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A Pre-Trained EfficientNetV2-B0 Model for Breast Cancer Prediction

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Abstract: **Breast cancer remains a critical global health challenge where early and accurate diagnosis is essential for improving survival rates. Conventional diagnostic approaches are often limited by subjectivity and inconsistent accuracy, demanding the need for reliable computer-aided diagnostic systems. This study examined the use of the EfficientNetV2-B0 model, for breast cancer prediction using histopathological images. The images used in this study were obtained from the BreakHis database, which contains images of biopsies at varying levels of magnification that includes both benign and malignant samples. Images underwent comprehensive preprocessing, including size reduction, normalization, and application of augmentation techniques and random cropping to improve generalization. The dataset was divided into a training (70%) and testing (30%) set and all known benign cases were oversampled to eliminate class imbalance between the benign and malignant cases. EfficientNetV2-B0 was utilized to extract features and generate predictions. Additionally, ResNet50 and DenseNet121 were also used in this study for comparison purposes with EfficientNetV2-B0. Model training and evaluation were conducted in Python 3.11 using TensorFlow and Keras. Experimental results demonstrate that the EfficientNetV2-B0 model achieved performance of 99% prediction accuracy on the test set with precision of 100% and recall of 99%. In contrast, ResNet50, and DenseNet121 achieved lower accuracies of 89% and 94% respectively. The results demonstrated the robustness and diagnostic reliability of EfficientNetV2-B0 for breast cancer prediction over existing models. The EfficientNetV2-B0 model is therefore, recommended for integration into clinical workflows to assist pathologists, minimize diagnostic errors, and improve patient outcomes through timely and accurate detection**

Keywords: **Breast cancer prediction, histopathological images, efficientNetV2-B0, transfer learning, deep learning.**

I. INTRODUCTION

Breast cancer remains one of the most leading causes of cancer-related deaths globally. This posed a major public health challenge in both developed and developing nations [1],[2]. The World Health Organization (WHO) identifies breast cancer as the most common cancer among women worldwide, though it can rarely occur in men as well [3]. Breast cancer is broadly classified by whether they are non-invasive (in-situ), invasive or special types as depicted in Figure 1.

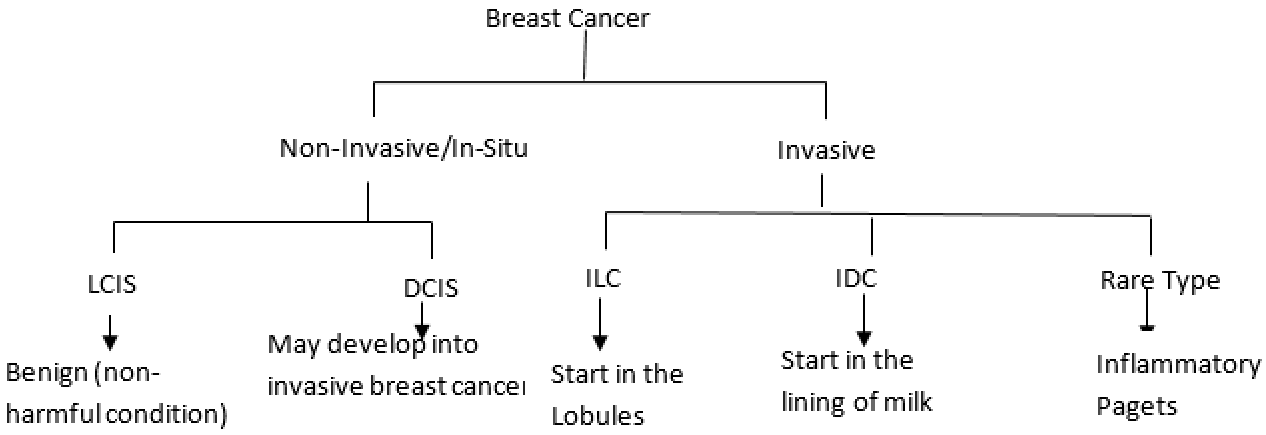


Fig. 1: Types of Breast Cancer

Non-invasive (In-situ) include Ductal Carcinoma in situ (DCIS) is stage 0, where abnormal cells are found in the lining of the milk duct but have not spread. Lobular Carcinoma in situ (LCIS) indicates abnormal cells in the lobules which have not developed into real cancer but increases future risk. Invasive type of breast cancer includes Invasive Ductal Carcinoma (IDC), Invasive Lobular Carcinoma (ILC). Examples of special types are Inflammatory Breast Cancer (IBC), Tripple-Negative Breast Cancer (TNBC), HER2-Positive and Pagets disease of the nipple [2].

