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Research Article

Machine Learning for Early Cancer Detection and Classification: AI-Based Medical Imaging Analysis in Healthcare

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Abstract

A common kind of cancer is breast cancer. Raising the survival rate of breast cancer patients is mainly dependent on breast cancer recurrence prognosis. The accuracy of cancer detection and diagnosis has increased with the progress of technology and ML approaches. Machine learning (ML) provides a number of statistical and probabilistic approaches. This study introduces a deep learning-based approach to automatically classify breast cancer images from the BreakHis dataset. Feature extraction was performed using a Convolutional Neural Network (CNN) to automatically detect significant tissue structures. The MobileNetV2 architecture was employed for its efficiency in handling large-scale data while maintaining high classification accuracy. The model achieved an impressive accuracy of 98.18%, with precision of 98.38%, sensitivity of 97.37%, and an F1score of 97.85%. When compared to other architectures, MobileNetV2 outperformed Xception, ResNet101, and EfficientNet, which demonstrated lower accuracy and sensitivity. These results highlight the potential of MobileNetV2 for reliable, fast, and cost-effective breast cancer detection, offering a promising tool for clinical applications.

Keywords: *Healthcare, Breast Cancer, Cancer Classification, Early Detection, Medical Imaging, Machine Learning (ML), Breast Cancer Histopathological Image Dataset.*

Introduction

Disease prevention, early diagnosis, and efficient treatment are becoming more important, and healthcare systems throughout the world are constantly adapting to meet these needs [1][2]. Among the numerous challenges faced by modern medicine, cancer stands out as one of the most serious and complex health issues[3]. In this condition, aberrant cells proliferate uncontrollably and have the potential to infiltrate neighboring tissues and metastasize (spread to other areas of the body)[4]. As the second leading cause of death worldwide, cancer demands timely intervention and accurate diagnostic strategies to improve survival rates and reduce the global health burden [5][6]. Cancer is a collection of connected disorders rather than a single illness that may impact almost any tissue or organ [7][8]. Common types include lung, colorectal, liver, prostate, and breast cancer, each with distinct biological behaviors and treatment responses [9][10].

Among these, breast cancer is particularly significant due to its high incidence among women worldwide. It is still the most common cancer in women and a major contributor to cancer-related deaths. Understanding the nature of breast cancer and the factors contributing to its development is essential in devising effective detection and treatment strategies[11]. Breast cancer may start in the breast's ducts or lobules and progress in a variety of ways, from benign to malignant and invasive [12][13]. Age, family history, hormone imbalances, and lifestyle choices are some of the risk factors that may greatly impact the probability of having the condition [14]. The importance of early identification in improving treatment results and lowering mortality from breast cancer cannot be overstated, considering its incidence and potential severity. The likelihood of a complete recovery and the efficacy of targeted treatments are both enhanced by early tumor detection [15].

To achieve early diagnosis, various imaging techniques have been employed, including mammography, ultrasound, and magnetic resonance imaging (MRI) [16][17]. These tools help visualize abnormalities in breast tissue and support clinical decision-making. However, the accuracy of these methods heavily relies on the experience and judgment of radiologists [18][19]. Human interpretation can vary and is susceptible to error, especially when analyzing subtle patterns or dense breast tissues. As a result,

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there is a pressing need for more consistent and objective diagnostic solutions. Modern technology has provided answers to these problems in the form of CAD tools, which aid doctors in making sense of medical imagery [19].

The most recent big deal in medical image analysis was when these systems started using ML and AI [20][21]. ML models can learn from massive datasets, identify complex patterns, and outperform humans in terms of prediction accuracy when using DL techniques [22][23]. By harnessing the power of ML, early-stage breast cancer can be detected with greater precision, and tumors can be classified more effectively based on their morphological and molecular features. As AI continues to evolve, its application in breast cancer detection and classification promises to transform healthcare by enabling faster, more accurate, and more accessible diagnostic services for patients worldwide.

Motivation and Contribution of Paper

The immediate and precise diagnosis is essential for successful treatment and patient survival, which is why this research is driven by the need to enhance early breast cancer detection via the use of histopathological imaging. The use of DL models, such as MobileNetV2, provides an automated, more efficient, and less error-prone alternative to traditional approaches. The study's overarching goal is to improve clinical outcomes by assisting pathologists in making more accurate diagnoses by tackling problems like class imbalance and feature complexity. This research mostly adds the following:

Utilized the Break His dataset, containing 9,109 histopathological images from 82 patients, for comprehensive analysis.

