



Review on Artificial Intelligence for breast cancer detection

Aiswarya J¹, Sanjith Shivan S², Umasankar S²

¹ Research Scholar, Department of Computer Applications, Sri Krishna Arts and Science College, Tamil Nadu, India

² Department of Computer Applications, Sri Krishna Arts and Science College, Tamil Nadu, India

DOI: <https://doi.org/10.66856/ijmrd.2026.13.3.13330>

Abstract

Breast cancer detection Artificial intelligence and early diagnosis. The incidence of breast cancer, among all the cancers affecting women worldwide, makes it the most prevalent one. Therefore, it causes many death. Early detection is the most important for better recovery.

Recently, Artificial Intelligence (AI), ML, and DL approaches are extensively utilized to assist clinicians with the accuracy and effectiveness of detecting breast cancer and other relevant health problems.

Breast cancers can be recognized by analysis performed on many types of image, including MRI, CT scan, X-rays, PET-CT scans and Ultrasound. The ability of AI models to interpret complex medical images accurately makes the diagnostic process quicker and reliable while simultaneously reducing diagnostic errors. In this research review, we introduce and cover the artificial intelligence approach toward breast cancer detection with the application of various types of algorithms such as, but not limited to, the Supervised Learning algorithms; Decision Tree (DT), Support Vector Machine (SVM), Logistic Regression, and Random Forest and the Deep Learning algorithms such as, the Convolutional Neural Network (CNN) & Transfer Learning (TL). This paper outlines used datasets ;Image preprocessing and Feature extraction in order to classify whether the image contains tumor or not, we will look at various performance evaluation metrics ; Accuracy (Acc), Precision (Pre), Recall (Rec) and F1 score (FS) which measure model performance by relating predicted results with actually labels and as well as Area under the Curve (AUC).

We cover also, pros and cons, issues and open questions in applying artificial intelligent systems to diagnostic imaging and some future studies which may lead to more efficient and interpret able systems which can help a great deal in saving many lives

Keywords: Breast cancer detection, Artificial intelligence, machine learning, deep learning, medical image analysis, mammography, CNN, diagnosis, classification, healthcare

Introduction

Breast cancer, the most commonly diagnosed type of cancer and a major cause of cancer-related deaths in women globally, arises from uncontrolled breast cell division that can lead to tumors that spread. Millions of cases of breast cancer are reported each year, and for many to improve chances of survival and a decrease in mortality rates, breast cancer must be identified in its early stages. Early methods for breast cancer identification include magnetic resonance imaging (MRI), mammography, ultrasound, and biopsy, which rely on specialists like pathologists and radiologists to conduct. Traditional breast cancer screening relies on humans' abilities, which can increase time or risk errors during diagnostics.

In the medical domain, machine intelligence or machine learning (ML) and deep learning (DL) has been implemented to replicate the cognitive skills of humans and computers as a transformative approach. ML is already being utilized in Medical image classification, early disease diagnosis, and clinical care decision support systems as these systems may evaluate a vast quantity of clinical data, find unusual patterns and classify images or cases, making it easier to assist radiologists. This research article aims to provide an overview of methods for detecting breast cancer, machine learning algorithm for the early detection of the cancer, feature extraction, datasets used, validation methodology, and future direction and the current scenario for developing new detection technologies in the current

scenario by using Artificial Intelligence. ML for breast cancer is very useful for predicting the malignant and benign class or classifying between two breast tumor types: malignant and benign tumors, the result was obtained by using different data mining models: Logistic Regression, decision trees, support vector machines (SVM), random forests, and Naive Bayes; DL is the next advanced step with impressive features where the results of the DL models outperform. The research aims at exploring various machine learning, and deep learning techniques used for breast cancer detection to achieve the higher efficiency and accuracy.

The results showed how Artificial Intelligence techniques for breast cancer diagnosis can really help doctors and lead to diagnosis and more patients surviving. Artificial Intelligence is changing the way we learn. It is one of the important technologies in education now. Artificial Intelligence has changed how schools collect and look at student information.

Traditionally teachers looked at test scores and homework to see how well students were doing. They also looked at attendance records. Did assessments by hand. These methods are helpful. They do not always find students who need help early on. Now with many people learning on computers and schools keeping lots of data they have a lot of information about students. Artificial Intelligence is helping schools use this information to support students and Artificial Intelligence is making a difference, in education.

Literature Review

1. Logistic Regression

Logistic Regression is a commonly utilized supervised machine learning algorithm used for the classification purposes and it's typically employed when we have a target variable which comes down to only two outcomes or outcomes. For instance, we often use Logistic Regression to perform the breast cancer diagnosis where tumors are classified as either benign (non-cancerous) or malignant (cancerous), with the help of a couple of input clinical and diagnostic characteristics. Though the algorithm is known as the regression model because it predicts the possibility of a given test case belongs to a specific class and has the value for that category is likely to fall into a probability value of somewhere between 0 to 1 and yet we use this algorithm as a classification purpose and it's one of the basic models for any medical diagnostic work. The sole purpose of this logistic regression model is to determine the chances of a breast cancer case being cancerous depending on input values from physical tests. The input variables used for such a problem could consist of the size, radius, area, and other

features of a tumour, which can be taken from the tests like X-ray, CT scan, and MR scans. These data is fed to the Logistic Regression model for it to learn the correlation between these characteristics and the final output. Once the learning process has completed, the trained model would predict either 'benign' or 'malicious' based on these test cases. In this, unlike linear regression, it doesn't predict exact continuous value, rather the prediction of logistic regression results into the value which is the probability that can exist in the range of 0 and 1 by implementing the use of sigmoid function (also known as logistic function). If this value will be greater than or equal to 0.5 then that test case would fall into the category of "malignant", whereas if the predicted value is lower than 0.5 it will be categorised as "benign". For the Breast cancer diagnostic problem, we often use a large dataset called Wisconsin Breast Cancer Diagnostic (WBCD) which have multiple entries of tests with hundreds of cells with a couple of hundred different tests to provide inputs to train the Logistic regression algorithm.

