RESEARCH PAPER

Machine Learning Based Classification Analysis of Benign and Malignant Breast Tumors: A Clinical Perspective

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Abstract**—**Cancer is a disease spared worldwide. Body's cells cultivate uncontrollably and reach to other parts of the body and propagate to other parts of bodies. As know all in general, cells grow and divide to produce new cells as the body requirements. Old or damaged cells die and are replaced by new cells. However, an old and damaged cell breaks down into cancer. Abnormal/damaged cells continue to live when they should die, and new cells form when they are no longer needed, such cells can form a tumor. One such cancer is known as breast cancer, and its early detection is crucial for the success of treatment and the survival of the patient. Accurate classification of skin lesions into malignant and benign categories is essential for timely treatment and reducing mortality rates. Various Machine Learning (ML) models are applied and compared for their effectiveness in diagnosing breast cancer using dermatological datasets. Performance measuring features accuracy, precision, recall, and F1-score are used to review the models. The promise of artificial intelligence as a reliable tool to assist dermatologists in clinical decision-making is highlighted by recent experimental results showing that specific algorithms perform better in diagnoses. In addition to improving diagnosis accuracy, the work helps create automated, dependable breast cancer detection systems that promote early intervention. The extensive use of AI and ML in breast cancer uncovering, diagnosis, and medication is transforming medical practice and improving how physicians detect and manage the disease. In this work, a labelled dataset of breast cancer has been used to compare Light Gradient Boosting (LightGBM) and Gradient Boosting. The Extreme Gradient Boosting (XGBoost) technique has been found to be more accurate than the LightGBM method.

Keywords—Machine Learning, Breast Cancer, Benign Tumor, Malignant Tumor, Medical Diagnostics
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I. INTRODUCTION

Both machine learning and artificial intelligence are cutting-edge, research-oriented technology. Machine learning is essentially a branch of artificial intelligence that examines how models or algorithms adapt to data so they may operate on their own without human assistance. Both of these technologies have shown to be revolutionary in the diagnosis, treatment, and detection of cancer [1]. Develop new models and use them for therapy and diagnostics. These technologies improve the speed and accuracy of diagnosis by enabling automated analysis of clinical and imaging data. Artificial intelligence (AI)-powered systems analyse mammograms, MRI scans, ultrasounds, and histopathology pictures to help discover problems early and often exceed traditional diagnostic methods [2].

In summary, AI and ML provide scalable, reliable, and rational explanations that improve clinical findings, boost early diagnosis, and increase the use of resources in the treatment of breast cancer [3]. Breast cancer is one of the most mutual and deadly cancers in the world, with a high rate of cancer-related morbidity and death in women. This situation starts when irregular breast cells proliferate out of control, which rapidly results in the creation of tumors that can be seen using imaging techniques or clinical assessment. Breast cancer usually starts in the lobules or milk ducts, and its aggressiveness and propensity for metastasis vary. For the purpose of diagnosis, prognosis, and treatment planning, it is essential to accurately distinguish between benign and malignant tumor types [4-6]. Because it directly disturbs treatment options, such as systemic chemotherapy and surgery, accurate tumor type classification is crucial. The productivity and accuracy of breast cancer classification have significantly increased to recent developments in medical imaging, histology, and computational diagnostic techniques, especially those powered by machine learning and deep learning. In order to increase early detection and survival rates, this study looks into and assesses mathematical techniques for

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distinguishing between benign and malignant breast tumors [7-9].

A number of ML algorithms, including SVM, RF, and XGBoost, along with deep models like Convolutional Neural Networks and Vision Transformers, have demonstrated remarkable efficacy in accurately, precisely, and recallably classifying breast tumors into benign and malignant categories. AI supports prognostic, recurrence risk assessment, and treatment planning predictive analytics in addition to categorization, particularly when integrating multi-modal data for individualized medical decision-making [10]. Transparency, clinician comprehension of model predictions, and increased confidence in AI-enabled diagnosis are all made possible by the adoption of explainable AI methods like SHAP and Grad-CAM.

