RESEARCH ARTICLE

Prediction and Diagnosis of Breast Cancer Using Machine and Modern Deep Learning Models

Seeta Devi[1]*, Ruchika Kaul Ghanekar[2,3], Jayshree Ashok Pande[4], Dipali Dumbre[1], Ranjana Chavan[1], Harshita Gupta[4]

Abstract

   Background &Objective: Carcinoma of the breast is one of the major issues causing death in women, especially in developing countries. Timely prediction, detection, diagnosis, and efficient therapies have become critical to reducing death rates. Increased use of artificial intelligence, machine, and deep learning techniques create more accurate and trustworthy models for predicting and detecting breast cancer. This study aims to examine the effectiveness of several machine and modern deep learning models for prediction and diagnosis of breast cancer. **Methods:** This research compares traditional machine learning classification methods to innovative techniques that use deep learning models. Established usual classification models such as k-Nearest Neighbors (kNN), Gradient Boosting, Support Vector Machine (SVM), Neural Network, CN2 rule inducer, Naive Bayes, Stochastic Gradient Descent (SGD), and Tree, and deep learning models such as Neural Decision Forest and Multilayer Perceptron used. The investigation, which was carried out using the Orange and Python tools, evaluates their diagnostic effectiveness in breast cancer detection. The evaluation uses UCI's publicly accessible Wisconsin Diagnostic Data Set, enabling transparency and accessibility in the study approach. **Result:** The mean radius ranges from 6.981 to 28.110, while the mean texture runs from 9.71 to 39.28 in malignant and benign cases. Gradient boosting and CN2 rule inducer classifiers outperform SVM in accuracy and sensitivity, whereas SVM has the lowest accuracy and sensitivity at 88%. The CN2 rule inducer classifier achieves the greatest ROC curve score for benign and malignant breast cancer datasets, with an AUC score of 0.98%. MLP displays distinguish positive and negative classes, with a higher AUC-ROC of 0.9959. with accuracy of 96.49%, precision of 96.57%, recall of 96.49%, and an F1-Score of 96.50%. **Conclusion:** Among the most commonly used classifier models, CN2 rule and GB performed better than other models. However, MLP from deep learning produced the greatest overall performance.

Keywords: Prediction- diagnosis- artificial Intelligence- machine learning algorithms- deep learning algorithms.

Introduction

   Cancer is a significant contributing factor to mortality and a serious barrier to increasing life expectancy in every country across the world. Female breast cancer, in particular, exhibited a significant increase with 2.3 million new cases, highlighting a concurrent rise in fatality rates. Breast cancer has a unique influence on women's life [1]. Strategies including increased awareness, early detection, and proactive diagnosis can potentially reduce mortality [2]. Gathering substantial data across many ailments in today's medical scene enhances studies and allows predictive insights. Technology assists physicians and pathologists in generating exact predictions, avoiding

excessive medical costs and assuring optimal treatment. Early detection can sometimes be a life-saving intervention [3]. Machine learning classification models of many types are essential in predicting and diagnosing breast cancer. Multiple research studies emphasize the need to use a variety of approaches to overcome issues in breast cancer prediction. Pathologists can better understand disease progression trends using several data mining ML models on the Wisconsin Breast Cancer diagnostic dataset [4].

   The use of machine learning algorithms in health data analysis, notably in the context of breast cancer, has resulted in significant advances. The Breast Cancer Wisconsin Data Set has been subjected to algorithms such as random forest, extreme learning machine, naive Bayes,

[1]Symbiosis College of Nursing (SCON), Symbiosis International Deemed University (SIDU), Pune- 412115, India. [2]Symbiosis Centre for Research and Innovation (SCRI), Symbiosis International (Deemed University) (SIDU), Pune, 412115, India. [3]Symbiosis School of Biological Sciences (SSBS), Symbiosis International (Deemed University) (SIDU), Pune, 412115, India. [4]Symbiosis Institute of Technology (SIT), Symbiosis International Deemed University (SIDU), Pune- 412115, India. *For Correspondence: drseetadevi1981@gmail.com

artificial neural networks, and support vector machine algorithms are used to predict cancer susceptibility, recurrence, survivorship, and treatment results [5]. Notably, advances in breast cancer detection and diagnosis have been made, improving patient outcomes through prompt intervention and tailored treatment strategies. ML algorithms have shown promise in predicting survival and determining the malignancy of breast tumors in the early stages [6].

The advantages of this study are many, as it aids in the promotion of rapid detection and timely modification of treatment methods. In addition, it has the potential to alter the current situation of breast cancer management by influencing aspects such as future research, the low cost, and global accessibility of healthcare services. Using ML techniques for carcinoma breast detection will assist in reducing healthcare expenses. Still, it also has the potential to have a positive and far-reaching impact on breast cancer therapy internationally.