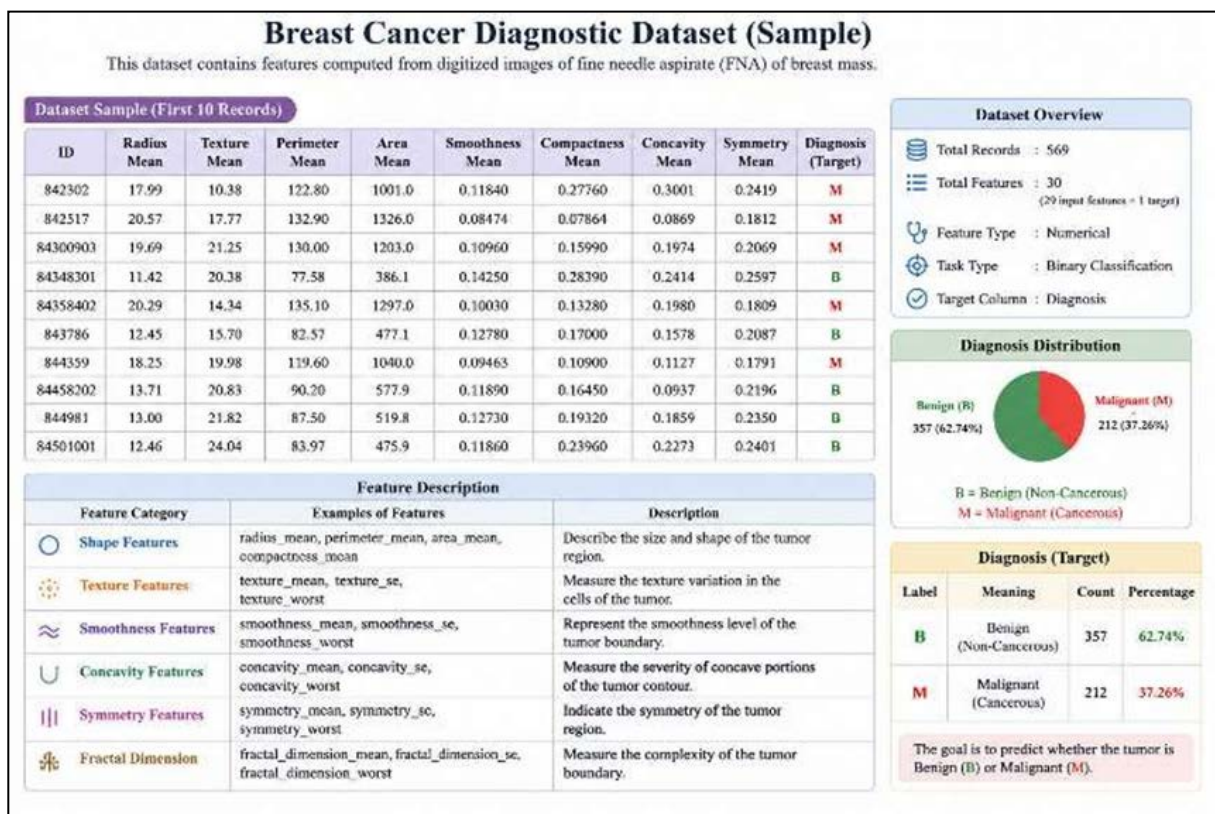


Fig 1: Dataset and diagnosis

This particular data is commonly used in academic research and also it works perfectly as a benchmark for Machine Learning algorithms that perform the breast cancer test. These tests results used for training the machine learning model include tests such as radius, texture, area, smoothness, compactness, concavity, symmetry, fractal dimension etc, which is computed from digital imaging and imaging techniques used to extract features for breast cancer cell classification. The performance of this algorithm can then be gauged by other metrics like, precision, recall, confusion matrix, ROC curve etc., along with overall accuracy which for Logistic regression on WBCD dataset is

seen to be around 95-98%. The significant benefits of using Logistic Regression are its speed and its interpretability. This machine learning model's speed means it works much better and faster when compared to the advanced models and its accuracy is significantly high and reliable. However, when working with large data sets of tumors, for example images of cell clusters, with complex structure like textures, a logistic regression might prove not efficient enough. For the classification tasks involving the extraction of complex features from images of cell clusters like texture, the other models like random forest, SVM or gradient boost are more efficient than logistic regression. This could be because of

logistic regressions tendency to produce a linear decision boundary and because it's not designed to learn non-linear associations between the input parameters and outcome which may result in less-optimal models on image based data.

2. Decision Tree

Decision Tree One of the most prevalent supervised machine learning algorithms is Decision Tree, used in classification and prediction tasks. It's extremely useful in situations when you're trying to classify information into definite categories by looking at a variety of features of information! For breast cancer, you'll use Decision Trees to classify tumours as either benign (not cancer) or malignant (cancer) by looking at various factors from the data of patients. They form a tree-like structure composed of nodes and branches, where branches indicate the outcomes of the decisions of the internal nodes, and the leaf node indicates the actual prediction. Because they work like how we human makes decision, these algorithms are very understandable by doctors and can be utilized in automated cancer detecting programs. It's so understandable that it's one of the most straightforward algorithms out there and commonly utilized by doctors. They basically make recursive partitioning on the information by selecting the "best" features each moment. You will assess the features, pick the feature that makes you have the least entropy, the greatest information, and/or least gini score to split your data, and continue doing it recursively until every one of the specimens in your database are classified to one thing, or the tree stops growing.