Improved the quality of the images by using preprocessing methods like Gabor filtering and normalization.

Employed data augmentation (brightness adjustment, flipping, rotation) to address class imbalance and improve model generalization.

Used CNN-based feature extraction to automatically capture important tissue structures.

Developed an efficient breast cancer detection model using the MobileNetV2 architecture on histopathological images.

Validated the model’s robustness through extensive evaluation using confusion matrix, ROC, loss, and precision-recall curves.

Justification and Novelty

The crucial yet difficult-to-interpret histological images used for early identification of breast cancer provide a compelling rationale for this research. The novelty lies in the application of the MobileNetV2 model, a lightweight and computationally efficient deep learning architecture, combined with extensive preprocessing and augmentation techniques to improve classification performance. Unlike conventional methods, this approach addresses class imbalance, enhances feature extraction, and achieves state-of-the-art accuracy, making it suitable for real-world clinical deployment in resource-constrained settings.

Structure of the paper

This paper is organized in the following way: Section II reviews related studies on ML techniques applied in breast cancer diagnosis. The assessment measures and data preparation procedures utilized in this research are described in Section III. An examination of model performance in comparison to visual representations is presented in Section IV. Section V concludes with a summary of the main conclusions and suggestions for further study.

1) Artificial Intelligence (AI) has fundamentally transformed the landscape of security, offering
2) advanced capabilities that significantly enhance threat detection and response. By leveraging
3) machine learning and predictive analytics, AI systems can analyze vast amounts of data to identify
4) patterns and anomalies indicative of potential threats. This capability is crucial for managing
5) the complexity and volume of modern threats, providing organizations with a powerful tool
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Literature Review

The literature review explores ML and DL applications for early cancer detection, analyzing AI-based medical imaging techniques. Table I summarizes previous studies on AI-based cancer detection, highlighting machine learning techniques, dataset model interpretability, and challenges.

Chikkala et al. (2025) There are four distinct parts to a BRNN: the Transfer Learning Backbone Branch, the GRU, the residual collaboration branch, and the Feature Fusion module. The BreaKHis breast cancer dataset, which includes 7,909 microscopic pictures from 82 individuals across 8 different classes, was used to evaluate the BRNN model. Compared to state-of-the-art approaches, their model achieved a better average classification accuracy of 97.25 percent [24].

Chang et al. (2025) After super pixel segmenting high-resolution image data into graph data, the model employs a causal attention method to identify and use significant causal features. A backdoor adjustment strategy further decouples causative variables from shortcut characteristics to improve the model's interpretability and resilience. The experimental evaluations performed on the 2018 BACH breast cancer image dataset demonstrate that CDA-GNN achieves a classification accuracy of 86.36%. Several measures, including F1-score and ROC, demonstrate that the proposed strategy is superior and generally applicable [25].

Rai et al. (2025) conducted two independent trials using their suggested method: one on a real dataset devoid of augmentation and the other on a real dataset with GAN augmentation addition. They employed a 5-fold cross-validation strategy in their trials, and their suggested model performed well on the actual dataset (87.16% precision, 86.87% recall, 86.84% F1score, and 86.87% accuracy) without explicitly training it. Consistent with the first experiment, the second one outperforms the genuine + GAN-augmented dataset in every way (96.36% accuracy, 96.35% recall, 96.35% F1score). Improving performance on the combined dataset, this multimodal strategy using Lightweight UNet improves recall by 9.48%, F1score by 9.51%, and accuracy by 9.48% [26].

Anusha and Madhavi (2025) On MRI datasets, it shows an outstanding AUC score of 98.94%, an F1score of 94.8%, and an overall accuracy of 97.0%, demonstrating that it is superior in terms of discrimination and provides more accurate delineation of anatomical structures. Such high performance is also replicated in the ultrasound and mammogram datasets, where AMFFR-Net predicts higher AUC, F1-score, and Dice coefficient values with lower HD95 values indicating accurate boundary detection[27].