The study's objective as follows

This study aimed to examine the effectiveness of common machine and modern deep-learning models on the prediction and diagnosis of breast cancer.

Related work

Recently, numerous research studies have used ML approaches in the medical care industry to diagnose breast cancer. Because these algorithms generate satisfying results, other researchers have adapted them to address complicated situations. Ongoing research provides valuable insights and suggestions for using ML models in carcinoma breast prediction and diagnosis. Numerous research studies have looked into ML approaches for breast cancer diagnosis, including kNN, NB, Tree, SVM, and Logistic regression. A study stressed the significance of early detection in improving breast cancer prognosis and survival. They emphasized using classification algorithms to develop models capable of reliably classifying breast cancer as malignant or benign [7]. Another study presented successful outcomes by employing refined machine learning algorithms, which led to greater skills in less invasive predictive medicine and improved treatment options for breast cancer [8]. Furthermore, RF and XG Boost models were proposed in a research to predict the probability of malignant breast, with accuracy rates of 74.73% and 0.73, respectively [9].

Another research used the EXSA GB approach to predict the onset of breast cancer and enhance survival rates [10]. An ensemble model including kNN, SVM, and DT was developed in a research and obtained 78% accuracy [11]. Besides, another study used several supervised learning algorithms on the Wisconsin dataset, with the Artificial Neural Network (ANN) and attained the greatest accuracy of 98.57% [5].

Furthermore, using quadratic kernel and SVM produced the maximum accuracy [12]. In terms of data reduction, both linear and nonlinear techniques are viable, with the decision depending on the unique nature of the correlations between dataset features [13]. An evaluation was undertaken to discover similarities and differences between Support Vector Machines (SVM), logistic regression, naive Bayes, and random forest [14]. The Wisconsin breast cancer dataset was used as a reference in another study. When Anaconda Data Science boards were used, RF obtained the greatest results with a precision of 0.997 with minimum error [15, 16]. Various forms of breast malignancy are classified using a NN (Neural Network) method, specifically focusing on the MLP. The primary task of the neural network is to categorize the input data into two breast cancer types: benign and malignant. A collective erudition strategy, acknowledged for its effectiveness, is employed to balance modification and prejudice. Improving classification performance is accomplished by combining individual classifiers to produce a unified classification model, a notion that has been well-established in several research investigations. Ensemble classification uses three fundamental techniques: stacking, boosting, and bagging. Stacking, for example, requires combining results from many categorization models into a single model [17].

In our review, we discovered a shortage of papers that evaluated the efficacy of machine learning and deep learning algorithms in detecting breast cancer. Recognizing this discrepancy, researchers became interested in comparing the efficacy of traditional and modern breast cancer prediction models.

Materials and Methods

Many classification techniques are used on breast cancer data, yet each classifier performs differently on the same dataset (Figure 1 depicts the general concept of the suggested breast cancer detection system). As a result, an ensemble strategy involving bagging and boosting is used. This method integrates data from many classifiers while also learning from previous classifiers. The first step in carrying this out is to collect data. Following that, the data is preprocessed for attribute selection. The dataset is partitioned, with 80% for training and 20% for testing. The collection contains labeled data with malignant and benign classifications. The training data is then used to develop a model using several classification approaches that have been supervised. The test data is analyzed using several classifiers, and the performance of these various classifiers is compared to each other and with deep learning models.

Source of Dataset and Information and data pre-processing

The Wisconsin Malignant Breast Diagnostic dataset, freely available at UCI ML repository, was used in this work. The collection includes data from 569 individuals who have malignant breast diseases. Researchers used numerous machine learning algorithm models to examine data and identify breast cancer in this study. ML is a subset of AI deployed for data classification using created models, most notably in breast cancer prediction analytics. It provides automated ways for evaluating large datasets. This work used machine learning (ML) techniques, and a scientific dataset of breast cancer patients was obtained from Kaggle (https://www.kaggle.com/uciml/breast-cancer-wisconsin-data). The information was evaluated

using several parameters from digitally accessible photos of fine needle aspirates of breast masses. These traits were especially used to differentiate benign from malignant tumors.

The effectiveness of medical treatment and the precision of the diagnosis are crucial factors influencing a patient's likelihood of surviving cancer and preventing recurrence; using the orange tool, the data were indiscriminately alienated in two sets to train and test the machine in an 80:20 ratio. Following this division, the model's efficacy is evaluated using test data once trained using the assigned training sets. The decision of whether or not a person will be affected depends on various feature values. The initial step involves gathering essential data for pre-processing to enhance its quality, which is achieved through various pre-processing methods. It includes just picking the properties that are required.