Features are usually measured and determined to be best by either Gini index, Information gain, or Entropy in order to be able to split your data optimally. One of the common datasets utilized in research using this algorithm is Wisconsin Breast Cancer Diagnostic (WBCD) dataset. In this data-set there's around 500 patient's records and several measurements collected by digitizing images of fine needle aspirate (FNA) tests of breast masses and then examining the cell features, and whether the tumour was malignant or benign. But, first, you want to ensure your information quality and remove duplicate and useless attributes (but you're also allowed to do that even without using Decision Trees) and fill in some information that's missing and clear unnecessary noise in information. Decision Trees don't require you to scale information before hand, although that can help the model in some cases; and after this stage you'll need to split your information into training set, and testing set to avoid overfitting, you might want to use cross validation to ensure its generalization. Decision Trees are perhaps the simplest machine learning algorithms you can implement! Unlike many complex and so called "black box" models that you would be totally unable to understand how it reached the decision, with decision trees, you will be able to interpret exactly why and how it decided the tumor is malign or benign. For example, it could first look at tumor's radius, then evaluate its smoothness, and then its compactness before concluding that it is malignant. The reasons behind decisions can always be represented to help doctors, and make it trustworthy for them in a medical

scenario. With this explainable nature it has been used for AI's in health-care for various cases. Another great perk is how efficient and quick Decision Tree models are. They aren't computationally intensive like deep learning algorithms and it can be trained easily, without the need of powerful processors or supercomputers. This makes it a good choice for less well-funded or less computationally available clinics and health-care facilities.

Another advantage is that Decision Trees can work with both numerical and categorical data and doesn't require explicit feature normalization or standardization beforehand, and they can auto-identify relevant diagnostic features that contributes to cancer diagnosis by itself, which could further lead to discovering more related features and biological insights that can help in treating cancer. After training the model, you evaluate its predictive power using a set of evaluation measures. For the binary classification case you have Accuracy, which represents the fraction of all samples that was classified correctly; Precision, which measure how many of the samples that the model predicted as cancerous actually are cancerous; Recall (sensitivity), which is the proportion of actually cancerous samples that were correctly identified as cancerous; Specificity, which indicates how many of the samples that are not cancerous were correctly identified as not cancerous; F1-Score, a measure which blends precision and recall; Confusion Matrix, a table of all outcomes; ROC curve and its Area Under the Curve (AUC) score, to assess the discriminative performance of the model. For a good decision tree classifier for this problem, we usually expect to get an Accuracy of above 93% to 97% (and this depends highly on data processing and feature selection). Although Decision Trees are beneficial, there are drawbacks as well, the main one is called overfitting, which happens when the tree grows too large and starts to fit noise and special data-points rather than the general pattern, leading to very poor performance on unseen data. This can be addressed by techniques like tree pruning, and adjusting other parameters like maximum depth, minimum sample split, and minimum leaf size.

Decision trees are also highly sensitive to input changes; slight modification in data can lead to entirely different trees; thus, creating non-robust and unreliable predictions. Decision Trees often can't model extremely non-linear relations so if the information consists of complex high resolution medical imaging information like mammograms or MRIs, then ensemble approaches like Random forest or deeper architectures such as Convolutional neural networks (CNN) are a more suitable choice. The Decision Tree classifier is used in Computer Aided Diagnosis programs to help doctors and oncologists find out if someone has breast cancer. Decision Tree algorithms are, like tools that help medical professionals make decisions. They do not replace the doctor. They do give them more information to think about. People trust the Decision Tree classifier because it is easy to read. This makes doctors feel more assured when they use computers to help them diagnose patients with breast cancer. The Decision Tree classifier is a thing because it is easy to understand and it helps doctors do their job better.