Research established that, in Malaysia, breast cancer accounts for about 25% of cancer deaths, with 5% of women at risk compared to 12.5% in Europe and the United States [4]. Similarly, Nigeria and other developing countries experience a growing breast cancer burden due to inadequate medical infrastructure [5]. However, as noted by Cancer.Net, every patient's experience is unique, with varying risk factors and recovery chances [6]. Breast cancer begins when breast cells grow uncontrollably, forming tumors that can be fatal if untreated [3]. The disease typically originates in the milk ducts or lobules and may spread to surrounding tissue, causing lumps or thickening [7]. The early stage, known as in-situ cancer, is not life threatening, but invasive forms can spread and become more dangerous [3]. Over three million women are affected yearly [8], with multiple contributing factors including genetics, hormonal imbalance, radiation, weight, and reproductive history [9], [10]. Lifestyle and dietary changes have also been linked to the rising incidence of the disease, and survival beyond five years after diagnosis remains difficult for many patients [11].

Early detection and accurate prediction play vital roles in improving treatment and survival outcomes [12]. Traditional method by Medical practitioners to identify and classify tumors using imaging and biopsy tests can be time-consuming and prone to error [13]. Therefore, computational and deep learning tools have become essential for assisting in diagnosing and predicting breast cancer more efficiently [14],[25]. These tools can help determine cancer stages early and guide proper therapy, thereby reducing mortality rates [11].

Despite the advancement in medical research and technologies, accurate and timely detection and diagnosis of breast cancer remain a critical concerns due to the diseases complexity and traditional diagnostic methods [23], this necessitate the need for a robust and integrated model capabilities to improve accuracy and reliability in breast cancer prediction. Hence, this study aims to present EfficientNetV2-B0 pre-trained model as the most efficient and accurate deep learning models for tumor prediction, providing valuable insights into how this model can enhance breast cancer diagnosis and prognosis. EfficientNetV2-B0 is highly suitable for breast cancer prediction, particularly in histopathological image dataset due to its superior balance of high accuracy, computational efficiency and robust feature extraction capabilities [24].

II. LITERATURE REVIEW

Breast cancer prediction has rapidly advanced with the adoption of machine learning and deep learning techniques making researchers now using more complex and powerful techniques to help in detecting cancer early and accurately. In [15] investigated the performance improvement of machine learning algorithms for breast cancer prediction using the Wisconsin Breast Cancer Diagnostic (WBCD) dataset. The study evaluated multiple classifiers including Support Vector Machine (SVM), Logistic Regression (LR), K-Nearest Neighbors (KNN), Decision Trees, Random Forest, Multi-Layer Perceptron (MLP), and bagging techniques. K-fold cross-validation and feature importance scoring were employed to enhance model reliability. Logistic Regression achieved the highest accuracy (99.14%) and AUC (99.6%), with Extra Trees and SVM achieving comparable results. However, the study acknowledged potential overfitting concerns due to the small and imbalanced nature of the WBCD dataset.

The authors in [13] conducted a comparative analysis of machine learning algorithms for early-stage breast cancer detection using the University of Wisconsin dataset. The study evaluated Logistic Regression, SVM, and KNN, with SVM demonstrating superior performance (92.98% accuracy) compared to Logistic Regression (87%) and KNN (91%). While the results highlight the potential of ML techniques for early detection, the study was limited to a single dataset, raising concerns about generalizability to diverse clinical populations. In [16], breast cancer prediction using various ML was presented. The assessed algorithms included SVM, Logistic Regression, Random Forest, XGBoost, AdaBoost, KNN, Naive Bayes, and a custom ensemble classifier. XGBoost achieved the highest accuracy (96.60%), followed closely by the ensemble method (96.54%) and Random Forest (96.25%). The authors noted that algorithm performance may vary depending on dataset characteristics and specific prediction tasks.

A breast cancer prediction model using k-Nearest Neighbor (kNN), SVM, Logistic Regression, and Gaussian Naive Bayes (NB) classifiers was presented in [17]. The experimental results revealed accuracy values of 0.99 for KNN, 0.96 for SVM, 0.97 for Logistic Regression, and 0.95 for Naive Bayes. While kNN demonstrated superior performance, the study acknowledged its susceptibility to the course of dimensionality. Sarkar and Ghose [8] employed the University of Wisconsin Madison Breast Cancer dataset to evaluate Logistic Regression, SVM, Random Forest, and Neural Networks for binary classification. Logistic Regression achieved the highest accuracy (98.24%), followed by SVM (97.28%), Neural Networks (97.19%), and Random Forest (94.13%). Authors in [12] conducted a study on breast cancer prediction using machine learning. The work compared three models namely, Logistic Regression, Decision Tree, and Random Forest using the Wisconsin Diagnostic Dataset, which comprised 357 benign and 212 malignant cases based on fine needle aspirate image features. Experimental study revealed Random Forest achieved the highest accuracy of 95% and a 93% cross-validation score using the top predictors. The findings also highlight the potential of machine learning for early breast cancer detection and diagnosis, while Logistic Regression and Decision Tree demonstrated competitive predictive performance, the ensemble approach of Random Forest captured complex data patterns more effectively, resulting in superior accuracy.

