



# Breast Cancer Prediction using Deep Learning

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**Abstract :** Breast cancer poses a severe exposure to women because it is one of the most prevalent diseases in women. Healthy cells in the breast begin to alter and expand out of control to form a tumor, which is a mass or sheet of cells. A tumor may be benign or malignant. Malignant describes a cancerous tumor's capacity to grow and spread to various body parts. A benign tumor is one that is still growing and has not yet spread. Given the constantly increasing danger of death from breast cancer, early cancer detection has become absolutely essential. Based on deep learning, it may be possible to predict breast cancer. Deep learning algorithm neural network is constructed for detection of breast cancer using different datasets namely Wisconsin Breast Cancer Dataset (WBCD), MIAS Mammography Dataset and Breast Cancer Histopathological Database (Breakhis). We have collected dataset and applied pre-processing algorithm for the data and then we splitted dataset in training and testing purpose and then we implemented model on training dataset. Three regular Machine Learning models, namely logistic regression (LR), decision tree (DT), random forest (RF) were compared with the Deep Learning Neural Network (NN). The accuracy of cancer detection by experienced physicians is 78%, while deep learning techniques can provide accuracy of up to 98%.

**IndexTerms - Breast Cancer, Malignant, Benign, Deep learning, NN, Machine learning, Decision Tree, Random Forest, Logistic Regression.**

## I. INTRODUCTION

Cancer is a condition in which the abnormal cells divide and destroy the normal body tissues. Cancer can affect any human body part, but breast cancer is found to be the most common cancer type. Risk factor for most cases of breast cancer is due to a combination of factors which are genetic and environmental. The risk factors that we cannot change or control is genetic factors such as family history, early menstruation, late menopause and dense breast tissue. The example of environmental and lifestyle risk factors that we have control of are being overweight or obese, lack of physical activity and drinking alcohol. Diagnosing a cancer at an early stage can bring down the fatality rate to a great extent. Deep learning is an artificial intelligence approach in which the machine is equipped with intelligence by trying to mimic the thought process of a human brain. This paper looks into the aspect of how a deep learning model can be used to detect the type of a breast cancer case.

## II. RELATED WORK

Detection of disease at early stage has become very crucial as the risk of death incurred by breast cancer is rising exponentially. In this paper, we compare five supervised machine learning techniques named support vector machine (SVM), K-nearest neighbours, random forests, artificial neural networks (ANNs) and logistic regression using a prominent machine learning database named UCI machine learning database. The performance is based on accuracy, sensitivity, specificity, precision, negative predictive value, false-negative rate, false-positive rate, F1 score, and Matthews Correlation Coefficient. ANNs technique is more consistent than any other techniques with highest accuracy of 98.57%, specificity of 96%, precision of 97.8%, F1 score is nearly 97% and lowest false-positive rate and false negative rate compared to other techniques. From these comparative study, we can conclude that machine learning techniques are able to detect the disease automatically with high accuracy [1].

Major number of deaths of women are caused by malignancy of tumor. Malignant tumour is a type of tumour that spreads into nearby cells or even around the whole body. Breast cancer can have an effect on both men and women, but it is more common in women. In this paper presents we study six supervised machine learning algorithms named k-Nearest Neighbourhood, Logistic Regression, Decision Tree, Random Forest, Support Vector Machine with radial basis function kernel. Deep learning using Adam Gradient Descent Learning was also applied because it combines the benefits of adaptive gradient algorithm and root mean square propagation by utilising their hyper parameters for the Wisconsin Breast Cancer Dataset (WBCD). This dataset consists of 30 features computed using fine-needle aspiration (FNA) of the breast mass. Specific hyperparametric modifications of each model are shown to improve the accuracy within the model and to compare each model with each other. The accuracy found by Adam Gradient Learning is highest with a score of 98.24% with minimum loss because it combines benefits of AdaGrad and RMSProp [2].

Breast cancer can be a common cause of death and is the only cancer that is prevalent among women worldwide. When the breast cancer dataset is loaded, features need to be retrieved, thus the classification model is frequently developed and used with machine learning calculations and used for prediction of benign and malignant. Benign cases are considered noncancerous, which is non-perilous. Harmful cancer begins with irregular cell development and may quickly spread or attack close-by tissue all together

that it is regularly hazardous. This paper is predicated on a dataset that is openly accessible from the UCI Machine Learning Repository. In this paper, we study k Nearest Neighbor (KNN), Support Vector Machine (SVM), Logistic Regression (LR), Naive Bayes (NB). This comparative study shows that k Nearest Neighbor's classification accuracy, precision, recall, f1 score, and Jaccard index outperform support vector machines, logistic regression, and Naive Bayes classification algorithm within the predictive breast cancer data from the UCI Machine Learning Repository Wisconsin breast cancer dataset. We have confirmed that k Nearest Neighbor provides significant performance classification algorithms in terms of accuracy, precision, recall, f1 value, and Jaccard index [3].