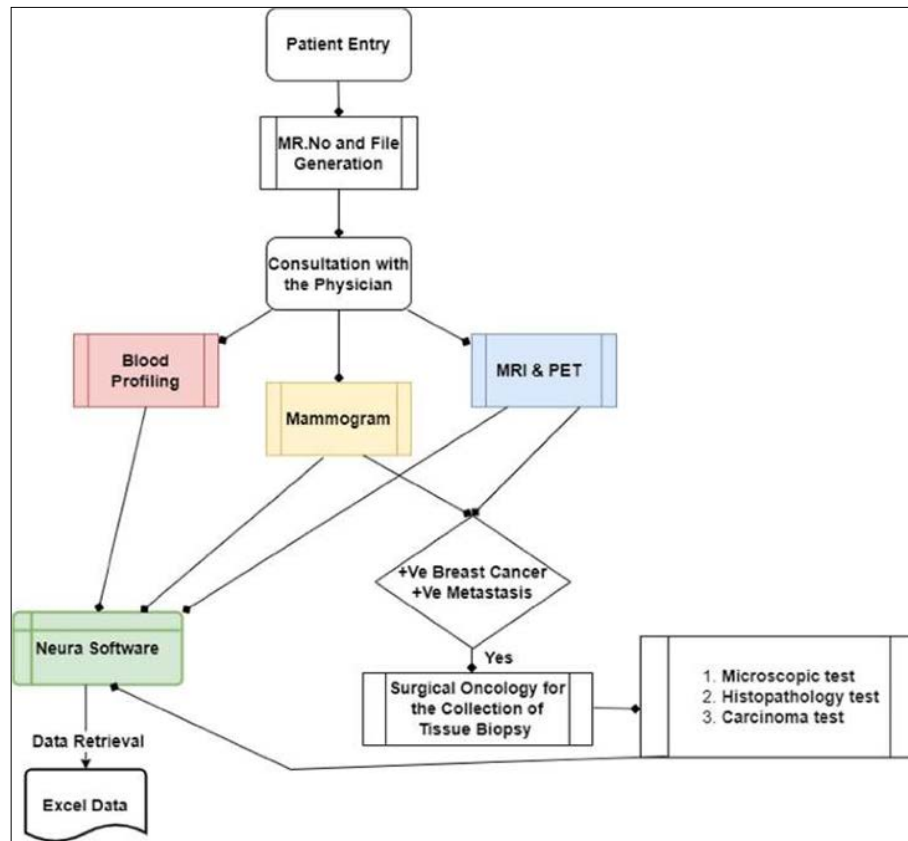


Fig 2: Prediction of Patient using Decision Tree

Random Forest

Random Forest is one of the most powerful and widely used supervised machine learning algorithms for breast cancer detection and classification. It fits into the category of ensemble learning algorithms, where multiple machine learning models are combined to improve prediction accuracy and reliability. In context of breast cancer diagnosis, Random Forest is used for classifying tumors as benign or malignant on the basis of results of certain clinical and diagnostic tests. Contrary to the standard Decision Tree, Random Forest is an ensemble algorithm which means that it uses multitude of decision trees to arrive at a prediction. Moreover, Random Forest has been shown to perform better than the standard decision tree by reducing overfitting and bias which leads to more accurate predictions. Due to its superior accuracy and ability to generalize well in medical domain, Random Forest has found wide application in diagnosis of diseases including breast cancer. The way in which Random Forest accomplishes this is that it constructs decision trees from randomly selected subset of data. When the data is randomly selected from the data set, the process is referred to as bootstrap sampling. Random Forest uses this method to create Decision Trees and then it uses all of these Decision Trees to make predictions. The main idea, behind Random Forest is to use Decision Trees to improve the accuracy of the predictions made by Random Forest⁷⁷. Each bootstrap sample is used to train an individual Decision Tree. The algorithm does not just pick data samples. It also picks a subset of input features for each Decision Tree when it is trying to find the best split at every node. This is called feature bagging. Feature bagging helps each Decision Tree learn things from the data. So the Decision Trees are all different. This means they do not all

make the mistakes when they are making predictions. The Random Forest model combines what each Decision Tree thinks. It does this by using a majority voting mechanism. Each tree in the decision forest indicates whether it deems the tumor to be benign or malignant. The random forest classifier then analyzes the results from all the decision trees in order to determine which classification is endorsed by the majority of them. This way of making decisions makes the Random Forest model more accurate and stable, than just using one Decision Tree. The Decision Trees work together to make a prediction. The Random Forest model uses all of the Decision Trees to make the prediction.

In breast cancer detection, the Random Forest algorithm is usually trained by using the Wisconsin Breast Cancer Diagnostic (WBCD) database. The database consists of 569 patient records, of which 357 were diagnosed with benign tumors, while 212 had malignant growths. The 30 variables represent the digitized images of fine needle aspiration tests. Thus, there are 30 numerical attributes in Random Forest, including tumor radius, texture, perimeter, area, smoothness, compactness, concavity, concave points, symmetry, and fractal dimension. All of these attributes are relevant for diagnosis since they help distinguish between benign and malignant tumors. Before training, it is critical to note that the data needs to be pre-processed. For example, some data may need to be deleted, or special symbols, such as "NaN," may need to be replaced if they are present in the data set. In addition, it is essential to make sure that the data set is divided into a training set and a test set. Usually, 80% of data is used for training, and 20% is used for testing; however, sometimes, 70% of data is used for training, and 30% is used for testing, and other variations are possible. Apart from that, it is possible to use cross-validation methods. Since Random Forest is an ensemble algorithm,

which combines many Decision Trees, there is no need for data normalization, or scaling.

An essential benefit of the Random Forest is that it prevents overfitting, which is inherent to Decision Trees. In other words, the algorithm reduces the risk that the same information, which was used to train the model, will be incorrectly predicted again. If applied to medical data, it means that the algorithm will not guess the same patient record each time. Instead, it will be able to generalize the information and provide consistent results. Moreover, the algorithm is less sensitive to the outliers, missing data values, and noisy measurements since it provides reliable predictions across various samples and sets of data. In addition, using the Random Forest, one can make an estimate of how meaningful each attribute is in terms of prediction. For instance, in case of breast cancer, it will be possible to identify which tumor characteristics contribute to malignancy. When predicting patient records, the Random Forest algorithm offers high performance, which is estimated by various statistical measures. Most often, medical researchers and practitioners use the accuracy threshold to evaluate how good their algorithm is. It basically represents a percentage of correctly predicted records. In addition, medical practitioners use other evaluation metrics, including precision, recall (or sensitivity), specificity, F1-score, confusion matrix, ROC curve, and AUC. For most tasks relating to tumor detection, the accuracy of the Random Forest algorithm is between 96% and 99%. In other words, the algorithm can correctly

predict 96 to 99% of cases. In medical practice, it would mean that doctors can correctly differentiate between malignant and benign tumors. Therefore, the algorithm has great potential in breast cancer detection by helping practitioners identify malignant tumors in early stages.

However, the Random Forest algorithm has some disadvantages, such as higher memory consumption as compared to other machine learning algorithms. Since the algorithm combines hundreds of Decision Trees, it requires more computing power and memory than, say, Logistic Regression. As a result, the model becomes slower in both training and prediction. In particular, there is no point in using the Random Forest algorithm on large-scale data, as there are too many trees to process. Another limitation is interpretability. While a single Decision Tree produces a straightforward sequence of decisions that can easily be understood by healthcare professionals, Random Forest combines the outputs of many Decision Trees, making the overall prediction process less transparent. Although feature importance scores provide some interpretability, the algorithm is generally considered less explainable than simpler models. Furthermore, Random Forest may not outperform deep learning algorithms such as Convolutional Neural Networks (CNNs) when working directly with high-resolution medical images because CNNs automatically learn complex visual features from imaging data. Nevertheless, for structured clinical datasets containing numerical diagnostic features, Random Forest remains one of the most effective machine learning techniques available.