The authors in [18] compared eleven ML algorithms for predicting breast cancer recurrence using a clinical dataset (n = 342) from Tianjin Medical University Cancer Institute. While Random Forest achieved the highest accuracy 98.1%, AdaBoost recorded 97.1% accuracy as a result of balanced performance across multiple metrics including AUC, sensitivity, specificity, PPV, NPV, and F1-score. However, small sample dataset limits generalizability and raises concerns about overfitting. A Hybrid Machine Learning-Fuzzy and Dimension Reduction (MLF-DR) model using the WBCD dataset was developed in [19]. Feature-based class, fuzzification and dimension reduction techniques (PCA and RFE) were applied, with Logistic Regression and Random Forest classifiers trained on the reduced fuzzy feature space. The LR-PCA model with eight components achieved the highest accuracy (99.1%), demonstrating that integrating fuzzy logic with dimension reduction enhances model generalization.

Authors in [20] proposed an attention-driven multimodal deep learning framework integrating clinical data, copy number alteration data, and gene expression data. The two-phase architecture employed a sigmoid-gated attention CNN for feature extraction, followed by dense and dropout layers for classification. The multimodal approach effectively captured complex interdependencies among diverse data modalities, improving breast cancer prognosis and classification performance. A CNN models for breast cancer prediction using the Dataset-BUSI-with-GT and BreakHis datasets was proposed in [21]. Transfer learning was implemented using pre-trained VGG19 as a baseline, with an enhanced CNN architecture incorporating global pooling, dropout layers, and optimized hyperparameters. The enhanced ResNet101 model achieved 89.98% validation accuracy on the BreakHis dataset, surpassing baseline CNN and VGG19 models. Authors in [22] proposed a hybrid deep learning architecture combining Bidirectional LSTM (BiLSTM) and 2D Convolutional Neural Network (Conv2D) for breast cancer prediction using histopathological images. Following preprocessing with autoencoders, the model achieved 98.8% accuracy, with sensitivity of 0.82 and specificity of 0.79. The relatively modest sensitivity-specificity balance suggests potential under-detection of malignant cases, a critical concern for clinical deployment.

Several studies have explored machine learning and deep learning approaches for breast cancer prediction using various datasets and algorithms. While these works demonstrate promising results, many faced limitations in dataset size, generalizability, model performance and lacked optimization for clinical use since they failed to eliminate false negative which is a critical requirement in medical diagnosis. This study addresses these gaps by applying the EfficientNetV2-B0 architecture to the BreakHis dataset, aiming to achieve superior accuracy and clinical reliability for breast cancer diagnosis.

III. METHODOLOGY

To achieve the objectives of this work, the architecture of the prediction model is presented in Figure 2.

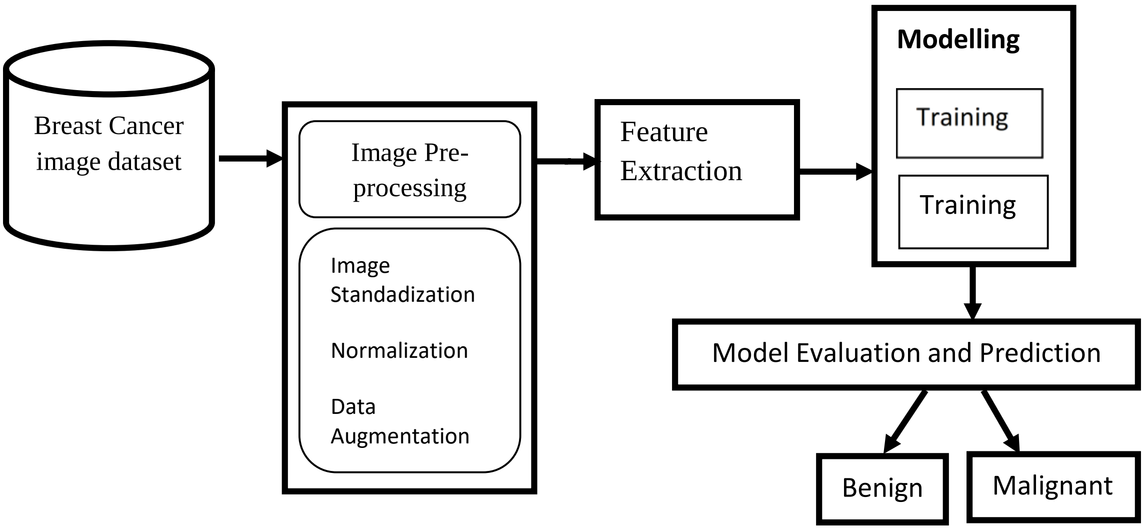
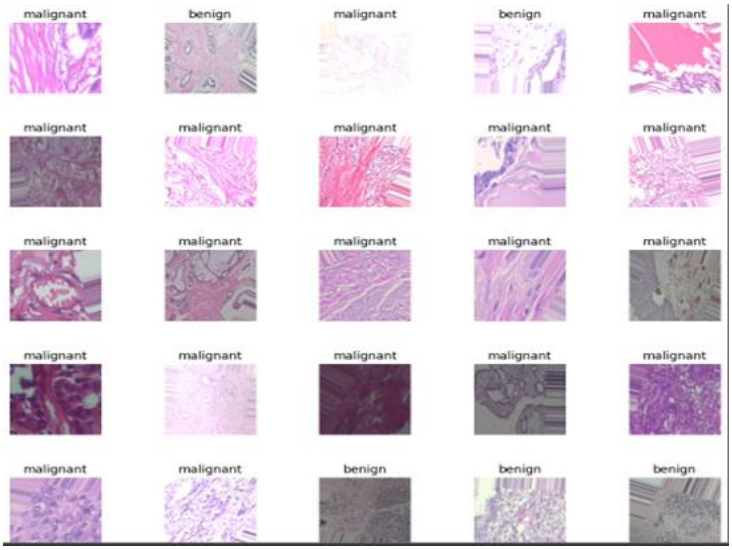