Cancer-related mortality is one of the largest problems that humanity in developing countries is currently confronting. Certain cancer kinds still lack a cure, despite the fact that there are many strategies to stop it from occurring in the first place. One of the most common malignancies is breast cancer, and effective treatment depends on early identification. An proper diagnosis is one of the most important steps in the treatment of breast cancer. This dataset was subjected to data visualisation and machine learning methods such as logistic regression, k-nearest neighbours, support vector machine, naive bayes, decision tree, random forest, and rotation forest. In this study, a number of machine learning and data mining techniques for the early detection of breast cancer were proposed. Simple and efficient strategies for comprehending and forecasting future data include data mining and machine learning. The best classification accuracy (98.1%) was obtained using the logistic regression model with all features included, and the suggested method demonstrated improved accuracy performances. These findings suggested that there may be new avenues for the early diagnosis of breast cancer [4].

Breast Cancer is the second major cause of women's death. This paper gives comparison between the performance of four algorithms which are used to predict breast cancer, which are SVM, Logistic Regression, Random Forest and KNN. The main goal is to minimize error and increase accuracy in prediction. Cancer starts when cells begin to grow out of control. The cause of Breast Cancer includes changes and mutations in DNA. There are seven phases in Machine learning which are 1. data preprocessing: converting raw data into understandable format, 2. data preparation: loading data in suitable place, 3. feature selection: selecting few parameters, Our target parameter is malignant (M) and benign (B), 3. feature projection and 4. feature scaling are used for transforming data, 5. model selection and 6. prediction. They found that the accuracy of SVM (97.13%) is higher than the accuracy of C4.5, Naive Bayes, and KNN. Final result is that SVM is the most effective and efficient method based on accuracy [5].

One of the most prevalent and significant causes of cancer in women is breast cancer. Computer-aided detection (CAD) systems play a major role in identification of breast cancer. Aim of the project is to classify and predict whether the person is suffering from carcinoma or not. In this paper, the result shows that Naive Bayes is the best classification model with precision of 97%. The k-Nearest-Neighbours (KNN) is a technique which is used for the classification of data in machine learning. It will perform classification by finding the nearest and similar data points within the corresponding dataset. The proposed method was implemented by using python. The entire dataset is divided into three subsets for training, testing, and validation. Random forest is capable of both regression and classification techniques. When the user adds input data, the system looks through the attributes and its values will have already been educated using a variety of datasets be validated and it gives the result. Random forest gives the best accuracy [6].

In this paper five classification models are used for classifying two different data sets related to breast cancer which are Breast Cancer Coimbra Dataset (BCCD) and Wisconsin Breast Cancer Database (WBCD). Classification models used are Decision Tree (DT), Random Forest (RF), Support Vector Machine (SVM), Neural Network (NN) and Logistics Regression (LR). Breast cancer is divided into malignant and benign. The goal of this study is to predict which model has highest accuracy. From Data sets some data is used for training and other data is used for testing the accuracy. After comparing the accuracy, F measure metric and ROC curve of five models we found that Random forest is most suitable for prediction on those two data sets [7].

In this study, we employ the Naive Bayes (NB) classifier and the k-nearest neighbour classifier (KNN). Machine learning is used for the creation and evaluation of algorithms that facilitate prediction, pattern recognition, and classification. ML is based on four steps: Collecting data, picking the model, training the model, testing the model. The main goal is to develop an effective machine learning approach for cancer classification. Each classifier's performance will be assessed based on its accuracy, testing process, and training process. Nine characteristics are required for breast cancer classification, including: 1. Clump Thickness, 2. Uniformity of Cell Size, 3. Uniformity of Cell Shape, 4. Marginal Adhesion, 5. Single Epithelial Cell Size, 6. Bare Nuclei; 7. Bland Chromatin, 8. Normal Nucleoli, 9. calculate the approximate number of mitoses that have occurred. Naive Bayesian Classifier (NBC): A Bayesian method is a basic result in probabilities and statistics, it can be defined as a framework to model decisions. To determine a data set's class or property, the KNN algorithm is utilised. A statistical approach called cross-validation is frequently used to audit and assess learning algorithms. Findings indicate that KNN was more effective than NB, with a 97.51% efficiency rate, yet even NB had a high accuracy rate of 96.19% [8].