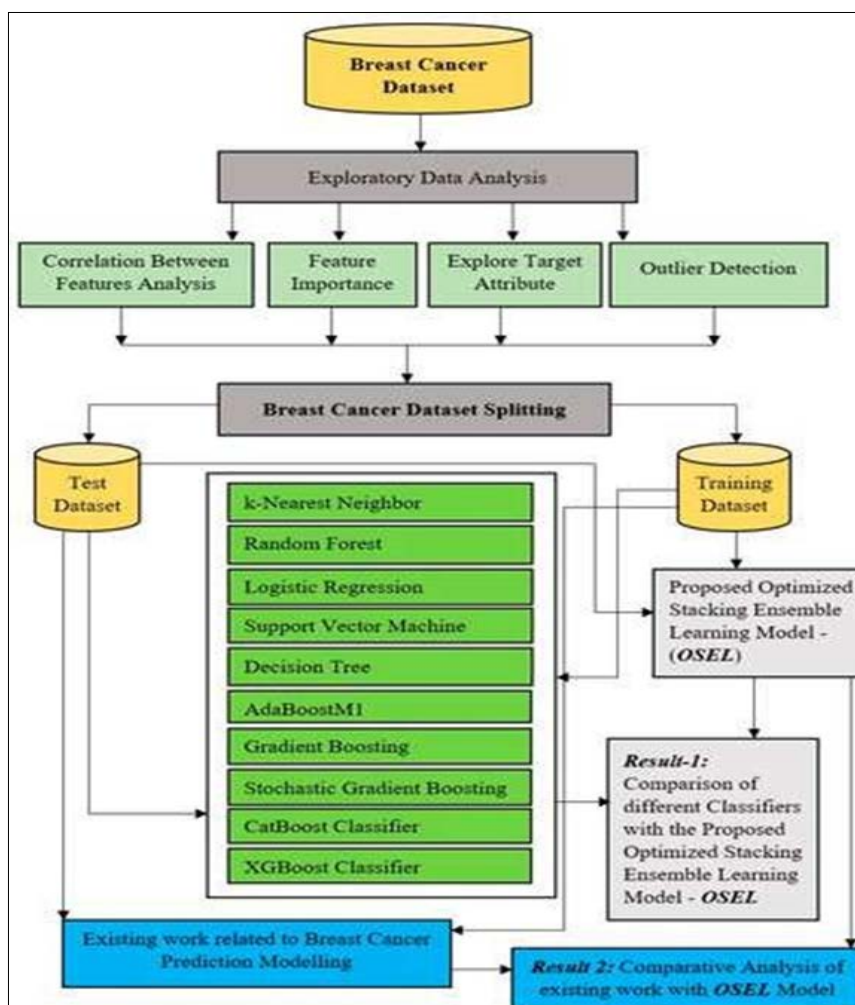


Fig 3: Random Forest in Machine Learning

In practice, the Random Forest algorithm is used in a wide range of computer-aided diagnosis (CAD) systems that help radiologists, pathologists, and oncologists in breast cancer screening and treatment. The algorithm is not intended to replace medical professionals but rather to serve as an auxiliary tool that analyses patients' data and yields plausible predictions based on them. In doing so, Random Forest helps reduce the rates of false-positive and false-negative diagnoses and enables medical workers to make better-informed decisions regarding the treatment. The algorithm helps identify crucial predictors associated with disease progression and serves as a valuable asset in medical research while enabling the establishment of individualized approaches to patients' care. Healthcare facilities and researchers continue to rely on the Random Forest classifier because of its accuracy, versatility, and impressive performance.

In essence, the Random Forest algorithm is one of the most accurate and reliable algorithms of machine learning that can be applied in various fields, including medical imaging and data analysis. Its capacity to perform well in binary classification tasks, paired with reduced computational complexity, makes it a great option for solving medical problems. It is resistant to overfitting and has demonstrated excellent performance in the presence of missing data. The algorithm is appropriate for implementation in the healthcare setting due to its ability to work with high-dimensional data, utilize crucial factors in making predictions, and identify unimportant variables that can be deleted from the data set. Although the newer deep learning algorithms demonstrate slightly better accuracy in image segmentation and detection tasks, Random Forest remains vital in medical research because of its ability to analyze structured data and help clinicians in providing care. After data preparation, parameter tuning, and validation, the Random Forest algorithm can reach accuracy rates of 96-99%, which makes it a valuable asset in the detection of breast cancer.

3. Support Vector Machine (SVM)

Support Vector Machine (SVM) is among the most efficient and popular supervised machine learning algorithms used for classification tasks. This algorithm offers an effective approach to tackle binary classification issues like detecting if a tumor is benign or malignant. The SVM is a robust classifier that works efficiently with high-dimensional data making it an ideal choice for diagnosis purposes where data sets tend to be large and complex. Its ability to generalize from complex data sets and achieve accurate classifications has made it an essential tool in computer-aided diagnosis systems for breast cancer detection. The basic concept of Support Vector Machine revolves around finding the best decision boundary, called a hyperplane that can separate input data points into different classes. When it comes to breast cancer detection, an SVM classifier is fed with diagnostic or clinical features extracted from either tissue samples or medical images. These features may include radius, texture, perimeter, area, smoothness, compactness, concavity, concave points, symmetry, and fractal dimension. The machine learning algorithm then attempts to find a hyperplane that best separates malignant tumors from benign tumors. In SVM, the hyperplane is determined by the data points that are closest to it. These points are known as support vectors. By maximizing the distance between the

hyperplane and the support vectors, an SVM classifier can reduce classification errors and increase its accuracy in making predictions.

The most significant advantage of an SVM is that it can perform both linear and non-linear classification, which makes it one of the most flexible and powerful machine learning algorithms. In instances where the data set is linearly separable, a Linear SVM can be used. However, most medical data sets, including breast cancer diagnostic data, tend to be non-linear, which means that a linear decision boundary may not be sufficient in capturing the underlying patterns in the data. In such cases, a kernel trick can be used to transform the input data into a higher-dimensional space, where a linear decision boundary can be formed. Several kernel functions are available that can be used in SVM, including Linear, Polynomial, Radial Basis Function (RBF), and Sigmoid. In the case of breast cancer, the RBF kernel is a good choice for the task because it is the best option for non-linear classification of medical data.

