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Enhancing Breast Cancer Classification with an Ensemble Transfer Learning Framework

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Abstract

Breast cancer remains one of the most formidable health challenges facing millions worldwide each year. Breast cancer poses a significant challenge to both patients and healthcare professionals. MRI, ultrasound, and mammography are conventional tools for the diagnosis of breast cancer. However, it can be time-consuming, and the results may be prone to human considerations. Researchers exploring the potential of deep learning and convolutional neural networks have shown promising success in automating image analysis across numerous applications. This study employs a transfer learning approach using a stacked ensemble model that combines MobileNetV2 and efficient-net v2 to classify breast cancer images. The breast cancer image dataset acquired from the Kaggle website known as BUSI(Breast ultrasound images). The proposed model exhibited superior performance in breast cancer picture classification, with an accuracy of 0.93. Our findings reveal that our suggested integrated framework might beat the state-of-the-art deep learning approaches of the baseline study by using all automated steps.

Keywords:Breast cancer, deep learning, classification, convolution neural networks (CNNs), and ensemble models.

1. Introduction

Breast cancer is a common and dangerous malignancy that affects women worldwide. Estimates [1] indicate that over 2 million new instances of breast cancer were detected in 2024 alone. Early and accurate detection of breast cancer improves patient survival rates and general well-being [2]. Breast cancer examination results can be classified into five types: negative, benign calcification, benign mass, malignant calcification, and malignant mass. Classifying these results is challenging due to the complicated, heterogeneous, and high-dimensional nature of the data [3]. Traditional approaches to Breast cancer diagnosis are based on mammography and histologist investigation, which can be time-consuming and prone to human error. The growth of deep learning technology, notably convolutional neural networks (CNNs), has resulted in a substantial shift toward automated image categorization systems that can help radiologists and pathologists diagnose breast cancer more reliably and efficiently. In machine learning, transfer learning is the method whereby a model developed for one job is reused or fine-tuned for another related task. Instead of training a deep neural network from scratch, transfer learning leverages pre-trained models (such as VGG16, Res Net, Dense Net, or Mobile Net) that have been trained on large datasets (e.g., ImageNet) and applies their learned features to new problems with limited data.

Ensemble deep learning techniques, which combine many models to increase classification performance, have shown promise in terms of system robustness and accuracy. The purpose of this document is to provide a complete overview of ensemble deep learning's potential for breast cancer image categorization.

Research Questions

RQ 1: How can breast cancer classification be performed using ensemble learning techniques?

RQ 2: How do we compare our proposed model with the baseline paper?

RQ 3: What are the statistical differences in classification accuracy among various individual models and the stacking ensemble approach for breast cancer image classification?

Research Objectives

1. To investigate and implement ensemble learning techniques for the classification of breast cancer using medical imaging data.
2. To evaluate and compare the performance of the proposed ensemble model against the baseline model presented in the reference study.
3. To analyze the statistical differences in classification accuracy among individual machine learning models and the stacking ensemble approach in the context of breast cancer image classification.

Related Work

A series of studies have offered frameworks for accurate breast cancer image classification. Numerous scholars have highlighted the significance of AI and deep learning models in healthcare. Deep learning has emerged as the most effective technique for analyzing and categorizing tumor diseases, owing to its high level of accuracy. This is mostly due to the extensive studies conducted on deep learning methods, particularly transfer learning (TL) technology, which utilizes pre-trained models.[1], [2]Many scholars have engaged artificial intelligence (AI), expert systems, and neural networks in the classifications of breast cancer images to enhance their accuracy[3]. Traditionally, the diagnosis of breast cancer relied on the manual examination of histopathology images by experienced pathologists. While pathologists possess extensive expertise, this approach is time-consuming, subject to inter-observer variability, and can be prone to errors, especially in distinguishing between subtle histologist sub-types [4], [5], [6]. Traditional machine learning approaches like Support Vector Machines (SVMs), Random Forests, and k-nearest Neighbors (k-NN) are typical techniques used for Classification tasks. While these methods improve efficiency, the reliable classification of breast cancer images remains difficult due to their complexity and variation[7].With progress in artificial intelligence (AI), mostly deep learning, there has been a weighty swing toward automatic breast cancer image classification. Furthermore, Deep learning models are becoming a growing trend due to their ability to handle complex problems with large datasets, increasing prediction accuracy, and robustness. [8]. Furthermore, the proposed ensemble was tested on the BreakHis dataset with the usage of VGG16, ResNet34, and ResNet50 models applied for classifying microscopic images into eight categories (four benign and four malignant). For both datasets, the 5-fold cross-validation technique was used for stringent training and testing. Initial experimental results showed a patch classification accuracy of 95.31% (for the BACH dataset) and 98.43% for WSI image classifications (BreakHis)[9].similarly another, Researcher apply the stacking ensemble method and the Extra tree, Random Forest, AdaBoost and Gradient Boosting, and KNN9 are selected as the base learners whereas the model of logistic regression is the final estimator. The performance of SELF in the setting of the BreakHis dataset and WBCD datasets has come up with approximately 95% and 99% testing accuracy in each case, respectively[10].