This paper aims to present a comparison of machine learning algorithms and techniques used for breast cancer prediction, namely Random Forest, kNN (k-Nearest-Neighbor) and Naive Bayes. The Wisconsin Diagnosis Breast Cancer data set was used as a training set to compare various machine learning techniques. ML is broadly categorized under three categories namely - reinforcement learning, supervised learning and unsupervised learning. Random Forest It is a supervised learning algorithm which gives an accuracy of 94.74%. The accuracy of kNN is found to be 95.90%. Naive Bayes's accuracy equals to 94.47%. The Naive Bayes algorithm deals only with classification problems whereas both KNN and Random Forest can deal with classification as well as regression problems. Accuracy is a good predictor for the degree of correctness in the training of the model. Recall is defined as the ratio of rightfully determined positive instances to all observations. Precision is defined as The degree of correctness in determining the positive outcomes. F1 score is the weighted average of Precision and Recall. The results shows that Random Forest's has the best recall performance measure but KNN has the best accuracy, precision and F1 Score over Naive Bayes and Random Forest [9].

One of the illnesses that causes a significant number of fatalities each year is breast cancer. Data may be effectively categorised using methods like data mining and classification. Weka's machine learning environment was used in all experiments on the classifiers covered in this study. WEKA incorporates machine learning methods for pre-processing data, classification, regression, clustering, and association rules. Relative absolute error (RAE), Mean absolute error (MAE), Root mean squared error (RMSE), and Kappa statistic (KS) (RRSE). The major goal is to evaluate each algorithm's efficiency and efficacy in terms of accuracy, precision, sensitivity, and specificity in order to determine whether or not the data classification was right. According to experimental findings, SVM provides the highest accuracy (97.13%) and lowest error rate [10].

Deep Learning algorithm of convolutional neural network to predict breast cancer using MIAS database. Firstly dataset got preprocessed and useful features are extracted using histogram and watershed model and then dataset got split into training and testing datasets. MIAS Dataset have contain 200 images in which 12 features got extracted. For this trained dataset they used convolutional neural network model, deep learning algorithm and achieved 98% accuracy [11].

The goal of this study is to develop a deep neural network that can identify breast cancer that is malignant. The dataset used for the study is the Wisconsin breast cancer dataset that consists of 569 data records and 30 set of features. All the layers in model are dense layers, number of neurons varies in each layer and activation functions used are RELU and sigmoid. Optimization through early stopping and dropouts were carried out to the model to reduce the over fitting problem. The neural network model showed F1 score of 98 for the benign class and F1 score of 99 for the malignant class [12].

Tanh, Rectifier, Maxout, and Exprectifier are some of the activation functions that are used in deep learning approaches. Vote(DT+NB+SVM), Random Forest, and AdaBoost are a few machine learning techniques that contrast with Naive Bayes, Decision Tree, Support Vector Machine, and Naive Bayes. This approach is based on a neural network with many feed-forward layers that can be trained using gradient distance by back-propagation. The pre-activation neuron, which is a nonlinear combination of inputs with weights and bias, was utilised by neurons in hidden layers prior to being transformed into activation functions. Deep learning and the activation function of the Exprectifier enabled accuracy of 96.99% when compared to conventional techniques [13].

The implementation of several models, including Logistic Regression, Support Vector Machine (SVM), K Nearest Neighbour (KNN), Multi-Layer Perceptron Classifier, and Artificial Neural Network (ANN), is highlighted in the study. With an accuracy of 96.5%, the trials have proven that SVM and Random Forest Classifier are the best for predictive analysis. Deep learning algorithms like CNN and ANN have been used to boost prediction accuracy. In the cases of ANN and CNN, the greatest accuracy attained is 99.3% and 97.3%, respectively [14].

This work provides a histopathology image for the detection of breast cancer cells (mitosis and non-mitosis). Mitosis is a crucial factor in the diagnosis and prognosis of breast cancer. This study's objective is to identify mitosis, a process by which breast cancer cells divide, using a deep layer CNN with the best possible accuracy. In order to detect breast cancer cells using histopathology images, this study presented three types of deep layer CNN architecture, referred to as 6-layer CNN, 13-layer CNN, and 17-layer CNN, respectively. The findings indicate that the 17-layer CNN provides the highest overall accuracy [15].

### III. MATERIALS AND METHODS

#### A. Datasets

We use different datasets namely Wisconsin Breast Cancer Dataset (WBCD), MIAS Mammography Dataset and Breast Cancer Histopathological Database (Breakhis) in our study for Breast cancer prediction.

With Breast Cancer Wisconsin (Diagnostic) Data Set Predict whether the cancer is benign or malignant. The WBCD dataset includes tumour traits that were extracted from digital breast fine needle aspirates (DFNA). This is a labelled dataset of 569 participants with 32 tumour conditional features, where the class label feature indicated whether the breast cancer was benign or aggressive (357 benign and 212 malignant).