Fig. 2: The Conceptual Model for the Breast Cancer Prediction

The process involves image acquisition, preprocessing stage, model development, training, testing, and prediction.

3.1 Dataset Acquisition and Processing

The dataset used for this study were obtained from the Breast Cancer Histopathological Image Classification (BreakHis) dataset, a publicly available repository developed in collaboration with the R&D Laboratory of Pathological Anatomy and Cytopathology in Paraná, Brazil. The dataset comprises 7,909 digitized microscopic images of breast tumor tissue collected from 82 patients. The images were captured at four magnification levels: 40X, 100X, 200X, and 400X. The dataset comprises of two classes, benign and malignant with total of 2,480 benign and 5,429 malignant tissue samples. All images are saved in PNG format at a resolution of 700×460 pixels in 3-channel RGB color. The data is anonymized in adherence to medical confidentiality standards. Figure 3 shows the sample images of the dataset collected.



. Fig. 3: Samples of Breast Cancer dataset images

To prepare the raw image data for deep learning models, the following preprocessing steps were implemented:

i. **Image Standardization:** All input images were resized to 224×224 pixels to match the input requirements of the selected model architectures.

ii. **Normalization:** Pixel values were normalized to a standard range between 0 and 1 to accelerate convergence during training.

iii. **Data Augmentation:** To mitigate overfitting and improve generalization, transformations such as horizontal flipping, rotation (limit 15°), brightness/contrast adjustments, and random cropping were applied.

iv. **Class Balancing:** Given the imbalance between benign (2,480) and malignant (5,429) samples, oversampling techniques were applied to the benign class during training to balance the dataset.

v. **Data Splitting:** The dataset was divided into training (70%) and testing (30%) subsets.

3.2 Model Architecture

This study employed three well established Convolutional Neural Network (CNN) architectures namely EfficientNetV2-B0, ResNet50, and DenseNet121 for the predictive task. These models were selected for their demonstrated effectiveness in image classification, especially within the medical imaging domain. EfficientNetV2-B0 served as the primary model, utilizing a compound scaling method that jointly optimizes network depth, width, and resolution. The architecture as depicted in Figure 4, employs Mobile Inverted Bottleneck Convolution (MBConv) blocks with Squeeze-and-Excitation (SE) optimization and fused convolutional layers for improved training efficiency on smaller image sizes. ResNet50 is a deep residual network that utilizes skip connections to mitigate the vanishing gradient problem, enabling the training of substantially deeper networks. DenseNet121 is a densely connected network where each layer receives feature maps from all preceding layers, promoting feature reuse and reducing parameter count. Transfer learning was applied by loading pre-trained weights (ImageNet) for all models. The final classification layers were replaced and fine-tuned on the BreakHis dataset. Initial layers were frozen to retain general features, while deeper layers were retrained for specific breast cancer classification.