Murillo, Skean and Giraldo (2023) merge Recasens's non-uniform sampling strategy with Shen's et al.'s technique for developing a breast cancer classifier. They find that their strategy outperforms the official partition by 0.7819 points on the test set using input photos of size 576 x 448 and a custom partition yields an AUC of 0.8543 on the test set employing the CBIS-DDSM dataset. Comparatively, the performance obtained with the official partition was 0.7621 AUC and with a custom partition it was 0.8456 AUC [28].

Luo (2024) explore a deep learning-based approach utilizing Swin Transformer with Dual-View Cross Attention to enhance breast cancer detection. Their approach obtained an accuracy of 0.81 and an AUC of 0.87 by using mammography pictures from the RSNA dataset. These findings highlight the promise of state-of-the-art DL methods for enhancing medical imaging-based breast cancer screening [29].

Ghadge et al. (2024) By concatenating relevant features, employ machine learning algorithms (SVM, RF, KNN, NN) for classification. The NN-based classifier achieves a remarkable 92%accuracy on the RSNA dataset, attributed to the incorporation of age and multiple views in the updated dataset. Notably, their approach outperforms advanced techniques, demonstrating a 94.5% accuracy on the MIAS dataset and an exceptional 96% accuracy on the DDSM dataset [30].

Gengtian, Bing and Guoyou (2023) suggested a method for detecting and classifying breast cancer that relies on DL and the EfficientNet architecture. The accuracy and AUC of their suggested method were 0.75 and 0.83, respectively, when they tested it on mammography pictures from the CBIS-DDSM dataset. Their findings show how well DL methods work for diagnosing and detecting breast cancer in medical imaging [31].

Table 1 Related work on Machine learning based Early Cancer Detection and Classification in Medical Imaging

References	Methodology	Dataset	Performance	Limitations & Future Work
Chikkala et al. (2025)	BRNN with transfer learning (ResNet50 + GRU) and feature fusion	BreaKHis (7,909 images, 8 classes, 82 patients)	97.25% accuracy	Limited to BreaKHis dataset; requires testing on diverse datasets to verify generalizability.
Chang et al. (2025)	Causal discovery attention-based GNN with superpixel segmentation and backdoor adjustment	BACH dataset	86.36% accuracy	Performance improvement needed for real-world applications; additional validation on clinical datasets.
Rai et al. (2025)	Hybrid CNN with hierarchical attention mechanism for breast cancer classification	CBIS-DDSM, INbreast	AUC: 0.8721 (CBIS-DDSM), 0.8012 (INbreast)	Requires additional testing with other histopathological datasets; generalization to different imaging techniques needs improvement.
Anusha and Madhavi (2025)	Multi-modal feature fusion and refinement for segmentation	MRI, Ultrasound, Mammogram datasets	AUC: 98.94%, F1-score: 94.8%, Accuracy: 97.0%	Model needs testing on more diverse real-world datasets; computational cost and inference speed require optimization.
Murillo, Skean and Giraldo (2023)	Non-uniform sampling approach integrated with Shen et al.'s classifier	CBIS-DDSM, INbreast	AUC: 0.8543 (high-res), 0.7819 (low-res)	Limited validation beyond CBIS-DDSM and INbreast; pixel-level annotation impact needs further analysis.
Luo (2024)	Swin Transformer with Dual-View Cross Attention	RSNA	Accuracy: 0.81; AUC: 0.87	Optimize performance for smaller datasets and test other imaging modalities
Ghadge et al. (2024)	Feature extraction via CNNs + ML classifiers (SVM, RF, KNN, NN)	RSNA, MIAS, DDSM	RSNA: 92% accuracy, MIAS: 94.5%, DDSM: 96%	Further integration with clinical data; multi-modal imaging analysis required for robust detection.
Gengtian, Bing and Guoyou, (2023)	EfficientNet architecture for classification	CBIS-DDSM	Accuracy: 0.75; AUC: 0.83	Expand feature extraction methods and increase model interpretability

Methodology

Figure 1 shows the organized sequence of procedures used in the approach for early breast cancer diagnosis utilizing histopathology images. To start, it gathered the BreakHis dataset, which includes 9,109 pictures of breast tumor tissues, both benign and malignant. After that, image preprocessing was performed, where each image was resized to 700×460 pixels, normalized, and filtered using Gabor filtering to reduce noise while preserving important spatial features. Next, methods for enhancing data variety and correcting class imbalance were implemented, such as brightness modification, flipping, and rotation.