Following the preparation of the data, multiple machine models are used to train the data. After training, the model's performance is evaluated using test data. This approach employs various machine learning algorithms in conjunction with an ensemble classifier. After preparing the data, several machine models are employed to train it. Subsequently, the performance of the model is assessed using test data. This approach combines different ML algorithms and a collective classification model. The objective of collective erudition is to create an enhanced predictive model by amalgamating outcomes from multiple learning algorithms. It is achieved by blending various supervised learners to augment the model's predictive capabilities. In this context, multiple algorithms, including kNN, gradient boosting, SVM, neural network, CN2 rule inducer, naive Bayes, tree, and SGD. Various classification and deep learning approaches are used to predict malignancy on a pre-processed breast cancer dataset.

Models for breast cancer prediction
kNN
This uses all training data for similarity-based classification, computing distances for label assignment.

SVM
This uses hyperplanes without the essential information for preceding distribution.

NB
This method relies on Bayes' theorem and conducts predictions based on likelihoods.

DT
This approach classifies occurrences based on feature values and splits them using the Gini Indexor Information Gain. Labels are represented by leaf nodes.

Gradient Boosting
This strategy lowers mistakes by emphasizing cases with prior model flaws, improving overall forecast accuracy by sequentially developing an ensemble of weak learners, generally decision trees.

Neural Networks
Inspired by the human brain, this model, which comprises linked nodes or neurons, excels at learning detailed patterns and correlations, making it useful for tasks like classification and regression.

Stochastic Gradient Descent
SGD iteratively refines model parameters to minimize the loss function, improving training efficiency and convergence.

Multilayer Perceptrons (MLP)
Are multilayer neural networks that use nonlinear activation functions to perform difficult tasks.

Neural Decision Forests
are ensembles of decision trees or tiny neural networks designed to increase performance, nonlinearity, and interpretability. They combine elements from classic decision forests with neural network principles to improve model capabilities.

The Orange mining tool is used to identify the best machine-learning classification approaches presented in this paper. This platform simplifies the construction of numerous algorithms, allowing for rapid analysis and exploration of datasets and contributing to the study's computational framework and analytical outputs. Researchers used the Python software framework to evaluate the efficiency of deep learning models. A thorough comparison was conducted, with the accuracy and Receiver Operating Characteristic Area Under the Curve (ROC AUC) values scrutinized.

Results

The Wisconsin Hospital diagnosed 569 patients with breast malignancy, and this data was used for this study. Sixty-three percent of these individuals were classified with benign diseases, whereas thirty-seven percent were diagnosed with malignant cases.

The characteristics of cell nuclei that may be relevant in the context of breast cancer diagnosis. Radius_Mean, Texture_Mean, Perimeter_Mean, and Area_Mean are the qualities that describe the average size and form of cell nuclei. The table displays the Worst Features, which are Radius_Worst, Perimeter_Worst, and Area_Worst, representing cell nuclei's most undesirable (biggest) size and form properties. Mean radius, for example, runs from 6.981 to 28.110, with a mean value of 14.12729, while Mean texture goes from 9.71 to 39.28. All the hyper-parameters were fine-tuned, and the prediction was carried out, as shown in Table 2; CN2 introducer and Gradient Boosting showed better prediction output than the remaining predictors (Table 1).

Various commonly used ML classification and deep learning models were applied to the Wisconsin Breast Cancer dataset, and their performance was assessed using metrics including Accuracy, AUC, precision, and recall.

The researcher used the AUC statistic to evaluate model performance explicitly. The outcomes were divided into traditional machine learning methods and ensemble

Table 1. Values of Geometrical and Textural Features among benign and Malignant Tumors of a Breast Mass Showing Mean Values and Dispersion

Features	Mean	Dispersion	Minimum Value	Maximum Value
Radius_Mean	14.12729	0.24923	6.981	28.11
Texture_Mean	19.2896	0.2228	9.71	39.28
Perimeter_Mean	91.969	0.264	43.79	188.5
Area_Mean	654.889	0.537	143.5	2501
Concavity_Mean	0.0887993	0.896963	0	0.4268
Concave Points_Mean	0.0489191	0.792506	0	0.2012
Symmetry_Mean	0.181162	0.151192	0.106	0.304
Fractal_Dimension_Mean	0.0627976	0.1123316	0.04996	0.09744
Radius_Worst	16.26919	0.29682	7.93	36.04
Perimeter_Worst	107.2612	0.646	185.2	4254
Area_Worst	880.583	0.646	185.2	4254
Smoothness_Worst	0.1323686	0.1723396	0.07117	0.2226
Symmetry_Worst	0.290076	0.213093	0.1565	0.6638
Diagnosis	Benign=65%		Malignancy =35%	

Table 2. Prediction Output Using Commonly Used Classification Models

Model	AUC	CA	F1	Precision	Recall	MCC
kNN	0.992	0.907	0.903	0.919	0.907	0.808
Gradient Boosting	1	1	1	1	1	1
SVM	0.992	0.889	0.884	0.906	0.889	0.773
Neural Network	0.988	0.895	0.89	0.91	0.895	0.783
CN2 rule inducer	1	1	1	1	1	1
Naive Bayes	0.985	0.942	0.942	0.942	0.942	0.876
Tree	0.988	0.989	0.989	0.99	0.989	0.977
SGD	0.985	0.989	0.988	0.988	0.988	0.974

approaches: TN, FN, TP, and FP acronyms used in the confusion matrix.