In summary, AI and ML provide scalable, reliable, and rational explanations that improve clinical findings, boost early diagnosis, and increase the use of resources in the treatment of breast cancer. Breast cancer is one of the most mutual and deadly cancers in the world, with a high rate of cancer-related morbidity and death in women. This situation starts when irregular breast cells proliferate out of control, which rapidly results in the creation of tumors that can be seen using imaging techniques or clinical assessment [11, 12]. Breast cancer usually starts in the lobules or milk ducts, and its aggressiveness and propensity for metastasis vary. For the purpose of diagnosis, prognosis, and treatment forecasting, it is mandatory to accurately distinguish between benign and malignant tumor classification. Because it directly impacts treatment options, like systemic chemotherapy and surgery, accurate tumor type classification is crucial [13]. The productivity and accuracy of breast cancer classification have significantly increased to current developments in medical imaging, histology, and computational diagnostic procedures, especially those powered by ML and DL. In order to increase early recognition and survival rates, this study looks into and assesses mathematical techniques for distinguishing between benign and malignant breast tumors [14, 15].

A. Risk Factors and Causes

Genetic, hormonal, environmental, and lifestyle issues contributes to the development of breast cancer. Aging, a personal history of breast cancer, and inherited genetic abnormalities, especially in the BRCA1 and BRCA2 genes, are high-risk presences. Radiation, extended estrogen exposure, hormonal disorders, and lifestyle decisions such as consuming alcohol, being obese, and not physical work are additional risk factors. To direct early intervention and individualized medication options, a comprehensive consideration of these risk factors is crucial [16].

B. Symptoms

Initial symptoms of breast cancer may have lumps or thickening in the breast, variations in size or shape, skin dimpling, or clear changes in the nipple, such as inversion, pain, or discharge. Knowing these primary cautionary signs are essential for better clinical results and early analysis.

C. Diagnosis

Mammography, ultrasound, MRI, and biopsy are among the imaging and histopathological procedures used in diagnostic workup to identify malignant tumors. Recent advances in computer technology, particularly ML and DL algorithms, improve the final results of diagnosis by evaluating imaging data more quickly and accurately [17].

D. Treatment

The type, stage, and aggressiveness of patient directly impact the breast cancer and have a major impact on medication. Radiation, chemotherapy, hormone therapy, targeted therapy, and surgery are examples of modern techniques that are typically combined to improve therapeutic efficacy. The use of recently created AI-based predictive models to enhance medication response, lower the chance of frequency, and enhance treatment planning is growing. Early disclosure and treatment are important to increasing patient survival chances because malignant tumors, such as melanoma, can spread rapidly to other parts of the body. Even though benign tumors cannot spread, they occasionally need to be treated to avoid complications or additional growth.

A significant diagnostic challenge in breast cancer is the accurate and rapid diversity between benign and malignant tumors. Histopathological analysis and dermoscopy are two traditional diagnostic techniques, rely largely on human decision, which is laborious and prone to errors. Advances in computing mechanisms, mainly in the areas of AI and ML, have made it possible to automate the segregation process. Due to malignant property of tumors like melanoma can spread quickly to other areas of the body, early findings and treatment are essential to improve patient survival.

Benign tumors may not spread, but sometimes require medical cure to prevent difficulties or further development. This research aimed on evaluating various ML models and comparing for breast cancer diagnosis in terms of segregating tumors as benign or malignant. With near about 2.9 million cases in 2021 alone and accounting for over 29% of all cancer cases, breast cancer is the most commonplace disease among women. The disease emerges when cells of breast multiply irregularly and converts into tumors that are palpable during a clinical diagnosis or visible on X-rays. For clinical oncology, verify differences between benign (non-malignant) and malignant (cancerous) tumors is crucial. This difference is important because it gets the tumor's biological potential, aggressiveness, and treatment mechanism. In this study, SVM is used to perform classification analysis on breast cancer data to increase diagnostic accuracy and promote early detection strategies. In addition to aiding in efficient treatment planning, both benign and malignant isolation significantly improves patient survival rates [18].