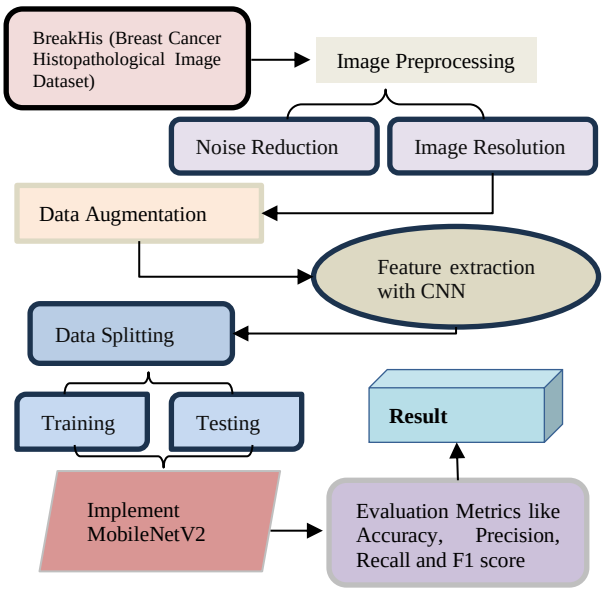

Fig.1 Flowchart for Breast Cancer Detection

After that, the dataset was split 80:20 for training and testing. Then, a CNN was used for automatic feature extraction of key tissue structures. After that, the MobileNetV2 model was implemented, utilizing depthwise separable convolutions, inverted residuals, and linear bottlenecks to create an efficient and lightweight model architecture. Then, the model was trained using a Learning Rate of 0.01, ReLU activation, 50 epochs, a dropout rate of 0.5, and a Batch Size of 5. Accuracy, precision, recall, F1score, Confusion Matrix, ROC, and Loss Curves were some of the measures used to assess the performance.

Each step and methodology process are explained in briefly in next section.

Data Collection

There are 9,109 photographs of breast tumor tissues obtained under the microscope in the BreakHis (Breast Cancer Histopathological Image Dataset) from 82 individuals. The dataset was created using the SOB (excisional biopsy) method. Separated into 2,480 noncancerous and 5,429 cancerous samples. The data sample is provided below:

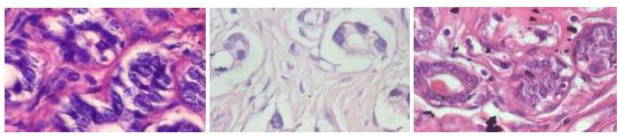

Fig.2 Dataset Sample Images

Figure 2 displays three H&E-stained histopathological sample images from the dataset. These samples

represent the diverse tissue morphologies the MobileNetV2 model must differentiate in classification tasks.

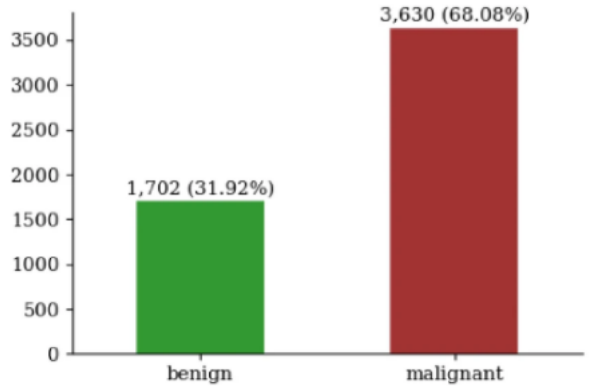

Fig.3 Distribution of Data

Figure 3 displays a class distribution in the histopathological dataset, showing significant class imbalance. The dataset contains 1,702 benign samples (31.92% of the total) represented by the green bar, and 3,630 malignant samples (68.08% of the total) represented by the red bar. The malignant class is over twice as common as the benign class, requiring techniques like class weighting or data augmentation to balance the dataset and improve model performance.