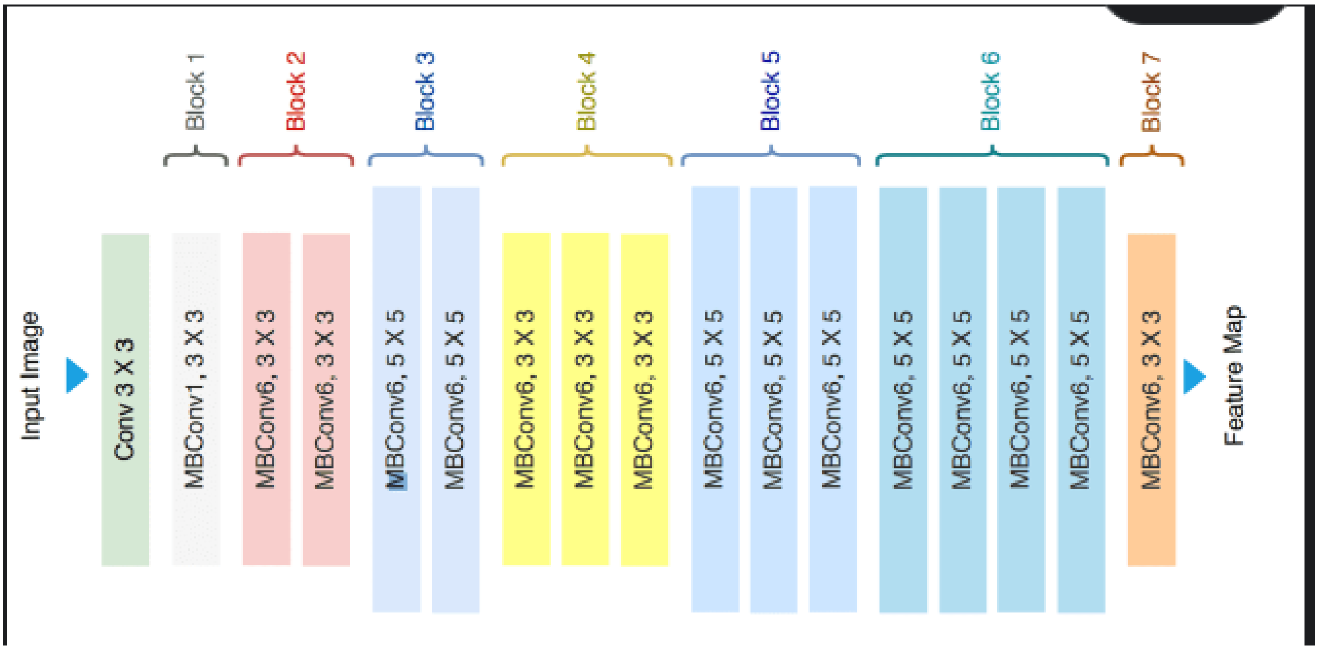


Fig. 4: The architecture of the EfficientNetV2-B0 prediction model [24]

IV. THE EXPERIMENTAL SETUP AND RESULT

The experimental study was carried out on a personal computer core i5 with 4GB RAM, 250GB HDD 205 GHz processor with 64-bit Operating System. The software requirements include Python 3.11 with TensorFlow and Keras libraries. Training was conducted using the following adjusted hyperparameters of the CNN model as shown in Table 1.

Table 1: Hyperparameters used in CNN training process

meters	Parameter values
Optimizer	Stochastic Gradient Descent (SGD)
Learning rate	0.00001
Batch size	32
Epochs	00
Loss function	Categorical cross-entropy

4.1 Performance Evaluation Metrics

The performance evaluation metrics is based on accuracy, precision, recall and F1 score as expressed in equations 1-4.

i. Precision is defined by True Positive (TP) divided by the summation of True Positive (TP) and False Positive (FP) is expressed as follows:

$$Precision = \frac{TP}{TP+FP} \qquad (1)$$

ii. Recall is True Positive divided by the summation of True Positive and False Negative is expressed as follows:

$$Recall = \frac{TP}{TP+FN} \qquad (2)$$

iii. F1-score is defined by 2 times precision times recall divided by the summation of Precision and Recall is expressed as follows:

$$F! - score = 2 * \frac{Precision \times Recall}{Precision \times Recall} \qquad (3)$$

iv. Accuracy is the summation of true Negative and True Positive divided by the summation of True Negative, True Positive, False Positive and False Negative

$$Accuracy = \frac{TN+TP}{TN+FN+TP+FN} \qquad (4)$$

4.2 Performance of the Breast Cancer Prediction models

Table 2

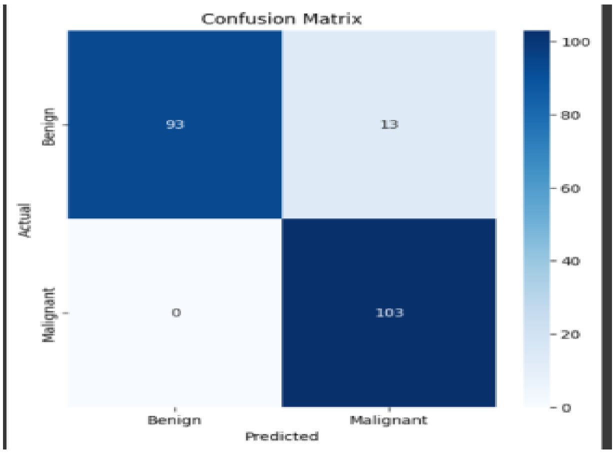
Model	**Precision (%)**	**Recall (%)**	**F1-Score (%)**	**Support**
EfficientNetV2-B0				
Benign	99	100	99	106
Malignant	100	99	99	103
Accuracy			99	
Macro Avg	99	99	99	209
Weighted Avg	99	99	99	209
DenseNet121				
Benign	100	88	93	106
Malignant	89	100	94	103
Accuracy			94	
Macro Avg	94	94	94	209
Weighted Avg	94	94	94	209
ResNet50				
Benign	100	79	88	106
Malignant	82	100	90	103
Accuracy			89	
Macro Avg	91	98	89	209
Weighted Avg	91	89	89	209

The results of the evaluated models, as presented in Table 2 establishes the proposed EfficientNetV2-B0 model as the superior architecture for this diagnostic task, achieving an overall accuracy of 99%. This performance significantly exceeds that of the benchmark models, DenseNet121 (94%) and ResNet50 (89%). A critical examination of class wise metrics reveals the clinical relevance of these results. While both DenseNet121 and ResNet50 achieved perfect recall (100%) for the malignant class, this sensitivity came at the cost of poor precision (89% and 82%, respectively) and, consequently, a low recall for the benign class (88% and 79%). This imbalance indicates a high false positive rate, where benign cases are frequently misclassified as malignant.