Accuracy

Accuracy gauges how well the model predicts both positive and negative instances overall. A higher accuracy
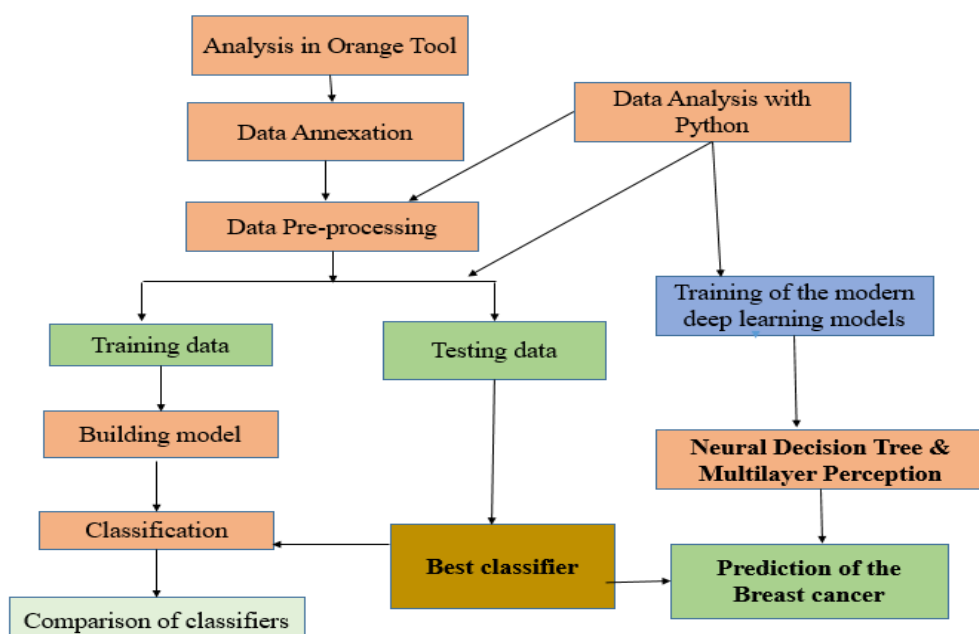
Figure 1. Flow Diagram of Proposed Model
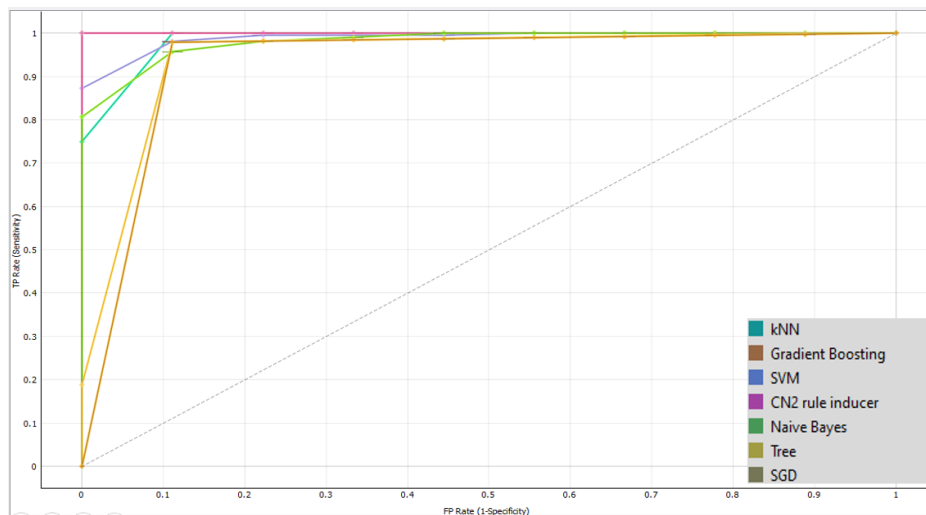
Figure 2. ROC Analysis of Malignant Tumour

Table 3. Prediction Output Using Modern Deep Leaning Model (NDF and MLP)

Metrics	Neural Decision Forest	Multilayer Perceptron
AUC-ROC	0.9667	0.9959
Accuracy	95.61%	96.49%
Precision	100%	96.57%
Recall	89.36%	96.49%
F1-Score	94.38%	96.50%

indicates better overall prediction performance.