Image Preprocessing

Data preprocessing plays a critical role in data analysis and machine learning projects. In this study, we carried out data transformation involving handling missing or damaged data and converting data into a suitable format for machine learning algorithms. Missing values were carefully imputed to avoid bias and maintain prediction accuracy, while categorical variables were label-encoded to convert them into numerical values. Additionally, continuous numerical features (Total Charges, Monthly Charges, Tenure Months) were normalized using Min-Max Scaler to fit within a predefined range, typically 0-1. These preprocessing steps ensure that the data is appropriately prepared for the machine learning

Algorithms used in this study

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Image preprocessing is a crucial step in deep learning that enhances image quality and optimizes data for model training. It involves several techniques such as resizing, normalization, noise reduction, contrast adjustment, and data augmentation. Some steps for preprocessing are given below.

Image Resolution: The pictures are saved in PNG format and have a pixel size of 700 × 460 and an 8-bit RGB depth.

Noise Reduction: The efficiency of Gabor Filtering in decreasing noise while preserving substantial spatial frequency data was a deciding factor.

Data Augmentation

Data Augmentation is a smart way to increase a sample size, overcome overfitting, and improve classification accuracy. Basic augmentation procedures and color modifications including brightness, flipping, and rotation are used in the data augmentation process. Randomly rotating pictures adds zero-pixel borders to the edges.

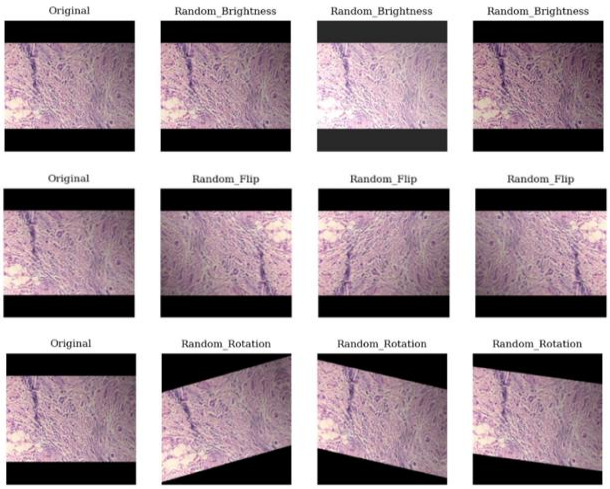

Fig.4 After Data Augmentation

Figure 4 showcases the outcomes of applying various data augmentation techniques to an original image. The first row illustrates the effect of "Random Brightness," where the original image is displayed alongside three variations exhibiting different brightness levels. The second row demonstrates "Random Flip," presenting the original image and three horizontally flipped versions. Finally, the third row depicts "Random Rotation," showing the original image followed by three rotated versions at different angles.

Feature Extraction with CNN

Feature extraction in CNNs enables automatic identification of key details like nuclei, glands, and tissue boundaries from histopathological images.

Models such as CNN optimize feature extraction through techniques like bottleneck blocks, depth wise convolutions, Max-Pooling, and residual connections for efficient and scalable performance.

Data Splitting

Splitting a dataset into training and testing sets to assess machine learning models is the procedure known as data splitting. 80% data for training and 20% data for testing.

Proposed MobileNetV2

The foundation of MobileNetV2 is the depthwise separable of MobileNetV1, which in turn adds the residual structure. The discovery of Linear Bottlenecks and Inverted Residuals followed ReLU's discovery of a severe information loss issue on Feature Maps with a limited number of channels [32]. The structural simplicity of MobileNetV1 is preserved in MobileNetV2 [33], allowing for the same level of precision without the need for extra specific procedures. Currently, MobileNetV2 is concentrating on learning how neural networks operate so that it can design the simplest network architecture possible[34]. The foundational study topics include the use of optimization techniques to framework searches (e.g., genetic algorithms) and reinforcement learning. Apart from adhering to the 33 depth-separable convolution, MobileNetV2's two primary advancements are Line bottlenecks and Inverted residuals. Performing both depthwise and pointwise convolutions makes up the depthwise separable convolution layer. The result was identical to that of ordinary 2D convolution because, after the depthwise convolution, a pointwise convolution operation was used [35]. The smallest amount of parameters is required for pointwise convolution since it is a typical 2D convolution with a 1×1 kernel. Equation (1) shows the output of a depthwise separable convolution layer, which is identical to that of a regular 2D convolution but uses less parameters, making it more efficient.

$$Output[i,j,k] = \sum Input[i,p,q] * Filter[k,p,q] \quad (1)$$

where the convolutional layer's output feature map is called output. The convolutional layer's input feature map is the input. Input feature maps are subjected to a series of filters that make up the filter. With i and j standing for the spatial dimensions and k for the channel dimension, the indices for the output feature map are i, j, and k, respectively. The input feature map's indices are p and q, where p and q are the spatial dimensions.