A. Problem Statement

Despite extraordinary advances in medical imaging and diagnostic methods, accurately identifying breast tumors as benign or malignant remains a challenge. Diagnosis is generally vulnerable by the factors like image quality, inter- observer variability, and the presence of benign early-stage tumors. False positive results can force patients to undergo irrelevant procedures, resulting in clinical and mental trauma, while false negative findings can delay treatment for malignant circumstances and such type of false errors have serious questions. Classification systems should be robust, self-contained, and highly accurate to enable doctors to take reliable and reproducible diagnostic decisions [19].

B. Research Objectives

The intension of this paper is to get the effectiveness of both modern DL techniques and trendy ML algorithms in classifying breast tumors into benign and malignant classes, reduce inter-observer variability and human error to improve diagnostic accuracy through computerized classification approaches, and facilitate the adoption of intelligent decision- support technology in healthcare processes for improved patient outcomes and early detection [20].

II. Related Work

A wide range of techniques, from conventional imaging and pathology to advanced computational algorithms, are used to diagnose breast cancer. Mammography, ultrasound, and magnetic resonance imaging (MRI) are the conventional diagnostic modalities; each has advantages and disadvantages of its own. For population-based screening, mammography is the recommended method; however, women with thick breasts have lower sensitivity. Recent developments in AI- based mammography risk prediction have been demonstrated to perform on par with, and in certain situations better than, traditional risk-factor-based models, signaling a shift towards customized, image-based screening procedures [1, 16].

The combination of AI-driven systems to reduce inter-observer variability, reduce errors, and improve evaluation consistency has sparked parallel developments in digital pathology and histology. The value of deep learning techniques in high-throughput pathology pipelines has been demonstrated by their success in the detection of invasive tumors, measurement of mitotic figures, prediction of lymph node metastases, and assessment of treatment response.

AI has also demonstrated practical use in real-world settings. A study carried out across Germany found that AI in mammography screening improved cancer diagnosis by 17.6% without increasing false positive rates [2, 3]. In studies on the classification of breast cancer, computational methods have taken the lead. Current CNN designs, such as ResNet, DenseNet, and VGG, have shown nearly 99% classification accuracy in a range of imaging modalities, such as histology, CT, MRI, ultrasound, and mammography. Ensemble models that integrate a number of different transfer learning networks have been found to attain accuracy scores of roughly 98.9% in histopathology classification on benchmarking datasets like BreaKHis [4].

The creation of lightweight architectures, like DRDA-Net in conjunction with MobileNet, which allow precise and effective tumor classification that can be applied in clinical settings with few resources, is increasing the viability of AI application in the treatment of breast cancer.

Transformers and contrastive learning methods are increasingly being applied in studies on breast cancer categorisation, along with CNN-based frameworks. For example, Supervised Contrastive Vision Transformer has achieved remarkable results on the histopathology datasets with an F1-score of 0.8188 and specificity of 0.8971. The results show that it has the potential to improve generalizability, especially when labeled data is sparse and traditional DL models fail. In the analysis of histological images, transformer-based ensemble models such as ViT-DeiT have also demonstrated high classification accuracy between benign and malignant classification [5].

Systematic studies further evidence the transformative impact of DL on workflows. “DL can be used for large-scale, generalisable data, therapeutic planning, prognosis prediction and diagnosis,” says a comprehensive study published in Breast Cancer Research. MRI-focused research [6, 7] has demonstrated that DL algorithms outperform radiologists in lesion diagnosis and classification, which facilitates clinical prioritisation. Finally, systematic assessments of deep learning diagnosis methods provide guidance for further research.

CNNs are most versatile and successful models, especially in histopathological and genomic image analysis, according to a deep systematic review of DL methods for breast cancer diagnosis. It emphasises improved diagnostic accuracy and a decreased reliance on manual feature engineering. The effectiveness of CNNs and hybrid models is highlighted in another systematic study that focusses on the classification of histopathology images, but it also highlights issues like overfitting, class imbalance, and data quality [8].