Accuracy = (True Positive + True Negative) / (Positive + Negative)

Precision

Precision signifies the percentage of occurrences the model correctly predicts as positive out of all instances; it denotes as positive. A high precision indicates the model makes fewer false positive errors.

Formula: Precision = TP / (TP + FP)

F1 Score

It depicts their harmonic mean, striking a harmonious balance between precision and recall. A score of 1 represents equilibrium between the two, whereas a value of 0 occurs when either one reaches a high elevation.

Formula: F1 Score = 2 x ((Precision*Recall) / (Precision + Recall))

AUC-ROC

The Area Under the Receiver Operating Characteristic Curve (AUC-ROC) measures a model's capacity to distinguish between positive and negative occurrences across multiple threshold levels. A higher AUC-ROC value indicates better performance of the model about classification.

Table 3 shows the test dataset performance of several classifiers and each classifier's particular hyper-parameters. For each model, the table includes the AUC score, classification accuracy, F1 score, precision, recall, and MCC score. Notably, gradient boosting and CN2 rule inducer classifiers outperform SVM in accuracy and sensitivity, whereas SVM has the lowest accuracy and sensitivity at 88%. The CN2 rule inducer classifier
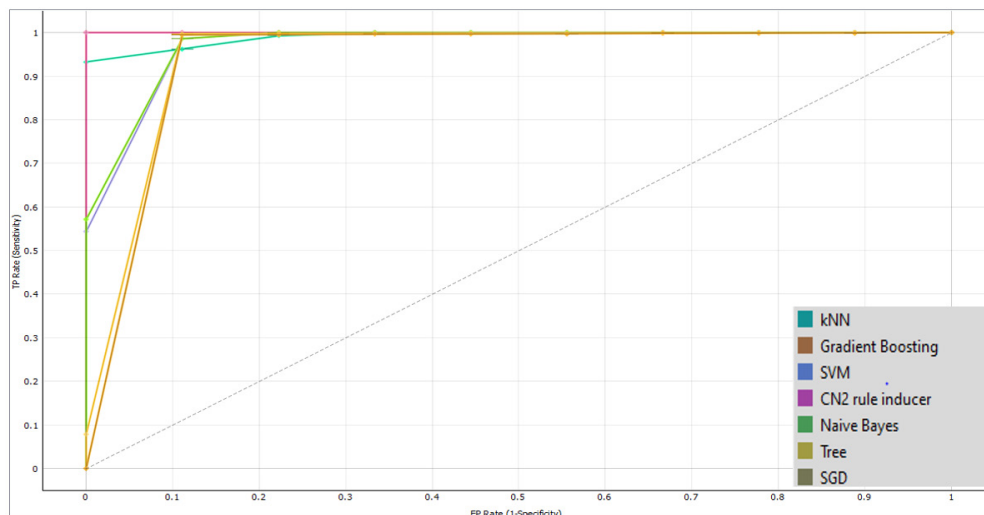
Figure 3. ROC Analysis of benign Tumour

a

Predicted

		B	M	Σ
Actual	**B**	87.1 %	0.0 %	357
	M	12.9 %	100.0 %	212
	Σ	410	159	569

b

Predicted

		B	M	Σ
Actual	**B**	100.0 %	0.0 %	357
	M	0.0 %	100.0 %	212
	Σ	357	212	569

c

Predicted

		B	M	Σ
Actual	**B**	100.0 %	0.0 %	357
	M	29.7 %	70.3 %	212
	Σ	420	149	569

d

Predicted

		B	M	Σ
Actual	**B**	100.0 %	0.0 %	357
	M	0.0 %	100.0 %	212
	Σ	357	212	569

e

Predicted

		B	M	Σ
Actual	**B**	95.2 %	4.8 %	357
	M	7.5 %	92.5 %	212
	Σ	356	213	569

f

Predicted

		B	M	Σ
Actual	**B**	99.7 %	0.3 %	357
	M	2.4 %	97.6 %	212
	Σ	361	208	569

g

Predicted

		B	M	Σ
Actual	**B**	99.4 %	0.6 %	357
	M	2.4 %	97.6 %	212
	Σ	360	209	569

Figure 4. Confusion matrix for various Machine learning algorithms. a, kNN; b, Gradiant Boosting; c, SVM; d, CN2 Rule inducer ; e, Naive Bayes; f, Tree; g, SGD

achieves the greatest ROC curve score for benign and malignant breast cancer datasets, with an AUC score of 0.98%, as shown in Figures 2 and 3.

The MLP performs better than the neural decision forest. It distinguishes between positive and negative classes, with a higher AUC-ROC of 0.9959. with accuracy of 96.49%, precision of 96.57%, recall of 96.49%, and an F1-Score of 96.50%. These findings show that the Multilayer Perceptron is a more resilient and accurate model for the classification job and should be considered in practical applications (Table 2).