Evaluation Parameter

Several performance measure indicators are utilized to assess the effectiveness of ML techniques. After assess the parameter, TP, FP, TN, and FN are combined to generate a confusion matrix for the actual and anticipated classes. The meaning of the terminologies is explained below.

True Positive (TP): it stands for the accurate identification of cancer patches [36].

False Positive (FP): symbolizes the areas that are identified as cancer regions by the model but are not the malignant section.

True Negative (TN): showcases the areas that do not contain cancer and the algorithm accurately detects them as such.

False Negative (FN): symbolizes the areas of a cancerous zone that are classified as non-cancerous.

The performance metrics are given below.

Accuracy

The percentage of right predictions as a percentage of all forecasts is called accuracy. It is an essential metric for medical imaging since it shows how well a model can classify tumors [37]. It is calculated in Equation (2).

$$Accuracy = \frac{TP+TN}{TP+FN+FP+TN} \quad (2)$$

Precision

Precision is of the utmost importance in medical diagnostics, especially because false positives might result in needless treatments or interventions. It is a way to check how well the model consistently gets a certain categorization right. Equation (3) presents the precision formula.

$$Precision = \frac{TP}{TP+FP} \quad (3)$$

Sensitivity or Recall

The sensitivity of a model is its ability to properly forecast the proportion of positive observations out of the total number of observations in the real class. It is calculated in the Equation (4).

$$Sensitivity = \frac{TP}{TP+FN} \quad (4)$$

F1-Score

The F1 Score is a balanced representation of the two metrics, Precision and Recall, which are represented by their harmonic means. The formula for the F1 score is shown in Equation (5).

$$F1\ score = 2 \times \frac{Precision \times Recall}{Precision + Recall} \quad (5)$$

ROC Curve

The ROC curve is a graphical representation of the relationship between sensitivity (TPR) and (1 - specificity) (FPR) at different test value cut-off points.

In most cases, a square box is used to represent this, and the axes on it run from zero to one. It compares the TPR with the FPR. The equations for these metrics are shown in Equations (6 and 7):

$$TPR = \frac{TP}{TP+FN} \quad (6)$$

$$FPR = \frac{FP}{FP+TN} \quad (7)$$

Loss

Particularly important in medical imaging multi-class classification jobs, where mistakes may have serious consequences. In order to bridge the gap between expected and actual values, weight modifications were guided throughout the training phase using the Categorical Cross-Entropy loss value function.

Results and Discussion

The simulation parameters and the suggested ML model's performance outcomes are examined in this section. On a PC with an Intel Core i5-8600 CPU, a 250 GB SSD, a GeForce 1050 Ti 4 GB, 16 GB of RAM, and a 1 TB HDD, the suggested method is tested using the Python 3.6.5 tool. Learnt parameters include an activation of ReLU, an epoch count of 50, a dropout of 0.5, and a batch size of 5. Key evaluation metrics, including accuracy/loss, precision, recall, and F1score (see Table II), are utilized to assess model effectiveness, ensuring accurate and early detection of cancer. The suggested model successfully classified malignant and non-cancerous tissue samples with a high accuracy of 98.18%. With a sensitivity (recall) of 97.37%, it proved it could accurately identify the majority of real positive instances, and a precision of 98.38%, it showed how well it reduced false positives. Furthermore, the F1-score of 97.85% shows that there is a balanced relationship between recall and precision, which further supports the dependability and robustness of MobileNetV2 for early breast cancer diagnosis utilizing histopathological images.