There are 322 digitised films in the MIAS Mammography database, which is available on a 2.3GB 8mm (ExaByte) cassette. Also, it includes the "truth" markings made by the radiologist on any potential abnormality sites. All of the photos in the database have been padded or clipped to a 1024x1024 resolution and lowered to a 200 micron pixel edge. The University of Essex's Pilot European Image Processing Archive (PEIPA) provides access to mammographic pictures. The following list includes movies from the MIAS database and offers pertinent information: MIAS database reference number in the first column. F [Fatty], G [Fatty-glandular], and D [Dense-glandular] are the characteristics of background tissue in the second column. Third column: Type of abnormality present: ARCH (architectural distortion), CIRC (well-defined), SPIC (spiculated masses), MISC (other, ill-defined masses), ASYM (asymmetry), NORM (normal). 4th column: Anomaly severity: B for benign, M for malignant. 5th and 6th columns: x, y picture coordinates of abnormality's centre. 7th column: Rough radius of a circle encompassing the anomaly in pixels.

For the Breast Cancer Histopathological Imaging Classification (BreakHis), 9,109 microscopic images of breast tumour tissue from 82 patients were collected using various magnification settings (40X, 100X, 200X, and 400X). Adenosis, fibroadenoma, ductal carcinoma, and lobular carcinoma tumours with a 400X magnifying factor were used as sources of data for our study.

#### B. Model Implementation

In this stage we implemented supervised Machine Learning models, namely logistic regression (LR), decision tree (DT), random forest (RF) and Deep Learning Neural Network (NN). In which we have to pass input data and get output. The flow chart of the implementation is as shown in Figure 1.

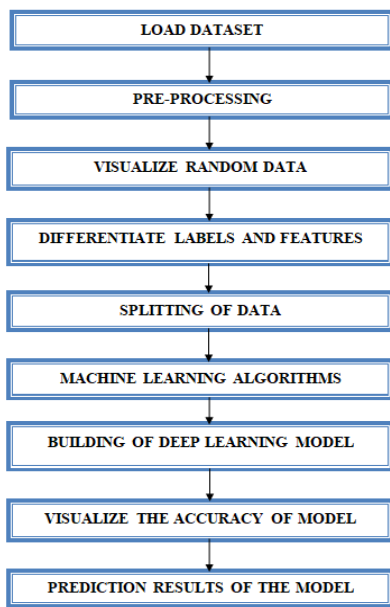


Figure 1: Flow chart of the Implementation.

a) **Pre-Processing:** Throughout the photography and processing of slides, a large number of deviations could occur. The brightness of the backdrop in the resulting histopathological image is not always consistent with the foreground because the image is acquired in a compressed format. To effectively separate sick cells in histopathological images, malignant cell nuclei must be recognised in histological images. It is necessary to perform some preliminary processing to smooth out the pixels and increase contrast in order to get a greater overall visual distinction between the cell nuclei (target region) and the surrounding area (intercellular matter).

b) **Visualize Random Data:**

	mean radius	mean texture	mean perimeter	mean area	mean smoothness	mean compactness
0	17.99	10.38	122.80	1001.0	0.11840	0.27760
1	20.57	17.77	132.90	1326.0	0.08474	0.07864
2	19.69	21.25	130.00	1203.0	0.10960	0.15990
3	11.42	20.38	77.58	386.1	0.14250	0.28390
4	20.29	14.34	135.10	1297.0	0.10030	0.13280

5 rows × 30 columns

Figure 2: Wisconsin Breast Cancer Dataset.

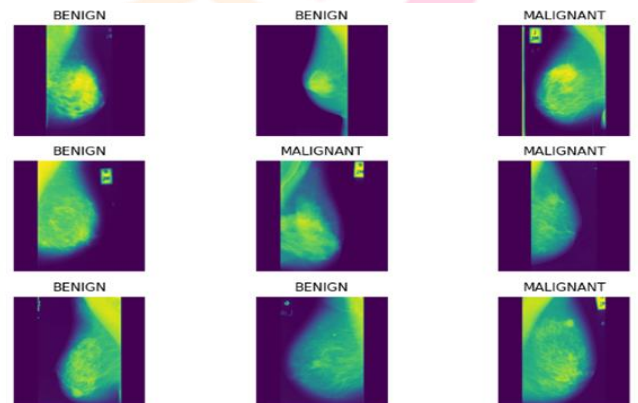


Figure 3: MIAS Mammography Dataset.