In the field of computer modelling, Ensemble Transfer Learning techniques that combine VGG-16, ResNet-50, DenseNet-201, and Xception have outperformed traditional Transformer and MLP models and achieved remarkable accuracy (98.9%) on datasets related to breast histopathology. On the BreaKHis dataset, a hybrid model built on DRDA-Net and MobileNet also performed well, providing a computationally effective choice appropriate for implementation in resource-constrained settings [9]. Furthermore, a DenseNet-based model improved with attention mechanisms and multi-level transfer learning was proposed in a 2024 study, and it was able to diagnose diseased breast images with an accuracy of over 84% [10, 11].

Beyond imaging, a comparison of ten algorithms, including CNNs, RNNs, XGBoost, and SVM, revealed that SVM had the best accuracy (~98.25%) in tumour classification using structured clinical data [12, 17]. DenseNet201 produced the highest results (accuracy 89.4%, AUC 95.8%) when 11 deep learning architectures were used in a study to categories biopsy images in the context of image- specific techniques.

Moreover, the field of explainable AI (XAI) is gaining traction, as transparency and model interpretability are crucial in clinical contexts. A 2024 scoping review focusing on XAI in breast cancer detection found that SHAP (SHapley Additive exPlanations) is the most popular technique for explaining model outputs and improving trust in AI tools, particularly in ensemble tree-based models [13-15].

Every year, millions of people are affected by breast cancer, which is still one of the most common and deadly illnesses in the world. Optimizing treatment plans and increasing survival rates depend heavily on early and precise diagnosis. Conventional diagnostic procedures, such as ultrasonography, biopsy, and mammography, take a lot of time and heavily rely on radiologists' skill. Recent developments in ML and AI have provided effective, automated methods for dividing breast tumors into benign and malignant groups in order to get around these restrictions [18].

Using organized datasets like the Wisconsin Breast Cancer Dataset (WBCD), early research used traditional machine learning methods including SVM, K-Nearest Neighbours (KNN), DT, and RF [19]. Because of their capacity to manage high-dimensional data and nonlinear decision limits, SVM and RF frequently outperformed other techniques in binary classification problems, achieving impressive results. Baseline comparisons were also provided by Naïve Bayes and Logistic Regression, which demonstrated competitive accuracy but restricted scalability with complex datasets [20].

III. METHODOLOGY

Classification is critical for diagnosis, prognosis, and treatment decisions, without it, doctors would not know whether to simply monitor a tumor or treat it aggressively. Logistic Regression, XGBoost, AdaBoost, Random Forest, SVM, and KNN are different pre-testing models which are applied and examined which method is the best on the same dataset. This study employs a comparative analysis framework to evaluate the performance of multiple ML algorithms in classifying breast cancer lesion as malignant or benign. Accuracy, precision, recall, F1-score, and computing efficiency are the main areas of examination. The data must be processed through a few processes. Steps in data processing are:

Collect data by collecting pictures of the breast or breast lesions from dermatology databases. Make sure that every piece of data is marked as benign or malignant. The Kaggle website is where it was gathered. 569 cases of breast cancer were gathered from the Breast Cancer Database to create the dataset. Digital images of tiny needle aspirates are used to generate 31 numerical features for each case. To guarantee comparability among features, the data was normalized and cleaned to eliminate missing or inconsistent values. Data cleaning involves removing faulty or poor-quality data and making sure that the dataset is consistently labelled. The process of finding, fixing, or eliminating mistakes and inconsistencies in datasets in order to enhance data quality and guarantee trustworthy analysis is known as data cleaning, data cleansing, or data preparation.