In Figure 4, the top-left corner of each model's matrix

accurately identifies positive cases instances when the actual label is positive and the model predicts it properly. True positive rates for benign and malignant tumors differ among models: Gradient Boosting (87.1%), SVM (100%), CN2 Rule Inducer (100%), Naive Bayes (100%), Tree (95.2%), and SGD (99.7%). This corresponds to the bottom-right corner, showing that negative situations where the actual label is negative have been correctly identified. With rates of 100%, 97.6%, and 97.6%, respectively, the CN2 Rule Inducer, Naive Bayes, and Tree models have the greatest percentages of accurately recognized true negative situations. In the bottom-left

Correlation Matrix

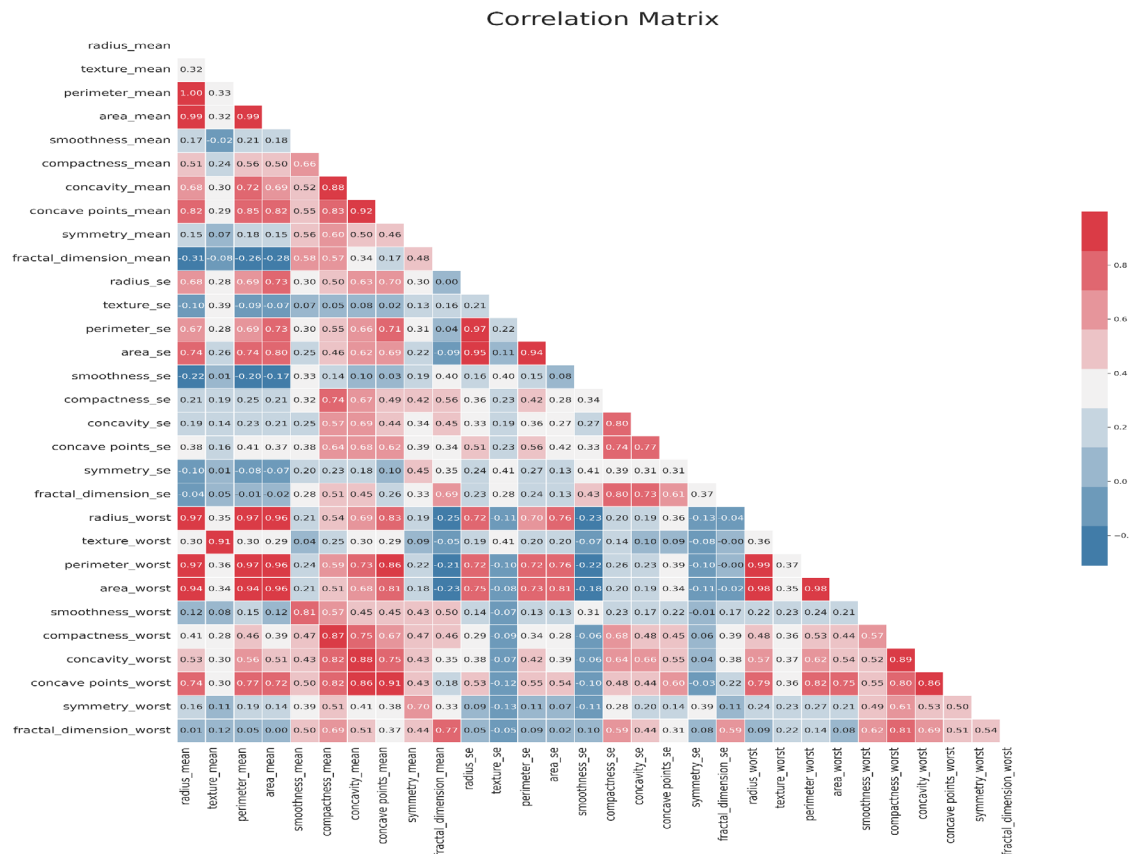|	radius_mean	texture_mean	perimeter_mean	area_mean	smoothness_mean	compactness_mean	concavity_mean	concave points_mean	symmetry_mean	fractal_dimension_mean	radius_se	texture_se	perimeter_se	area_se	smoothness_se	compactness_se	concavity_se	concave points_se	symmetry_se	fractal_dimension_se	radius_worst	texture_worst	perimeter_worst	area_worst	smoothness_worst	compactness_worst	concavity_worst	concave points_worst	symmetry_worst
texture_mean	0.32																												
perimeter_mean	1.00	0.33																											
area_mean	0.99	0.32	0.99																										
smoothness_mean	0.17	-0.02	0.21	0.18																									
compactness_mean	0.51	0.24	0.56	0.50	0.66																								
concavity_mean	0.68	0.30	0.72	0.69	0.52	0.88																							
concave points_mean	0.82	0.29	0.85	0.82	0.55	0.83	0.92																						
symmetry_mean	0.15	0.07	0.18	0.15	0.56	0.60	0.50	0.46																					
fractal_dimension_mean	-0.31	-0.08	-0.26	-0.28	0.58	0.57	0.34	0.17	0.48																				
radius_se	0.68	0.28	0.69	0.73	0.30	0.50	0.63	0.70	0.30	0.00																			
texture_se	0.10	0.39	-0.09	-0.07	0.07	0.05	0.08	0.02	0.13	0.16	0.21																		
perimeter_se	0.67	0.28	0.69	0.73	0.30	0.55	0.66	0.71	0.31	0.04	0.97	0.22																	
area_se	0.74	0.26	0.74	0.80	0.25	0.46	0.62	0.69	0.22	0.09	0.95	0.11	0.94																
smoothness_se	-0.22	0.01	-0.20	-0.17	0.33	0.14	0.10	0.03	0.19	0.40	0.16	0.40	0.15	0.08															
compactness_se	0.21	0.19	0.25	0.21	0.32	0.74	0.67	0.49	0.42	0.56	0.36	0.23	0.42	0.28	0.34														