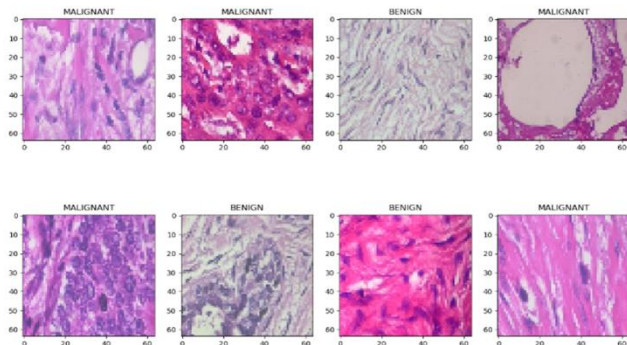


Figure 4: Breakhis Dataset.

c) **Splitting of Data:** We split the dataset into training and testing using the `train_test_split()` method and Apply that to `categorical()` method to transform data before we pass it to our machine learning and deep learning model for training. In order to be compatible with the models, it transforms the classes into a collection of numbers in the correct vector form. In our study we splitted the dataset into 80:20 and 70:30 ratio for analysis.

d) **Supervised Machine Learning Algorithms:** Three regular Supervised Machine Learning models, namely logistic regression, decision tree and random forest are used in our model.

The method of modelling the likelihood of a discrete result given an input variable is known as logistic regression. The most typical type of logistic regression models a binary outcome, such as true or false, yes or no, etc. Using multinomial logistic regression, events with more than two distinct possible outcomes can be modelled. When attempting to establish which category a

new sample most closely resembles, classification problems are a good place to employ logistic regression as an analysis technique.

A supervised learning method for solving classification and regression issues is the decision tree. It is a tree-structured classifier, with each leaf node denoting the classification result and inner nodes denoting the dataset's features. As opposed to Leaf nodes, which are the results of decisions and have no further branches, Decision nodes are used to make decisions and have numerous branches.

Random Forest can be used to solve Classification and Regression problems in machine learning. It is based on the concept of ensemble learning, which is a technique for combining several classifiers to handle challenging problems and improve model performance. In order to increase the projected accuracy of the input dataset, the Random Forest classifier averages the results from multiple decision trees applied to various subsets of the input dataset. The random forest uses forecasts from each decision tree and predicts the outcome based on the votes of the majority of projections, as opposed to relying solely on one decision tree. The greater number of trees in the forest prevents higher accuracy and overfitting.

**e) Deep Learning Neural Network:** Artificial systems called neural networks were influenced by biological neural networks. These systems acquire task-specific knowledge by being exposed to a variety of datasets and examples.

Convolutional neural networks were employed to diagnose breast cancer. Layers of synthetic neurons fundamentally make up convolutional neural networks. The only thing that artificial neurons are are mathematical functions that compute the weighted sum of several inputs and output an activation value. The layers produce a number of activation maps when we feed an image into the convolutional network. A patch of pixels is provided as input to the neuron, which is then multiplied by the weight, added, and finally passed via the activation function. Neurons produce output that is linear. So, when a neuron's output is transferred to another neuron, a new line of output is produced. We offer activation functions, such as Sigmoid and ReLU, to prevent and manage this issue. Another crucial component of the convolutional layer, the kernel, essentially examines the input data and extracts all of the characteristics.

#### IV. RESULTS AND DISCUSSIONS

The evaluated performance of the different classification methods for breast cancer into benign tumor and malignant tumor classes was performed on different datasets namely Wisconsin Breast Cancer Data Set, MIAS Mammography and Breast Cancer Histopathological Dataset. The accuracies of the proposed model are tabulated below in Table I.

**TABLE I**  
**PERFORMANCE COMPARISON**

DATASET	SPLIT RATIO	METHOD	ACCURACY IN (%)
WBCD	70 : 30	Random Forest	94.152
		Decision Tree	96.491
		Logistic Regression	98.246
		Neural Network	98.246
	80 : 20	Random Forest	92.983
		Decision Tree	92.105
		Logistic Regression	97.368
		Neural Network	96.491
MIAS Mammography	70 : 30	Random Forest	75.774
		Decision Tree	76.556
		Logistic Regression	56.907
		Neural Network	98.805
	80 : 20	Random Forest	74.374
		Decision Tree	68.089
		Logistic Regression	56.557
		Neural Network	96.095
Breast Cancer Histopathological Imaging Classification (BreakHis)	70 : 30	Random Forest	86.352
		Decision Tree	76.640
		Logistic Regression	82.415
		Neural Network	87.927
	80 : 20	Random Forest	86.221
		Decision Tree	78.347
		Logistic Regression	83.465
		Neural Network	86.614

##### A. Prediction results

```
1/1 [=====] - 0s 31ms/step
[[0.9219501 0.00173833]]
[0]
Tumor is Malignant

1/1 [=====] - 0s 29ms/step
[[0.17060125 0.83260137]]
[1]
Tumor is benign
```

Figure 5: Prediction result of Wisconsin Breast Cancer Dataset.