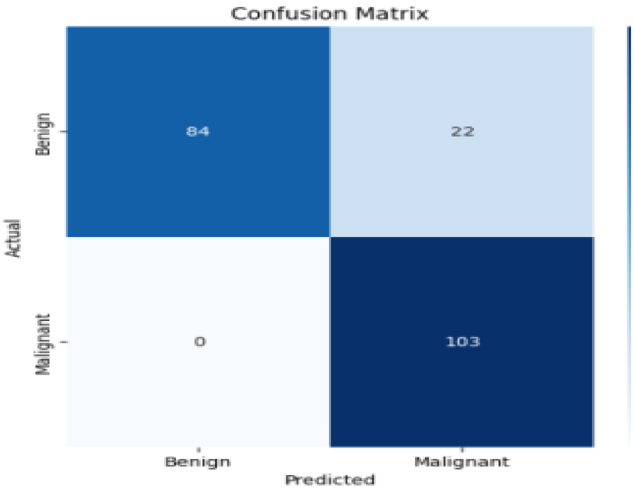
In contrast, the EfficientNetV2-B0 model demonstrates an optimal equilibrium between sensitivity and specificity. It achieved a near-perfect recall of 99% and a perfect precision of 100% for the malignant class, ensuring that cancerous cases are both reliably detected and accurately flagged. Simultaneously, the model attained perfect recall (100%) for the benign class, confirming its ability to correctly identify healthy patients. This simultaneous optimization results in a Macro and Weighted Average of 99% across all metrics, indicating robust and unbiased performance. The elimination of false negative for the benign class and the maximization of precision for the malignant class positions EfficientNetV2-B0 as the most clinically viable model, minimizing both the risk of missed diagnoses and unnecessary patient anxiety from false positives. The confusion matrix results for the three CNN architectures on the test set are presented in Table 3 and Figures 4 a,b and c .

Table 3: Confusion Matrix Results for CNN Models

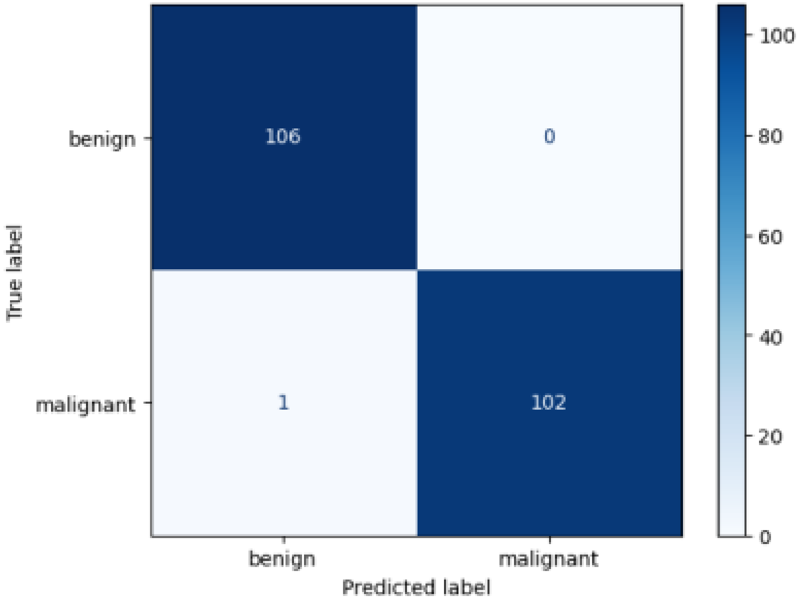
Model	**True Positive**	**False Positive**	**True Negative**	**False Negative**
DenseNet121	103	13	93	0
ResNet50	103	22	84	0
EfficientNetV2-B0	102	0	106	1



a. DenseNet121 model



b. ResNet50 model



c. EfficientNetV2-B0 model

Fig. 4: Confusion Matrix results for (a) DenseNet121, (b) ResNet50 and (c) EfficientNetV2-B0 Models.

EfficientNetV2-B0 achieved zero false positives, indicating perfect precision with no benign cases misclassified as malignant. It recorded the highest true positive count with only one false negative, reflecting an optimal balance between sensitivity and specificity. In contrast, DenseNet121 and ResNet50 achieved perfect recall (zero false negatives) but incurred significantly higher false positive counts (13 and 22, respectively), suggesting a conservative tendency that prioritizes sensitivity over precision. These results demonstrate that EfficientNetV2-B0 provides superior diagnostic reliability for applications where missing a positive case carries significant clinical consequence, as it maintained perfect precision while minimizing missed detections. The proposed model was compared with recent studies in the field. Table 4 presents the comparative analysis the findings.

