations, potentially yielding a higher risk of false negatives and false positives. The introduction of innovative deep learning models contributes to enhancing the accuracy of mammogram screening, thereby aiding radiologists in their assessments.

Prediction and classification in this context are formidable challenges due to the often-small size of tumours relative to the entire breast image. Deep learning necessitates extensive, meticulously labelled training datasets to bolster its accuracy. The process often involves pre-training the model on a substantial dataset, followed by fine-tuning for classification purposes [20].

Convolution Neural Network (CNN)

CNN, represented by Convolutional Neural Networks, stands as a sophisticated model endowed with the ability to autonomously learn and discern critical features within medical images [21]. In the classification of tumours as benign or malignant, CNN exhibits a remarkable capacity to deliver high accuracy with a low error rate.

The core components of CNN encompass convolutional layers, pooling layers, fully connected layers, activation functions, and the output layer [22]. Within the framework of CNN, kernels play a pivotal role in feature extraction from input images. The various dimensions of kernels, influenced by their distinct heights and widths, yield output images of varying dimensional sizes. In a similar fashion, kernels within the pooling layer serve to extract either the average or maximum number of features, while subsampling serves to reduce the dimensions of the images. Ultimately, the fully connected layer takes the output and classifies it into different classes through the application of the SoftMax activation function [23, 24] (Figure 6).

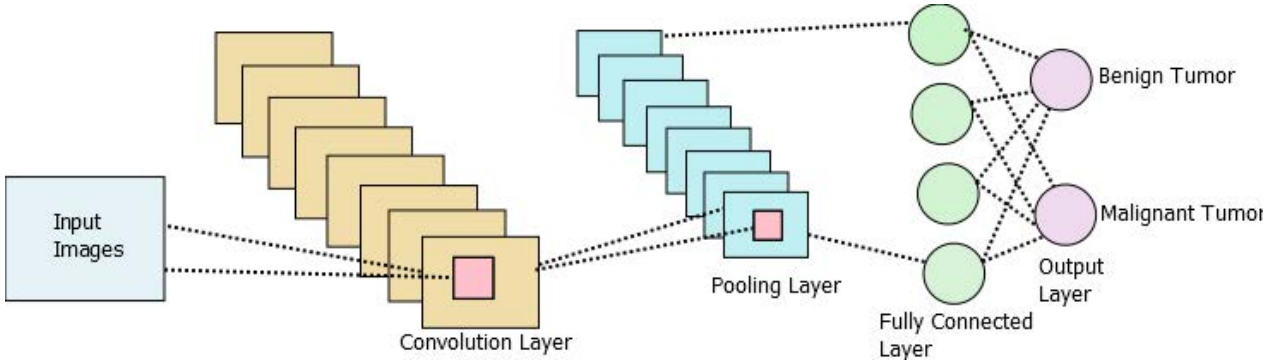

Fig. 6. Classification of breast cancer using CNN model

Alex net

The implementation of Alex Net is instrumental in achieving superior accuracy for the early detection of malignant breast tumours, ultimately contributing to a reduction in mortality rates. Alex Net is structured with five convolution layers, three pooling layers, and two fully connected layers, working in tandem with data augmentation techniques applied to breast mammograms for the purpose of classifying benign and malignant masses.

In the initial stages of the process, the mammogram image is transformed into grayscale and subsequently into a binary format. Tumour identification hinges on the pixel count within this binary object. If the binary object's pixel count with the highest value equals 1, the tumour is classified as malignant, whereas if the highest pixel count value is 0, it is categorized as a benign tumour. The final output image results from the multiplication of the input image by the binary image. In the case of the WBCD dataset, featuring 569 pertinent images and 30 attributes, which is modelled utilizing Alex Net, the achieved accuracy rate reaches an impressive 95.70% [25].

Visual Geometry Group Network (VGGNET)

The Visual Geometry Group Network (VGG Network) is a deep Convolutional Neural Network (CNN) distinguished by its incorporation of either 16 or 19 convolutional layers. The augmentation of convolution layers equips the network with the capacity to accommodate more intricate functions, thus enhancing its capability to attain high accuracy in output classification. This network accepts input images sized at 224 × 224 pixels, which are then processed through the convolutional layer. Subsequently, they pass through the Rectified Linear Unit (ReLU) function, where 3 × 3 minimal receptive field filters are employed. The ReLU function generates an output of 1 if the input is positive, and 0 otherwise.

In practice, the VGGNET-16 model was applied to a dataset comprising 2,795 images, each of dimensions 224 × 224 pixels, and it demonstrated an impressive accuracy rate of 92.7% [26].

Google net

The Google Net architecture is comprised of an impressive 22 deep layers. For its construction, approximately 100 layers are utilized, allowing for the inclusion of multiple filter sizes to effectively extract features of various dimensions. This enhancement in single-layer feature extraction proves instrumental in the effective extraction of breast cancer features.

Within the Google Net framework, three filter sizes 1 × 1, 3 × 3, and 5 × 5 are employed to perform the convolution operation on the input data. This process is complemented by max-pooling operations in tandem with convolution, using rectified linear activation functions. The output from this phase is then forwarded to the subsequent inception module to reduce the dimensionality of the feature set.