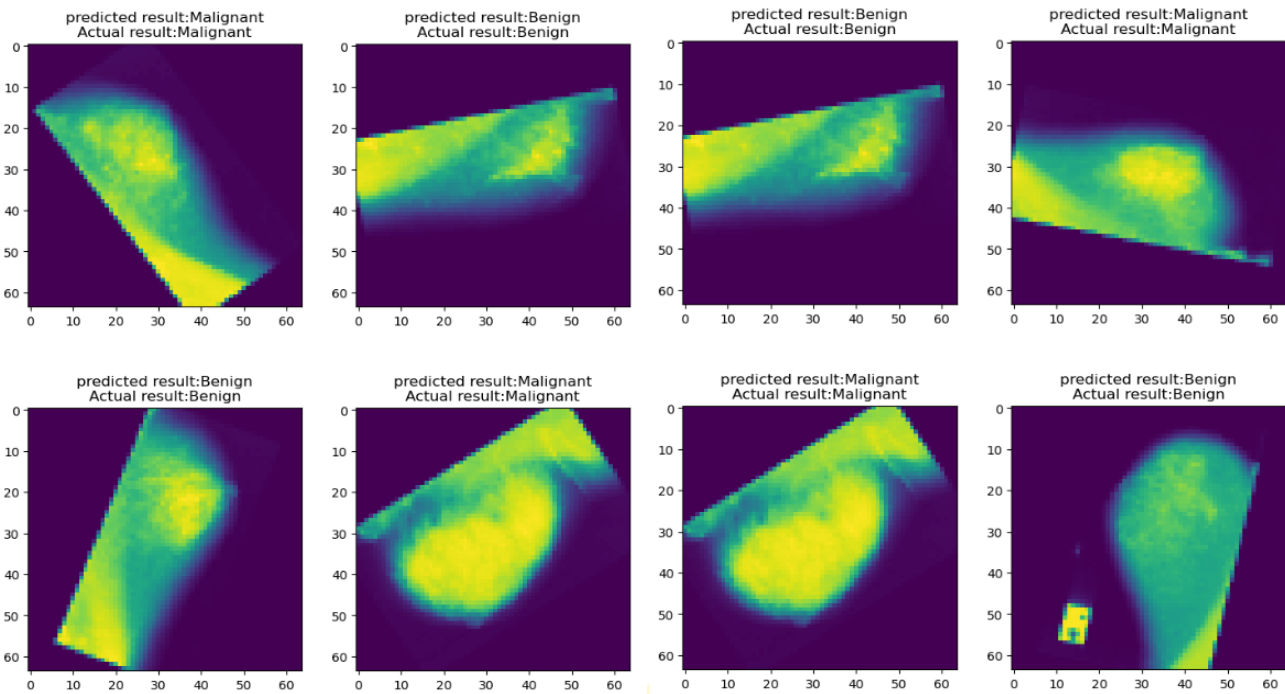


Figure 6: Prediction result of MIAS Mammography Dataset.