Support Vector Machine is often trained on the Wisconsin Breast Cancer Diagnostic (WBCD) data set, which is one of the most popular data sets in medical data mining. The data set consists of 569 patient records, with 357 and 212 patients having benign and malignant tumors, respectively. Each patient record consists of 30 different diagnostic features extracted from Fine Needle Aspiration (FNA) images, such as tumor radius, texture, perimeter, area, smoothness, compactness, concavity, concave points, symmetry, and fractal dimension. Prior to training an SVM model, the data set is often preprocessed to remove irrelevant information, such as missing data points, and reduce the overall dimensionality of the data. This can include selecting or extracting the most informative features to train the model on. In addition, the data must be normalized or standardized to have the same scale and range so that the SVM Classifier can achieve better results. Unlike Decision Trees and Random Forest, this algorithm is sensitive to the data's scale, which requires the data to undergo preprocessing. The data must also be divided into training and testing sets, with a recommended ratio of 80:20 or 70:30. The validation process also can be done using cross-validation. The Support Vector Machine algorithm has some outstanding advantages, including the ability to work with high-dimensional data and overcome the curse of dimensionality. SVM is appropriate for medical diagnoses since it rarely overfits, especially when the number of features is higher than the number of observations. In addition, it shows accurate results when working with a small amount of data, which is usually the case in medical research since collecting the necessary amount of data for training can be challenging. Since SVM is based on a linear model, it rarely produces false positives and negatives and is not significantly affected by outliers.

The accuracy of the Support Vector Machine can be evaluated by such metrics as accuracy, precision, recall or sensitivity, specificity, F1-score, confusion matrix, ROC curve, and AUC. These metrics describe the performance of SVM in terms of the correct identification of malignant tumors and the absence of false-positive and false-negative results. According to many research studies, SVM shows the best accuracy scores, which are usually between 96% and 99%, which is why it is one of the most effective algorithms used in medical research. At the same time, the most critical metric for this particular task is sensitivity,

which describes a model’s ability to detect positive cases correctly. For instance, in cases of breast cancer diagnoses,

there is no other choice but to remove the tumor, and only an accurate model will help save lives.

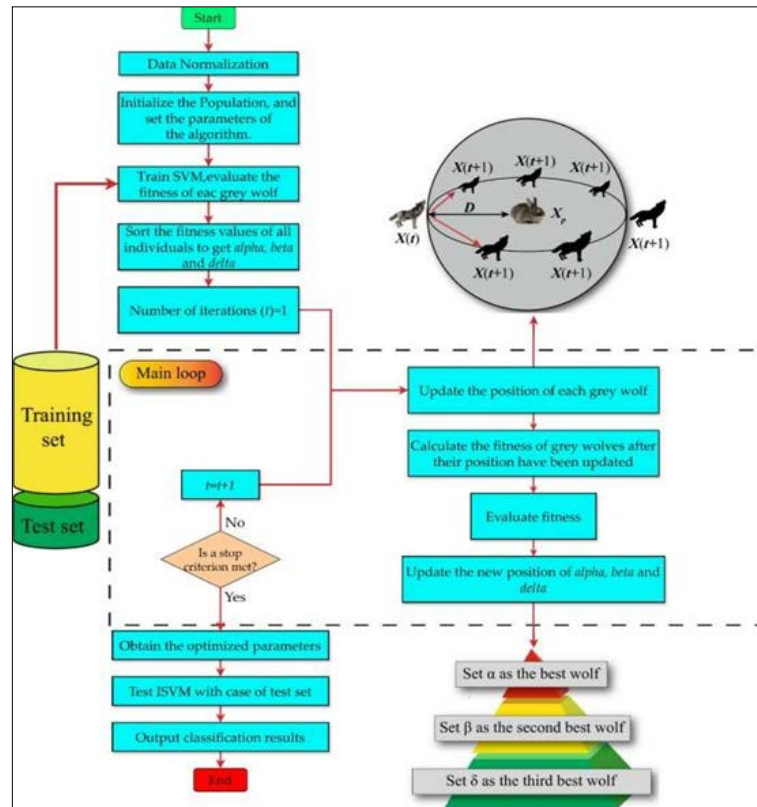


Fig 4: Support Vector Machine

Though it has numerous advantages, Support Vector Machine has a number of disadvantages as well. Firstly, finding an optimal kernel function and regularisation parameter C , and determining such hyperparameters as the kernel coefficient (γ) is a complex task. Secondly, if one has a large amount of data, the support vector machine (SVM) algorithm might become slow because of its computational complexity. Secondly, when dealing with huge amounts of data, the SVM classifier becomes slower since the optimization process becomes computationally expensive. Thirdly, there is the issue of interpretability. Unlike Decision Trees, which clearly show how input features influence the outcome, SVM’s mathematical model is too complex for an average healthcare professional to understand, making its use in medical practice inappropriate due to the need to provide justification for every result. Lastly, though Support Vector Machine is a powerful algorithm for analyzing structured data, such as patients’ records, Deep Learning approaches demonstrate better accuracy in medical image analysis, especially when using CNNs for image processing. In medical practice, Support Vector Machine finds its applications in developing Computer-Aided Diagnosis systems for breast cancer detection. Typically, such systems operate by analyzing patients’ scans and giving an indication for suspicion of tumor presence. In this context, it should be noted that SVM is presented as an efficient decision-making tool that helps oncology doctors accurately diagnose malignant tumors. In this regard, it is possible to note that the algorithm can contribute to the early detection of breast cancer, which is essential for successful therapy. Additionally, the method can be instrumentalized in analyzing medical records to

identify potential biomarkers or predict the natural history of the disease. Overall, it is possible to conclude that Support Vector Machine is an effective classifier that can be used in the medical field to process structured data.

Overall, it is possible to suggest that SVM is a highly efficient algorithm that is beneficial for various forms of medical practice, including tumor detection and analysis of health records. The ability of the algorithm to maximize soft margins and accurately classify data points, including the cases of multidimensionality and nonlinear decision boundaries, makes it a favorable choice among other machine learning methods. Though it has been partially overtaken by Deep Learning methods, which demonstrate better performance when it comes to image analysis, SVM remains one of the most efficient methods of data classification. Moreover, when properly tuned, SVM shows accuracy up to 96 – 99%, making it a reliable source for developing diagnostic systems.