The receptive field's size is set at 224 × 224 pixels, encompassing RGB colour information with a zero mean [27]. In practice, Google Net was applied to a dataset containing breast histopathology images, and it outperformed Inception v3 and Alex Net in the classification of benign and malignant masses, achieving an impressive accuracy rate of 97.8% [28].

Residual Network (Res Net)

The Residual Network, often referred to as Res Net, is a Convolutional Neural Network characterized by an impressive 34 layers. The incorporation of a greater number of layers leads to the extraction of more intricate and complex features, ultimately enhancing the network's performance and accuracy.

Residual networks are constructed using residual blocks, and they introduce the concept of skip connections, allowing for the bypassing of certain network layers. These skip connections facilitate the model in learning identity functions, thereby contributing to the network's overall performance. A shortcut connection is introduced to enable identity mapping across consecutive convolutions [29].

In practical implementation, the Res Net model was employed for the analysis of mammogram images within the Mammogram Image Analysis Society dataset. This dataset comprises 322 breast mammogram images categorized as malignant, benign, and normal. The Res Net model achieved an outstanding accuracy rate of 98.39% [30-32] (Figure 7).

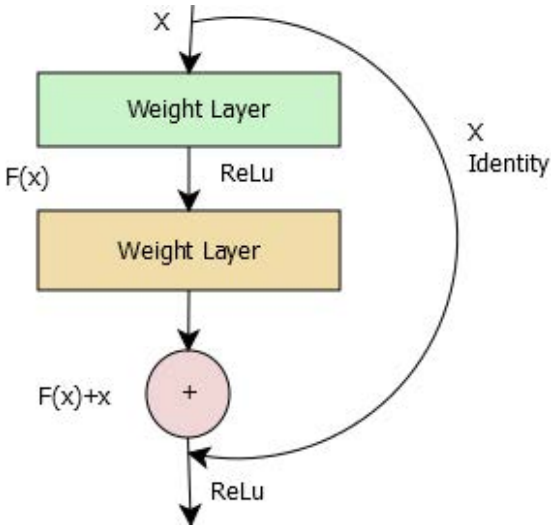

Fig. 7. Residual block of Res Net

Each residual block is represented in the form of:

$$qi = h(xi) + (xi, Wi) \quad (6)$$

$$xi + 1 = f(qi) \quad (7)$$

Where xi is input, xi+1 is output of it block, F is residual mapping function, h(xi)=xi is identity function, f is Re Lu function

Comparative analysis

Following tables shows the comparative analysis of ML and DL models (Table 1 and 2).

Tab. 1. Accuracy of classical machine learning models

Reference Paper	Dataset	Naive Bayes Classifier	SVM	KNN	Decision Tree
(OmarIbrahimObaid et.al., 2018)	Wisconsin breast cancer	78.54%	78.10%	76.70%	73.70%
(HibaAsri et.al., 2016)		85.12%	87.13%	85.28%	81.23%
(AliAlBataineh, 2019)		83.62%	86.42%	86.27%	81.00%
(Dada Emmanuel Gbenga et.al., 2017)		76.48%	77.07%	76.34%	76.48%

Tab. 2. Accuracy of deep learning models

Reference Paper	Dataset	Res Net	VGG Net	Google Net	Alex Net
(Zhantao Cao et.al., 2019)	Sichuan Provincial People's Hospital	85%	81.20%	80.80%	80.50%
Adeyinka P et.al., (2019)	Mammographic Image Analysis Society (MIAS)	98.39%	98.68%	95.06%	94.50%
Lazaros Tsochatzidis et.al., (2019)	DDSM-400	94.30%	94.80%	95.80%	93.30%
Lazaros Tsochatzidis et.al., (2019)	CBIS-DDSM	94.90%	91.60%	92.00%	85.30%

SanaUllah Khan et.al (2019)	ImageNet	94.35%	94.15%	93.50%	93.20%
Dr. D. Shanthi (2022)[33]	Breast Cancer	95.30%	96.70%	89.4%%	93.80%

CONCLUSION

Accurate diagnosis and classification of breast cancer are pivotal tasks in the field of medical diagnosis. A multitude of machine learning algorithms have been implemented for classification tasks using feature datasets. However, these machine learning algorithms encounter challenges when new predictive features are introduced, which can impact their accuracy. With the advancements in medical technology, many diagnostic laboratories have embraced image-based medical diagnostic approaches, such as MRI and Mammograms. These approaches have led to the generation of vast image datasets. Traditional machine learning models are well-suited for feature-based raw data but are less equipped to handle image data without specialized image processing. To address this issue, various deep learning algorithms have been deployed on diverse image datasets, including Ultrasound, Mammogram, MRI, and Histopathological images. These deep learning models have demonstrated improvements in classifier accuracy when compared to traditional machine learning models. However, it's worth noting that literature observations have indicated that deep learning models trained with image data may exhibit considerably higher false positive rates. For instance, Mammogram images often exhibit disconnected mass regions, some of which may resemble denser normal breast tissue. Deep learning models can struggle with classifying such images accurately, even misidentifying normal breast tissue as cancerous. This challenge is partly attributed to the segmentation algorithms used, which rely on pixel distances for mass distribution. In terms of future prospects, the focus is on applying more efficient preprocessing and segmentation algorithms. These algorithms aim to extract the breast boundary region with greater precision, effectively identifying highly and densely distributed cancerous masses while mitigating false positives.

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