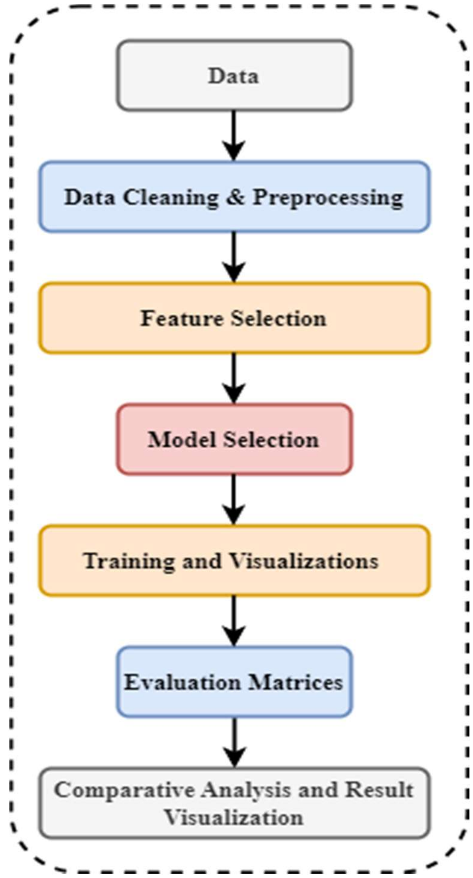

Figure 1: Data Preprocessing and Result Visualization

A. *Data pre-processing:*

It involved standardization of feature values to zero mean and unit variance. Additionally, synthetic minority oversampling was performed to balance the class distribution, thereby reducing bias in classification performance.

B. *Comparative Methods*

Six ML classifiers were evaluated. SVM with RBF kernel, RF with 100 estimators, K-Nearest Neighbors (KNN) with k=5, Logistic Regression XGBoost and AdaBoost. All models were implemented using Python's scikit-learn library.

C. *Results*

Results are presented using bar charts and comparative performance is summarized in a tabular format to facilitate clear interpretation.

IV. RESULTS AND DISCUSSION

The dataset is collected from Kaggle Online website. The size of dataset is (569, 33) i.e. 569 rows (entry) and 33 columns (features). After cleaning the dataset, the number of features gets reduced to 31 and the names of the features are as follows:

['id', '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', 'fractal_dimension_worst']

Of the 569 cases of breast cancer in the current dataset, 212 (37.25%) were found to be malignant and 357 (62.75%) to be benign (Figure 2). Malignant fields are malignant tumors that require prompt to get and treatment because they have the potential to invade nearby tissue and spread to other locations. Depending on their size, location, and accompanying symptoms, benign cases which are often less aggressive and non-cancerous may nevertheless need clinical monitoring or surgery. This distribution shows an intrinsic class imbalance, with benign instances outnumbering malignant cases, a characteristic that was incorporated throughout future statistical analysis and ML model construction to avoid classification bias.

TABLE I. ANALYSIS ON VARIOUS PERSPECTIVES

Id	Diagnosis	Radius mean	Compa-ctness worst	Concavity worst	concave points worst	Symmetry worst	Fractal Dimension worst
0	842302	M	0.1622	0.6656	0.7119	0.2654	0.4601
1	842517	M	0.1238	0.1866	0.2416	0.186	0.275
2	84300903	M	0.1444	0.4245	0.4504	0.243	0.3613
3	84348301	M	0.2098	0.8663	0.6869	0.2575	0.6638
4	84358402	M	0.1374	0.205	0.4	0.1625	0.2364

Several ML methods, such as RF, XGBoost, SVM, and LR, were used in the experimental evaluation on the dermatological datasets that were accessible. Each model was assessed using accuracy, precision, recall, and F1-score. The comparative performance results are shown in Table 2, display(df.head()).