4. Convolutional Neural Network (CNN)

The Convolutional Neural Network is one of the best and most advanced deep learning algorithms used in Breast Cancer Detection and Classification. This algorithm is primarily used in the analysis of image data and is highly effective in the identification of patterns such as mammograms, ultrasound images, MRI scans, and Histopathologic images. Unlike other artificial neural networks that require manual feature extraction from medical images, CNNs can autonomously learn key features directly from the data. This unique characteristic improves its accuracy in classifying benign and malignant breast tumors, making it one of the most popular algorithms in

medical image analysis and computer-aided detection of breast cancer. The working principle of Convolutional Neural Networks can be explained by discussing how they perform the recognition of breast cancer in medical images. First, in general, any Convolutional Neural Network (CNN) is consisted of several types of layers: input, convolutional, activation, pooling, fully connected, and output layer. The input layer gets the medical image of a breast as input data. Then, the convolutional layer scans it through multiple convolutional filters and extracts vital features like edges, shapes, and contours of neoplasms. The convolution operation helps to reduce image size and allows recognizing key elements distinguishing benign from malignant tumors. After that, the pooling operation is applied to further reduce the size of convolutional layers outputs, retaining important information. The activation function is vital to allow CNN to learn and identify patterns in data, which are not linearly separable. Usually, the Rectified Linear Unit (ReLU) function is used to add nonlinearity. Fully connected layers receive pooled convolutional outputs and process them in order to classify tumors in benign or malignant forms. Finally, an output layer reports the classification result of a tumor: malignant or benign.

The performance of CNN is usually evaluated using multiple classification metrics, including accuracy, precision, recall or sensitivity, specificity, F1-score, a confusion matrix, Receiver Operating Characteristic (ROC) curve, and Area Under the Curve (AUC). For medical image recognition tasks, most of these metrics should have high values in order to ensure sufficient performance of CNN, distinguishing benign from malignant tumors, avoiding false-negative and false-positive results. According to the research studies, for most of the standard benchmarks of breast cancer recognition, CNN demonstrated the average accuracy of 97 – 99%. For majority of CNN architectures, the accuracy is comparable to an experienced human radiologist in terms of malignancy probability of tumor classification. Thus, CNN can be successfully used in real-time medical settings in order to assist humans in diagnosing breast cancer, improving healthcare outcomes. Another strength of CNN is its ability to learn non-linear relationships between input features in medical images.

Most medical images are usually complex as they contain a wide range of information such as tumor morphology, size, shape, margin definition, density, and texture. Traditional machine learning algorithms such as Logistic Regression and Decision Trees are not capable of learning complex non-linear patterns in medical images. However, CNN can effectively detect intricate patterns and irregularities in imaging data, making it suitable for analyzing mammography, ultrasonography, MRI scans, and histopathological images. Besides, CNN can be combined with transfer learning techniques that allow fine-tuning of the algorithm using a big set of images and improving the accuracy of medical image classification. For instance, such methods as VGG16, ResNet50, DenseNet121, InceptionV3, EfficientNet, and MobileNet are transfer learning techniques applicable to medical image classification tasks. Thus, transfer learning can help reduce the amount of training data required while improving the performance of CNN in classifying benign from malignant tumors.

Even though CNN has several strengths in classifying medical images, it also comes with some weaknesses or shortcomings. For instance, CNN requires a large dataset to train the algorithm to detect tumors in medical images accurately. First, acquiring medical images is usually costly since it requires advanced imaging modalities such as MRI and scanners. Moreover, medical images need to be annotated by qualified radiologists and pathologists before they can be used to train a CNN model. Secondly, CNN requires a powerful Graphics Processing Unit (GPU) to train the model using a large set of images. The main limitation of training a CNN is the amount of time it takes to train the algorithm, which makes it computationally expensive, especially when working with large datasets. Another disadvantage is that a CNN is a black-box type of model, which means that it is not human-interpretable. Most clinicians would not want to use a CNN in practice, such as in computer-aided diagnosis, because they would be unable to assess how the model arrives at its conclusions. The use of post-processing algorithms such as Grad-CAM and saliency maps render a CNN interpretable by design in that they enable the identification of the image features that have the highest impact on the model's prediction.