concavity_se	0.19	0.14	0.23	0.21	0.25	0.57	0.69	0.44	0.34	0.45	0.33	0.19	0.36	0.27	0.27	0.80													
concave points_se	0.38	0.16	0.41	0.37	0.38	0.64	0.68	0.62	0.39	0.34	0.51	0.23	0.56	0.42	0.33	0.74	0.77												
symmetry_se	-0.10	0.01	-0.08	-0.07	0.20	0.23	0.18	0.10	0.45	0.35	0.24	0.41	0.27	0.13	0.41	0.39	0.31	0.31											
fractal_dimension_se	0.04	0.05	-0.01	-0.02	0.28	0.51	0.45	0.26	0.33	0.69	0.23	0.28	0.24	0.13	0.43	0.80	0.73	0.61	0.37										
radius_worst	0.97	0.35	0.97	0.96	0.21	0.54	0.69	0.83	0.19	-0.25	0.72	0.11	0.70	0.76	-0.23	0.20	0.19	0.36	-0.13	-0.04									
texture_worst	0.30	0.91	0.30	0.29	0.04	0.25	0.30	0.29	0.09	-0.05	0.19	0.41	0.20	0.20	-0.07	0.14	0.10	0.09	-0.05	-0.00	0.36								
perimeter_worst	0.97	0.36	0.97	0.96	0.24	0.59	0.73	0.86	0.22	-0.21	0.72	-0.10	0.72	0.76	-0.22	0.26	0.23	0.39	-0.10	-0.00	0.99	0.37							
area_worst	0.94	0.34	0.94	0.96	0.21	0.51	0.68	0.81	0.18	-0.23	0.73	-0.08	0.73	0.81	-0.18	0.23	0.22	0.35	-0.08	0.02	0.98	0.35	0.98						
smoothness_worst	0.12	0.08	0.15	0.12	0.81	0.57	0.45	0.45	0.43	0.50	0.14	-0.07	0.13	0.13	0.31	0.23	0.17	0.22	0.23	0.24	0.21	0.22	0.24	0.21					
compactness_worst	0.41	0.28	0.46	0.39	0.47	0.87	0.75	0.67	0.47	0.46	0.29	0.09	0.34	0.28	-0.06	0.68	0.48	0.45	0.06	0.39	0.48	0.36	0.53	0.44	0.57				
concavity_worst	0.53	0.30	0.56	0.51	0.43	0.82	0.88	0.75	0.43	0.35	0.38	0.07	0.42	0.39	-0.06	0.64	0.66	0.55	0.04	0.38	0.57	0.37	0.62	0.54	0.52	0.89			
concave points_worst	0.74	0.30	0.77	0.72	0.50	0.82	0.86	0.91	0.43	0.18	0.53	-0.12	0.55	0.54	-0.10	0.48	0.44	0.60	-0.03	0.22	0.79	0.36	0.82	0.75	0.55	0.80	0.86		
symmetry_worst	0.16	0.11	0.19	0.14	0.39	0.51	0.41	0.38	0.70	0.33	0.09	-0.13	0.11	0.07	-0.11	0.28	0.20	0.14	0.39	0.11	0.24	0.23	0.27	0.21	0.49	0.61	0.53	0.50	
fractal_dimension_worst	0.01	0.05	0.05	0.00	0.50	0.69	0.51	0.37	0.44	0.77	0.05	0.05	0.22	0.14	0.02	0.10	0.69	0.51	0.54										

Figure 5. Correlation Matrix between Each Feature

corner are False Positive (FP) examples, in which the model predicts positive events with a negative actual label. The percentages of false positives for the kNN, SVM, Naive Bayes, Tree, and SGD models are 12.9%, 29.7%, 7.5%, 2.4%, and 2.4%. False Negatives (FN), or inaccurate predictions of negative situations, are extremely low for Naive Bayes (4.8%), Tree (0.3%), and SGD (0.6%) (Figure 5).