Table 5: Comparative Analysis Table

Author (Year)	Method	Accuracy (%)	Precision (%)	Recall (%)
Poornajaf & Yousefi (2023)	Logistic Regression	99	99	100
Agana et al. (2023)	BiLSTM-Conv2D	98	61	82
Aprilia & Susanto (2024)	SVM (Ultrasound)	79	79	79
Proposed Study	**EfficientNetV2-B0**	**99**	**100**	**99**

As presented in Table 4, the proposed EfficientNetV2-B0 model demonstrates competitive performance against existing methods, achieving an accuracy of 99% and a superior precision of 100%. While the logistic regression model by Poornajaf & Yousefi (2023) also reports 99% accuracy, its lower precision (99%) compared to our model suggests a higher rate of false positives. Furthermore, our approach significantly outperforms the Bidirectional Long Short-Term Memory with 2D Convolutional Neural Network (BiLSTM-Conv2D) model proposed by Agana et al. (2023), which exhibited considerably lower precision (61%) and recall (82%). The results also show a substantial improvement over traditional machine learning methods like the SVM approach used by Aprilia & Susanto (2024), highlighting the advantage of using deep learning with histopathological images for more robust feature extraction. The superior performance of EfficientNetV2-B0 can be attributed to its compound scaling method, which optimizes depth, width, and resolution simultaneously. This allows the model to capture fine-grained details in histopathological images without a disproportionate increase in computational cost. The use of transfer learning further enhanced performance by leveraging features learned from large-scale natural image datasets.

The elimination of false negatives is the most significant clinical contribution of this study. In breast cancer screening, sensitivity is often prioritized over specificity to ensure no cancerous cases are overlooked. The model's ability to achieve 100% recall for malignant cases suggests it is highly suitable as a second-opinion tool for pathologists.

V. CONCLUSION

This study successfully developed a robust deep learning system for the binary classification of breast cancer histopathological images. The proposed model, based on the EfficientNetV2-B0 architecture, achieved an accuracy of 99% on the BreakHis dataset. Its most significant achievement is 100% precision for malignant cases with zero false positives, ensuring that no benign case is misclassified as cancer and eliminating unnecessary patient anxiety and invasive procedures. Complementing this, the model attained 99% recall for malignant cases, detecting cancer-positive cases with near-perfect sensitivity a critical factor for clinical deployment.

The results demonstrate the profound potential of advanced CNNs and transfer learning in enhancing the accuracy and efficiency of medical diagnostics. By providing a highly reliable, automated second opinion, such a system can assist pathologists in reducing diagnostic errors and improving patient outcomes through earlier and more accurate detection.

For future work, we plan to validate the model's generalizability on larger and more diverse multi-source datasets. Furthermore, integrating this model into a user-friendly web-based application could facilitate its adoption in clinical workflows, making advanced diagnostic AI accessible to a broader range of healthcare providers.

REFERENCES

[1] D. Sandeep, and G. N. B. Bethel. “A survey on Accurate Breast Cancer Detection and Classification using Machine Learning Approach”. E3S web of Conference, *01116*. 2021.

[2] A. Mehak, T,M. Ali, A. Nawaz, and L.S. Parwati. “Breast Cancer Predictions using Machine Learning Algorithms”. Engineering Proceedings. 107-129. 2025. https://doi.org/10.3390/engproc2025107129.

[3] *Breast cancer*. “World Health Organization”. 2023. https://www.who.int/news-room/fact-sheets/detail/breast-cancer..

[4] S. H. Nallamala, P. Mishra, and S. V. Koneru, “Breast Cancer Detection Using Machine Learning” international Journal of Recent Technology and Engineering, ISSN: 2277-3878, Volume 8, Issue 2S3, pp. 1402-1405. 2019..

[5] G. Omiko “Breast Cancer: How poor awareness, dearth of facilities, professionals, spike cases in Nigeria”. The Guardian Nigeria News - Nigeria and World News. Retrieved December 22, 2023, from https://guardian.ng/saturday-magazine/breast-cancer-how-poor-awareness-dearth-of-facilities-professionals-spike-cases-in-nigeria/

[6] *Breast Cancer - Statistics*. (2023). Cancer.Net. Retrieved December 22, 2023, from https://www.cancer.net/cancer-types/breast-cancer/statistics

[7] S. Mundhe, P. N. Wadkar and S. Misa, “Analysis of Breast Cancer Dataset and it’s prediction”. International Institute of Management Science (IIMS). ISBN: 978-81-927230-0-10, 2022.

[8] H. Sarkar and R. Ghose “Breast Cancer Prediction using Machine Learning”. International Research Journal of Engineering and technology (IRJET). Volume 10, Issue 03, pp. 148-153. 2023. Available at: www.irjet.net.