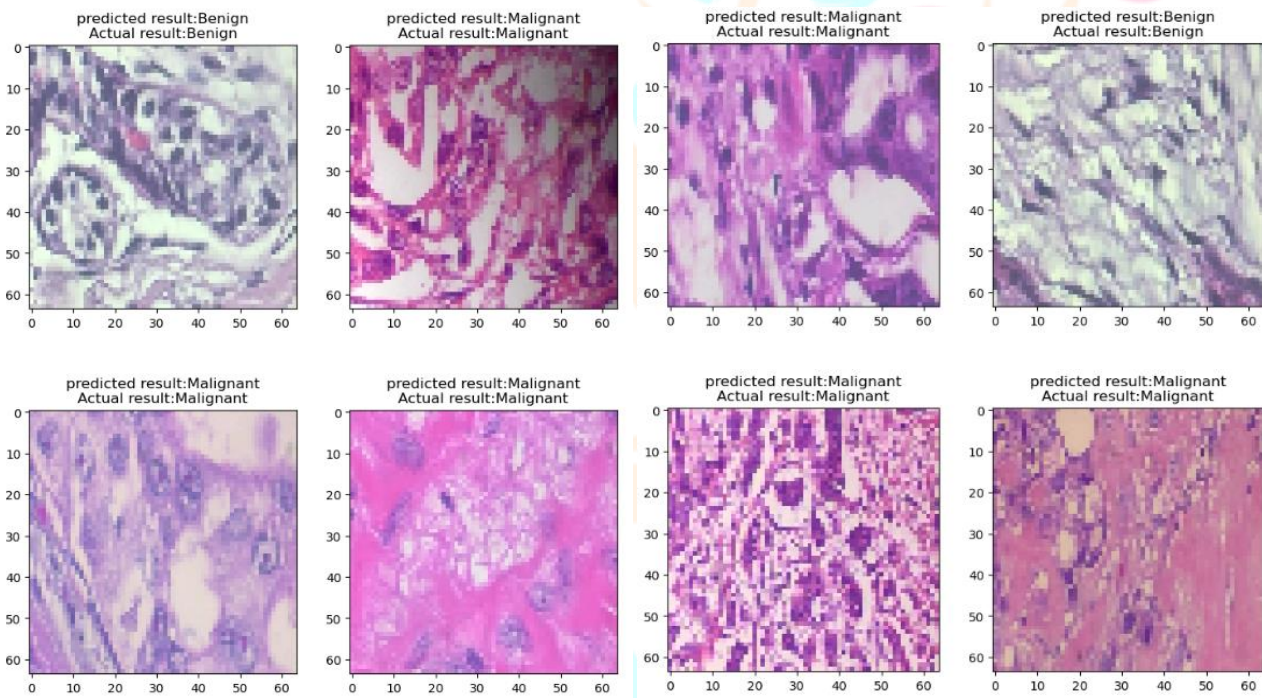


Figure 7: Prediction result of Breakhis Dataset.

**B. Accuracy per Epochs of Neural Network**

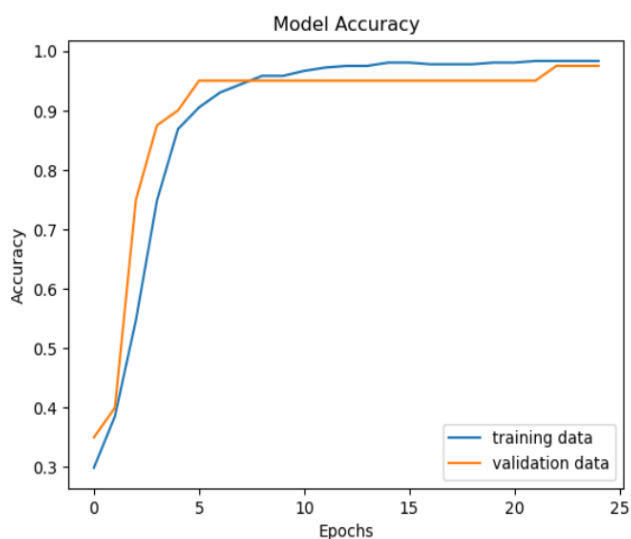


Figure 8: Result of WBCD Dataset with 70:30 Split Ratio.

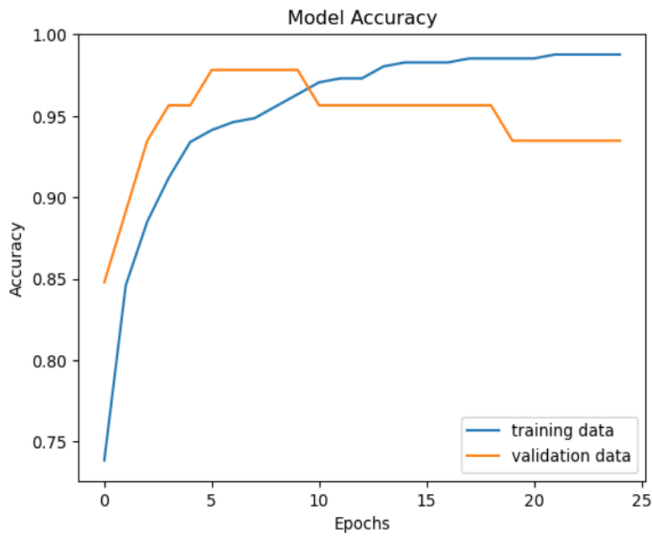


Figure 9: Result of WBCD Dataset with 80:20 Split Ratio.

Figure 11: Result of MIAS Mammography with 80:20 Split Ratio.

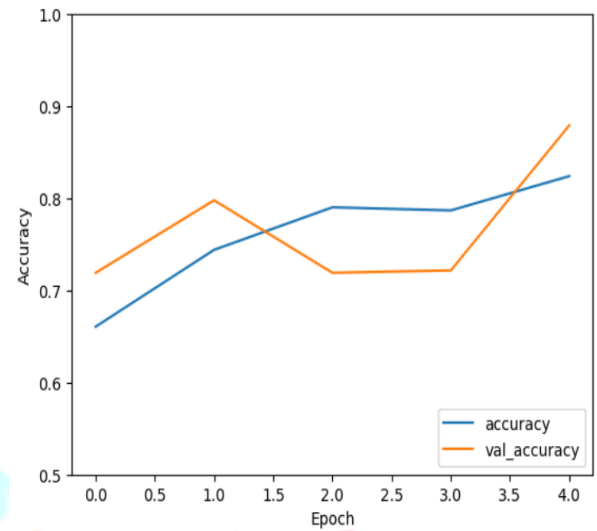


Figure 12: Result of Breakhis Dataset with 70:30 Split Ratio.