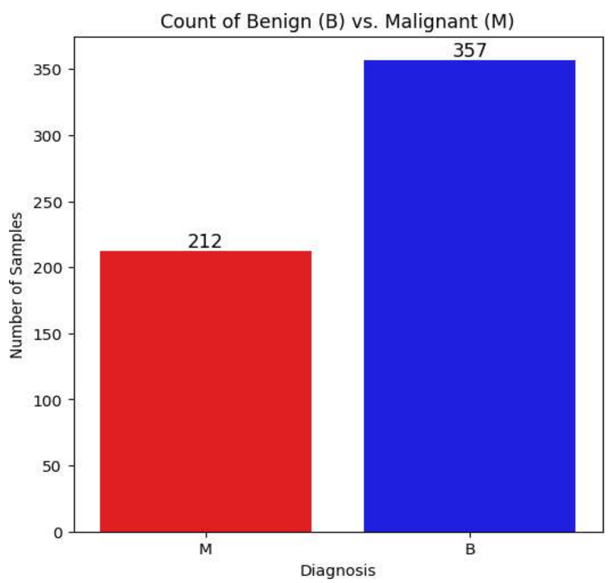

Figure 2: Distribution of Benign and Malignant

TABLE II. Comparative Evaluation of Several Models

Model	Accuracy	Precision (M)	Recall (M)	F1-score (M)
Logistic Regression	0.94736	0.9736	0.88095	0.925
XGBoost	0.94736	0.9879	0.85714	0.92307
AdaBoost	0.93859	0.9587	0.83333	0.90909
Random Forest	0.93859	0.9598	0.83333	0.90909
SVM	0.91228	0.9896	0.76190	0.86486
KNN	0.91228	0.9705	0.78571	0.86842

Observations and Insights

- Best Overall Accuracy: Out of the models that were compared, Logistic Regression and XGBoost both had the best accuracy (0.94736), indicating that they were more predictive overall.
- Perfect Precision Models: SVM, Random Forest, AdaBoost, and XGBoost all achieved 1.0 precision for malignant tumors, meaning that no benign tumors were mistakenly identified as malignant. This is essential for minimizing unnecessary patient stress and procedures, as well as false positives.
- Highest Recall (Sensitivity): Logistic Regression has the best recall (0.88095), followed by XGBoost (0.85714). High recall is necessary for cancer detection in order to prevent the malignant instances from being unnoticed.
- Balanced Performance (F1-score): Logistic Regression had the highest F1-score (0.925), giving the optimal balance between precision and recall. Additionally, XGBoost's high F1-score of 0.92307indicated balanced performance suitable for clinical usage.

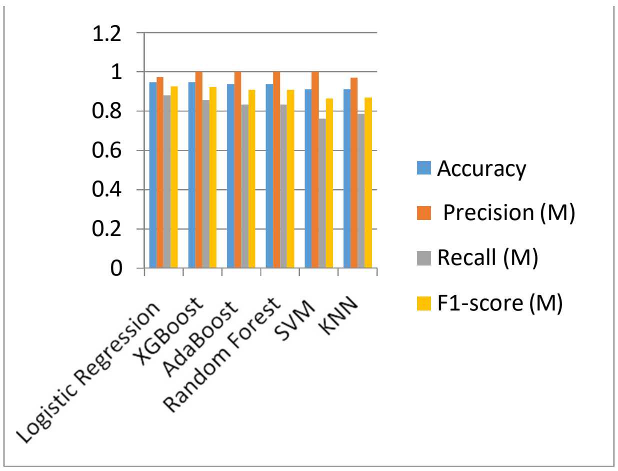

Figure 3: Comparison of Machine Learning Algorithms on Various Parameters

Implications for Clinical Deployment

- Logistic Regression is a good contender as it has high accuracy, high recall, and is interpretable, making it a good fit where model transparency is an issue.
- XGBoost also performs well overall, providing ideal precision and competitive F1-score, making it the best choice when reducing false positives is essential.
- As seen, AdaBoost and Random Forest are best, but their memory is slightly lower, which may cause some dangerous cases to be missed.
- SVM and KNN exhibit good feat but lower F1-score and recall, making their application in vital clinical decision-making constrained.

V. CONCLUSION AND FUTURE SCOPE

Breast tumors were categorized into benign and malignant groups using several algorithms. AI's potential as an oncologist's assistant was highlighted by the experimental evaluation, which revealed that some models, particularly complex ensemble and deep learning architectures, achieve good diagnostic accuracy, precision, and recall. These automated classification techniques help speed up decision-making, reduce diagnostic errors, and increase early detection rates. Research emphasizes on adding multi-modal medical data, such as mammography, MRI, and histopathology images, to increase dataset variety and improve model generalizability. Explainable AI approaches must be included in order to increase clinical trust and regulatory approval. Real-time, resource-efficient models should also be developed and applied in healthcare settings with limited resources to provide early breast cancer screening and detection to a larger population.

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