Table 2 Performance of the MobileNetV2 model for breast cancer detection on Histopathological Image data

Metrics	MobileNetV2
Accuracy	98.18
Precision	98.38
Sensitivity	97.37
F1-score	97.85

Figure 5 presents a performance of a model in forecasting between two classes: Benign and Malignant. The grid displays four critical values: 179 cases were accurately classified as benign (TN, 29.64%), 414 cases as malignant (TP, 68.54%), 9 cases as benign were erroneously classified as malignant (FP, 1.49%), and 2 cases as malignant were erroneously classified as benign (FN, 0.33%). These values provide a clear picture of the model's accuracy in classifying each category and the types of errors it makes.

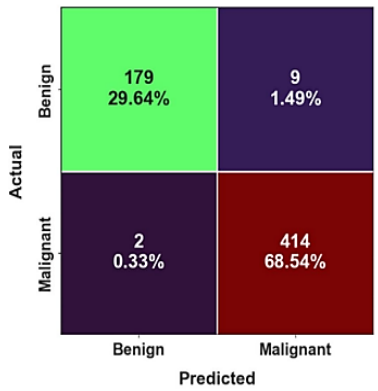

Fig.5 Plot Confusion matrix of MobileNetV2

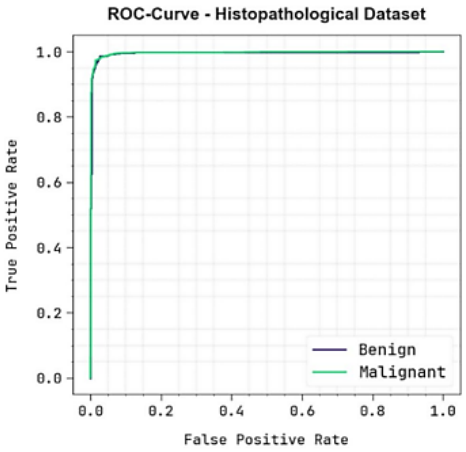

Fig.6 ROC Curve for MobileNetV2

Figure 6 represents a ROC curve for a model trained on a histopathological dataset for early breast cancer detection. The plot of the TPR versus the FPR provides an evaluation of the model's capability to differentiate among benign and malignant tumors. The near-perfect curve shape approaching (0,1) indicates a high-performing model with excellent discrimination capability.

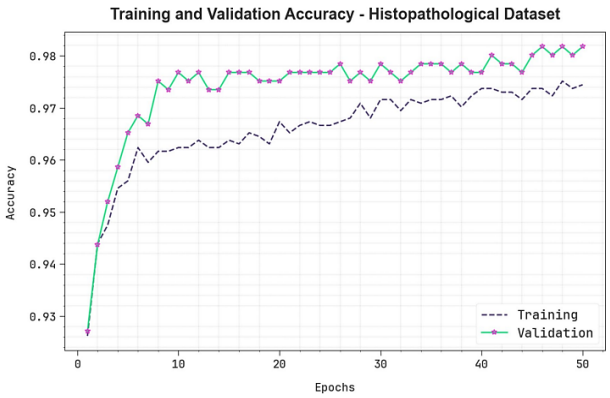

Fig.7 Plot Accuracy curve for the MobileNetV2

A histopathological dataset utilized for early breast cancer diagnosis has an accuracy curve for training and

validation, as shown in Figure 7. The y-axis displays the model's accuracy, while the x-axis shows the total number of epochs. Training and validation accuracy both reached about 98%, as shown in the graph, which indicates a consistent increase across epochs. The minimal gap between the two curves suggests a well-generalized model with low overfitting.

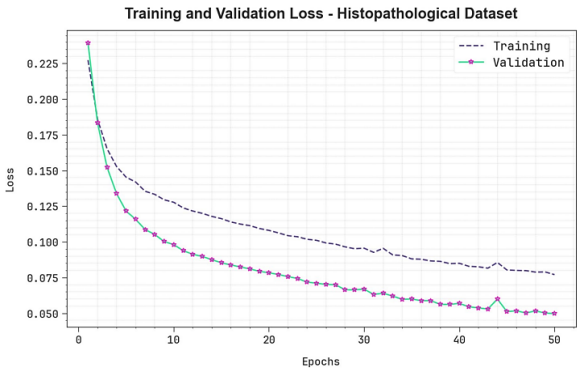

Fig.8 Plot Loss curve for MobileNetV2

Figure 8 displays training and validation loss curves for a MobileNetV2 model on a histopathological dataset over 50 epochs. Both curves show a rapid initial decrease followed by a gradual decline. The validation loss (purple line) remains consistently below the training loss (black dashed line), indicating good generalization without overfitting. A small validation loss spike appears around epoch 40 before returning to the downward trend, with final values reaching approximately 0.05.