[9] R. Challa, R. Bijjala, and D. M. Sreenivas “Breast Cancer Prediction Using Machine Learning”. International Journal for Research in Applied Science & Engineering Technology (IJRASET). Volume 10, Issue VI. ISSN:2321-9653, pp. 3560-3566. Available at: www.ijraset.com.

[10] V. K. Pokala, G. M. P. Puli, M. Ravipati, S. Pokala, and S. V. R. Krishna “Prediction of Breast Cancer, Comparative Review of Machine Learning Techniques and their Analysis”. International Research Journal of Engineering and Technology (IRJET). Volume 09, Issue 08. pp. 495–499. 2023 Available at: www.irjet.com.

[11] V. Apoorva, H. K.Yogish, and M. L..Chayadevi “Breast Cancer Prediction Using Machine Learning Techniques”. Proceedings of the 3rd International Conference on Integrated Intelligent Computing Communication & Security (ICIIC). Volume *4*, pp. 348–355. 2021.

[12] Y. Wei, D. Zhang, M. Gao, Y. Tian, Y. He, B. Huang, and C. Zheng, “Breast Cancer Prediction Based on Machine Learning”. Journal of Software Engineering and Applications, 16, pp.348–360. 2023 Available at: https://doi.org/ 10.4236/jsea.2023.168018.

[13] M. P. Wadkar, M. Shivaji, and D. S. Misal, "Comparative Analysis of different Machine Learning Algorithms used in Breast Cancer Prediction". UGC Care Journal. Vol. 47 Issue 1 No 10 ISSN:2278-6864, pp.32–39. 2023.

[14] M. Ashraf, K. Le, and X. Huang, "Information Gain and Adaptive Neuro-Fuzzy Inference System for Breast Cancer Diagnoses". 911–915. 2013.

[15] M. Poornajaf and S. Yousefi, "Improvement of the Performance of Machine Learning Algorithms in Predicting Breast Cancer" Frontier in Health Informatics. Pp.1-7. 2023. Available at: www.ijmi.ir.

[16] V. Sharma, V. Garg, S. Maggu, and B. Kapoor, "Breast Cancer Prediction using Machine Learning". International Journal for Research in Applied Science & Engineering Technology (IJRASET). Volume 11, Issue III. ISSN:2321-9653, pp. 1173-1180. 2023. Available at: www.ijraset.com.

[17] G. Singh. "Breast Cancer Prediction Using Machine Learning". International Journal of Scientific research in Computer Science, Engineering and Information Technology (IJSRCSEIT). Volume 6, Issue 4. pp.278-284. ISSN: 2456-*3307. 2020* Available at: www.ijsrcseit.com

[18] D. Zuo, L. Yang, Y. Jin, H. Qi, Y. Liu, and L. Ren, "Machine Learning-Based Models for the Prediction of Breast Cancer Recurrence Risk*"*. BMC Medical Informatics and Decision Making. pp.1–15. 2023.

[19] S. Prusty, P. Das, S. K. Dash, S. Patnaik, and S. G. P. Prusty, "Prediction of Breast Cancer using Integrated Machine Learning-Fuzzy and Dimension Reduction Techniques". Journal of Intelligent & Fuzzy Systems. Pp. 1633-1650. ISSN: 1064-1246. 2023.

[20] S. Kayikci, and T. M Khoshgoftaar, "Breast Cancer Prediction using Gated Attentive Multimodal Deep Learning". Journal of Big Data. pp.1-11. 2023. https://doi.org/10.1186/s40537-023-00749-w

[21] S. Chen, B. Han, L. Zhixin, and H. Wang, "Breast Cancer Prediction Based on the CNN Models". Applied and Computational Engineering, *8*(1), 657–666. 2023. https://doi.org/10.54254/2755-2721/8/20230293

[22] M. A. Agana, C. O. Agwu, and N. A. Ukpoho, "Breast Cancer Prediction and Control Using BiLSTM and Two-Dimensional Convolutional Neural Network". International Journal of Software Innovation, *11*(1), 1–19. 2023. Available at: https://doi.org/10.4018/IJSI.316169.

[23] O. Aknyemi, J.A. Kupolusi, and O.N. Omoragbon, "Prediction of Breast Cancer using Supervised Machine Learning and Deep Learning". African Journal of Biomedical Research. Vol. 28(1). pp. 2838-2847. 2025. https://doi.org/ 1053555/AJBR.v28IS.5039.

[24] M. Hassan, "Deep Learning for Breast Cancer Detection: Comparative Analysis of ConvNeXT and EfficientNet". International Conference on Computer and Information Technology (ICCIT). Cox's Bazar, Bagladesh. 979-8-3315-1909-4/24. 2024.

[25] K. Neha, A. Gupta, G.S. Pauwar, G.S. Waghale, and Goyal "Prediction of Breast Cancer using Deep Learning Algorithms and Gradient Boosting". Journal of Neonatal Surgery. 14(18s), pp. 380-387. 2025.