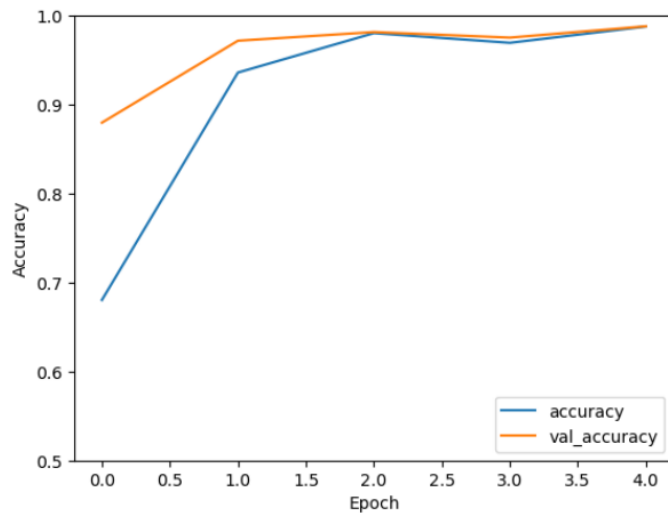


Figure 10: Result of MIAS Mammography with 70:30 Split Ratio.

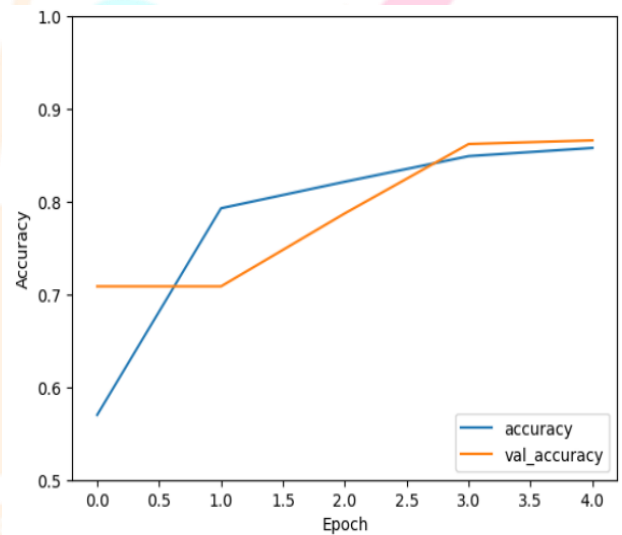
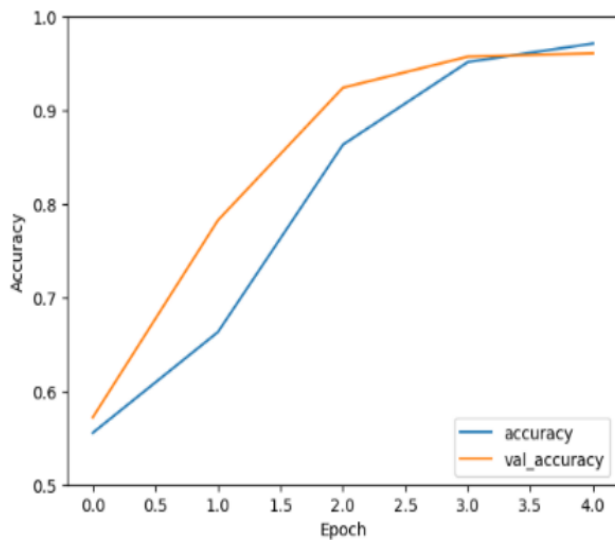


Figure 13: Result of Breakhis Dataset with 80:20 Split Ratio.



## V. CONCLUSION AND FUTURE WORK

Millions of individuals around the world have been impacted by cancer, and because it is fatal, people are frequently afraid of it. But, if cancer is detected at an early stage and treated appropriately, it can usually be cured. Convolutional neural networks were used in this study because, as we all know, they are frequently used in deep learning to classify image datasets. Following the model's implementation, we were able to obtain up to 98% accuracy.

In the future, we'll experiment with new features and real images dataset in an effort to diagnose breast cancer as accurately and effectively as possible. In the future, we'll test this approach not just for breast cancer but also for other types of cancer as well.

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