The Neural Decision Forest and Multilayer Perceptron models effectively predict breast cancer. The Multilayer Perceptron outperforms the Neural Decision Forest with a higher AUC-ROC of 0.9959. Notably, the Multilayer Perceptron outperforms the Neural Decision Forest with a respectable 96.49% accuracy. Precision for the Neural Decision Forest is flawless at 100%, while the Multilayer Perceptron is an astounding 96.57%. Furthermore, the Multilayer Perceptron outperforms in recall (96.49%) and F1-Score (96.50%), demonstrating its ability to detect true positives. The ROC curve values for NDF and MLP are 0.97 and 0.99, respectively. These findings highlight the Multilayer Perceptron's superior performance in predicting breast cancer (Table 3).

Discussion

Using the Breast Cancer Wisconsin (diagnostic) dataset, seven different classifications and two deep-learning models are examined for breast cancer categorization in this study. The Standard Scaler module is used for data preparation, while the Orange data mining tool and Python software are used for feature selection. Machine learning methods such as kNN, Gradient Boosting, SVM, Neural Network, CN2 rule introducer, Naive Bayes, Decision Tree, and SGD were used to build the machine models, while NDF and MLP techniques were used to build the deep learning models. The evaluation uses a confusion matrix to associate expected and actual results, measuring performance indicators such as accuracy, AUC, precision-recall curve, sensitivity, and f1-score. This research discovered a decrease in smoothness _worst and maximum area mean values after running the data in the tool, indicating a possible increase in false positives.

Examining the correlations between numerous aspects of carcinoma of the beast detection is critical to understanding how distinct characteristics relate to a patient's prognosis. Gradient boosting and CN2 rule introducer models regularly display the best efficiency after naive Bayes, Decision Tree, SGD, and kNN models.

Breast cancer is a common disease that affects women across the globe. It presents the possibility of a revolutionary influence on early identification and prognosis through machine-learning algorithms. There are two forms of ductal carcinoma: invasive and ductal in situ. Timely identification is critical for effective therapy, emphasizing the need to use precise screening methods. Mammography and USG are usually radiographic used to detect malignant tumours in the breast at an early stage. Significant advances in artificial intelligence have considerably improved mammography precision, giving rise to deep learning algorithms capable of identifying carcinoma of the breast in digital mammography. Furthermore, an MRI of the breast assists as an imaging

tool with great sensitivity and specificity. Artificial intelligence integrated tools emergent in the realm of patient care, with the goal of improving image processing and reducing reliance on human visual identification in detection of breast cancer.

Future ML research in breast cancer diagnostics may investigate a wide range of options, including refining existing models and incorporating fresh methodologies. Continuous development in breast cancer identification and treatment depends on the continued collaboration of data scientists, medical specialists, and researchers. Ongoing attempts to improve diagnostic tool accuracy and efficiency help to a more complete knowledge of the condition. As technology advances, the potential for creative uses to enhance patient outcomes grows [18]. The interaction of scientific competence and technological innovation continues to be critical in advancing breast cancer diagnosis and treatment.

In conclusion, finally, the Breast Cancer Wisconsin dataset was used to test several machine-learning and deep-learning models for breast cancer classification. Evaluation measures demonstrated the efficacy of models such as Gradient Boosting and the CN2 rule introducer. The study emphasized the importance of studying correlations in breast cancer screening, particularly the potential influence of machine-learning algorithms on early detection. Ongoing advances in artificial intelligence, notably in mammography and breast MRI, indicate intriguing avenues for enhancing diagnostic accuracy. Future research should concentrate on improving existing models and encouraging collaboration between data scientists and medical professionals to improve breast cancer detection and therapy.

Author Contribution Statement

Conceptualization, S.D.; methodology, S.D. DD.; software, S.D.; validation, S.D. RC.; formal analysis, S.D. DD.; investigation, S.D. JP; resources, S.D.; data curation, S.D.; writing JP, S.D.; writing, review and editing, S.D. DD.; supervision, S.D. RG.; project administration, S.D, RG.

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Approval
The researchers obtained institutional research committee (IRC) approval to conduct the study. Authors used secondary data, and ethical approval was not sought due to the study's nature, no direct human beings were involved.

Data Availability
The data presented in this research may be found in the UCI Machine Learning Repository, which can be found at https://archive.ics.uci.edu/dataset/17/breast+cancer+w isconsin+diagnostic.

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