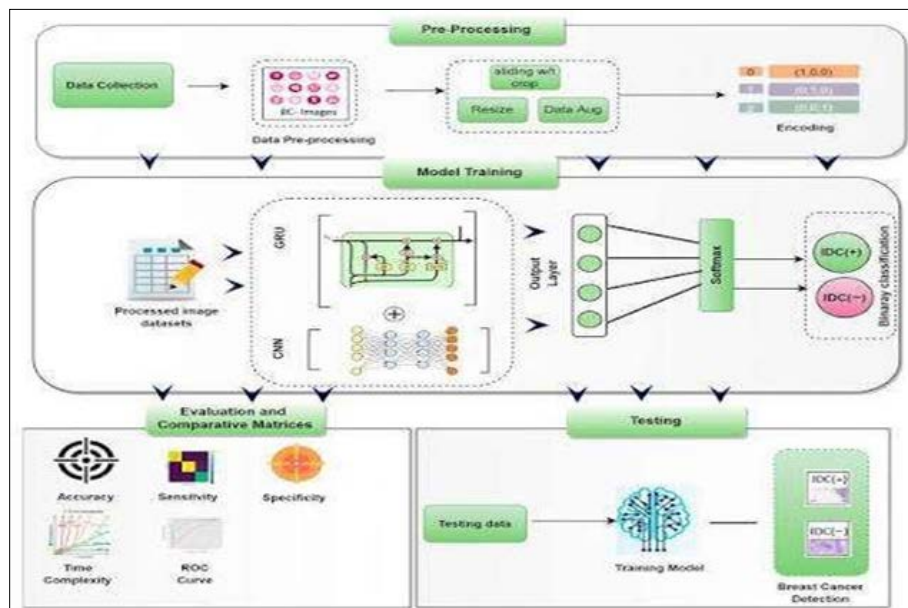


Fig 5: Repetition of CNN

In terms of practical implementation, CNN is mostly used in the context of Computer-Aided Diagnosis (CAD) for breast cancer screening. The primary application areas of Convolutional Neural Networks include medical image processing, visualization, and recognition, where it typically performs the analysis of mammography pictures and other imaging data. In this context, CNN is usually used as an auxiliary tool that helps pathologists and radiologists detect tumor sites, evaluate malignancy risk, and determine normal or abnormal tissues. Thus, it plays a critical role in diagnosis and treatment while being used as an advanced screening tool due to its ability to provide accurate results and reduce human intervention. In the early detection of breast cancer, timely and accurate identification of malignant tumors is vitally important to determine the further stages of treatment, tumor removal, and the prognosis of the disease. In addition, CNN is used in medical research for tumor segmentation, classification, and analysis, as well as for developing alternative AI-based approaches to healthcare.

To summarize, Convolutional Neural Network can be considered the best practice for tumor detection due to its ability to identify patterns automatically and achieve high accuracy rates in classification. Overall, CNN is a deep learning algorithm that excels at image recognition, making it a perfect candidate for tumor detection in mammography. The accuracy of such networks is normally very high due to the application of multiple convolutional layers that process images in great detail to extract relevant patterns and features. Thus, multiple factors contribute to the high efficacy of CNN in tumor screening, which allows it to become one of the essential parts of a variety of artificial intelligence systems. Although convolutional neural networks require extensive amounts of computational power and data to operate, their high accuracy rates make them a viable choice for early breast cancer detection. For example, networks of this type can achieve 97-99% accuracy rates in detecting malignancy, which makes them one of the most efficient ways of developing a successful treatment plan in breast cancer cases.

5. Transfer Learning

Transfer learning is one of the most sophisticated and effective deep learning methods that can be used for the

detection of breast cancer and medical image classification. Essentially, the concept of this approach is to utilize the information obtained from one machine learning model and apply it to train another one in order for the latter to perform its specific task. More concretely, Transfer Learning refers to a set of strategies that allow a neural network to train on some other data apart from the ones it will actually work with. For instance, scientists can use a pre-trained convolutional neural network that has already learned the most frequent patterns from natural images in order to re-train it on medical scans containing benign and malignant tumors. Since obtaining a high-quality medical data set is a complicated and time-consuming process, Transfer Learning is an extremely common approach for artificial intelligence-powered breast cancer classification.

The way Transfer Learning works is based on the fact that scientists do not have to start training their neural network from scratch every time they need to solve a new task. In other words, already trained networks can be used as tools to build other networks. The reason why it is possible is because the majority of deep learning methods are based on the same mathematical principles and algorithms. For example, a convolutional neural network that was trained to identify different objects in images can be utilized to detect breast cancer. The reason why it works is because the network already knows how to analyze the basic patterns in images, such as edges, corners, shapes, colors, and others. Even though natural images and medical scans have little in common, the majority of the learned patterns can still be used in the process of tumor detection. Specifically, when scientists employ Transfer Learning for medical image classification, they usually retain the part of the network that was responsible for learning the fundamental patterns while replacing the remaining part that is specific to the task of the network, such as the breast cancer classification head. After that, they fine-tune the new network using medical images so that it can learn to perform its task effectively. Overall, this method is extremely effective in medical image classification because it allows scientists to accomplish their goals while using limited data sets.

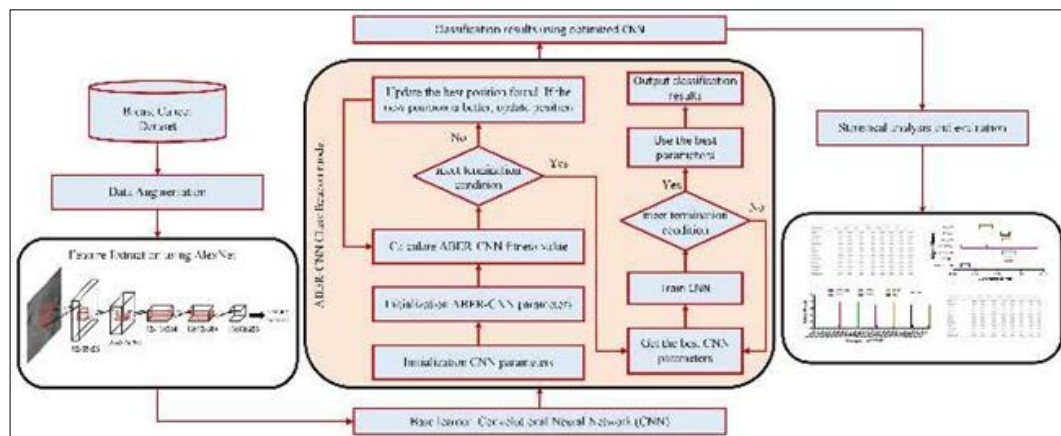


Fig 6: Transfer Learning Analysis

Conclusion

Artificial Intelligence appears to be a promising technology with regard to faster, better, and more reliable clinical

decisions in breast cancer diagnosis than many conventional techniques. In the present review article, the performance of six machine learning (ML) -based Artificial Intelligence

(AI) algorithms including Logistic Regression, Decision Tree, Random Forest, Support Vector Machine (SVM), Convolutional Neural Network (CNN), and Transfer Learning were assessed by considering their applications, advantages and disadvantages, and accuracy in breast cancer diagnosis. Each of the aforementioned ML algorithm seems to have a brilliant performance in detecting whether cancer is benign or malignant by learning from the patients' clinical information and imaging data to assist clinicians in their final decision-making.

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