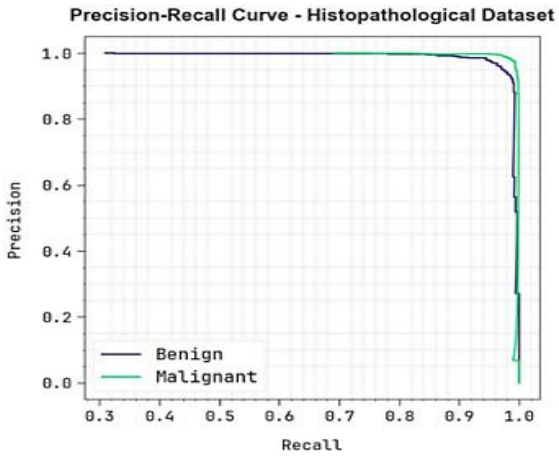

Fig.9 Precision-Recall curve for MobileNetV2

This precision-recall curve in Figure 9 classifying benign (blue) and malignant (green) samples. Both classes maintain near-perfect precision (close to 1.0) across most recall values (0.3-0.9), demonstrating excellent classification performance. The curves remain flat until approximately 0.95 recall before dropping sharply, indicating the model only struggles with the most difficult cases while achieving strong discriminative ability between benign and malignant samples with minimal precision-recall trade-off.

Comparison and Discussion

This section presents a performance comparison between the current model and the suggested one. The comparison is the same dataset and evaluation parameter that is shown in Table III. Among the models compared, MobileNetV2 demonstrated superior performance, achieving the highest accuracy of 98.18%, precision of 98.38%, sensitivity of 97.37%, and F1score of 97.85%, outperforming Xception, ResNet101, and EfficientNet. ResNet101 also showed strong results with an accuracy of 96.09% and balanced precision and sensitivity, whereas EfficientNet achieved a notable F1-score of 96.36%, despite a slightly lower sensitivity of 89.29%. The Xception model, although effective, had the lowest performance across all metrics. Overall, MobileNetV2's outstanding results highlight its effectiveness and reliability for accurate breast cancer detection from histopathological images.

Table 3 Comparative Evaluation of Models for breast Cancer Detection

Model	Accuracy	Precision	Sensitivity	F1-score
Xception [38]	89	90	90	89
ResNet101[39]	96.09	96.26	96.09	96.08
EfficientNet[40]	94.57	94.34	89.29	96.36
MobileNetV2	98.18	98.38	97.37	97.85

The proposed model offers several advantages, including high accuracy and efficiency in classifying benign and malignant breast cancer samples from histopathological images. It is perfect for contexts with limited resources since it uses MobileNetV2 to provide high performance at a reduced computational cost. The use of data augmentation helps mitigate class imbalance, while advanced feature extraction techniques ensure precise identification of critical tissue structures. These advantages enable faster, reliable, and automated cancer detection, supporting pathologists in clinical decision-making.

Conclusion and Future Work

One of the leading causes of mortality and a major health issue that is becoming more prevalent globally is cancer. Recent studies have shown that breast cancer is among the most prevalent cancers, particularly among women. Breast cancer survival rates and treatment costs may be improved with early diagnosis. Nevertheless, modern healthcare systems' reliance on early diagnostic techniques is not without its limitations. The MobileNetV2 model in this research showed remarkable performance in identifying breast cancer by histopathological pictures, with an F1score of 97.85%, accuracy of 98.18%, precision of 98.38%, and sensitivity of 97.37%. This study's findings demonstrate the promise of DL models as an automated tool for detecting breast cancer, which might greatly improve the accuracy of early detection.

There is a limitation to the model's capacity to handle varied real-world circumstances due to its dependence on a single dataset. Data augmentation helped with class imbalance, but for more complicated scenarios, it need even better solutions. Future work should focus on expanding the dataset, incorporating transfer learning, exploring multi-class classification for other tumor types, and optimizing the model for clinical deployment to ensure rapid and accurate breast cancer detection in various settings.

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