The proposed models were tested on two datasets of mammography. DDSM and CBIS-DDSM. To boost the performance of the task of breast lesion classification of mammographic scans, three pretrained convolution neural networks (CNNs), which are VGG16, InceptionV3, and VGG19, were used as base classifiers, and two ensemble models were also trained. Having a linear meta-learner in the form of logistic regression for classification, Ensemble Model 1, and Ensemble Model 2 with a neural net as the meta-learner for classification. The accuracy, sensitivity, and specificity for Ensemble Model 1 were 98.02%, 97.17%, and 98.87%, respectively, for the DDSM dataset, while for the DDSM dataset, Ensemble Model 2 had 98.10%, 97.01%, and 99.12[11].

Based on the diverse learning ideas, the study suggests an ensemble deep learning system for the early detection of breast cancer. In contrast to the contemporary ensemble learning approach that processes the whole picture, the suggested system solely processes the Suspected Nodule Regions (SNRs), extracted through an optimal dynamic thresholding technique, where the threshold changes according to the details of each provided image[12].

A Blended ensemble learning, a new method, has been used in the classification of breast cancer, and the model is good in the prediction analysis as the base classifier. The five machine learning methods, such as support vector machine, K-nearest neighbors, decision tree Classifier, random forests, and logistic regression, are used as base learners in a blended ensemble model. In this study, the incorporated base learners (individually) and the outcome of the Ensemble Learning are compared with several performance metrics, including accuracy, recall, precision, and F1-score for the early prediction of Breast Cancer. The percentage of noticeable enhancement is 98.14% compared with the basic learners with the Ensemble learning model[13].

Research on Breast cancer classification has mostly employed deep learning approaches, including CNNs and transfer learning. These methods have been effective in providing details for tumor classification[14], [15], [16]. The summary of the selected Deep learning approach is extracted here in Table 2.1.

Table 1: Summary of the selected study

Author(s)	Title of the study	Dataset	Technique	Limitation	Accuracy
Hiba et al (2023)[17]	A Convolutional Neural Network Deep Learning Approach for Enhanced Ultrasonography Breast Cancer Classification	Two dataset	CNN	The study focuses only on Iraq's population.	92%

Salman et al(2023) [18]	A Novel Deep-Learning Model for Breast Cancer Diagnostics Using Medical Images	Break His dataset	CNN, Google News	The high computing cost of CNN	93%
Sathishkumar et al(2024)[19]	Using Enhanced Convolutional Neural Networks to Predict and Classify Breast Cancer.	Medical Image Dataset	CNN	Data imbalance	95%
Ashwin et al (2024)	Hybridization of CNN Features for Multi-class Breast Cancer Classification	BUSI	VGG16 , CNN	Publicly accessible breast cancer databases abound with this restriction, which can compromise the general performance of the categorization system.	93%
Monticciolo et al(2021)[20]	Recommended Guidelines for Breast Cancer Screening include all women at average risk.	Mamo graphy images	CNN	Small dataset	93%
Rajendran et al(2023)	A Methodological Analysis of Breast Cancer Classification Based on Deep Learning	Medical Images	CNN	Small dataset	90%

Research Methodology

The development of an efficient meta-ensemble transfer learning model designed for the classification of breast cancer images, specifically utilizing the Breast Ultrasound Images (BUSI) dataset. The methodology encompasses data collection, augmentation, preprocessing, splitting, architecture proposal, and evaluation metrics to achieve robust and accurate classification performance. The overall framework representing the proposed methodology is depicted in Fig.1.

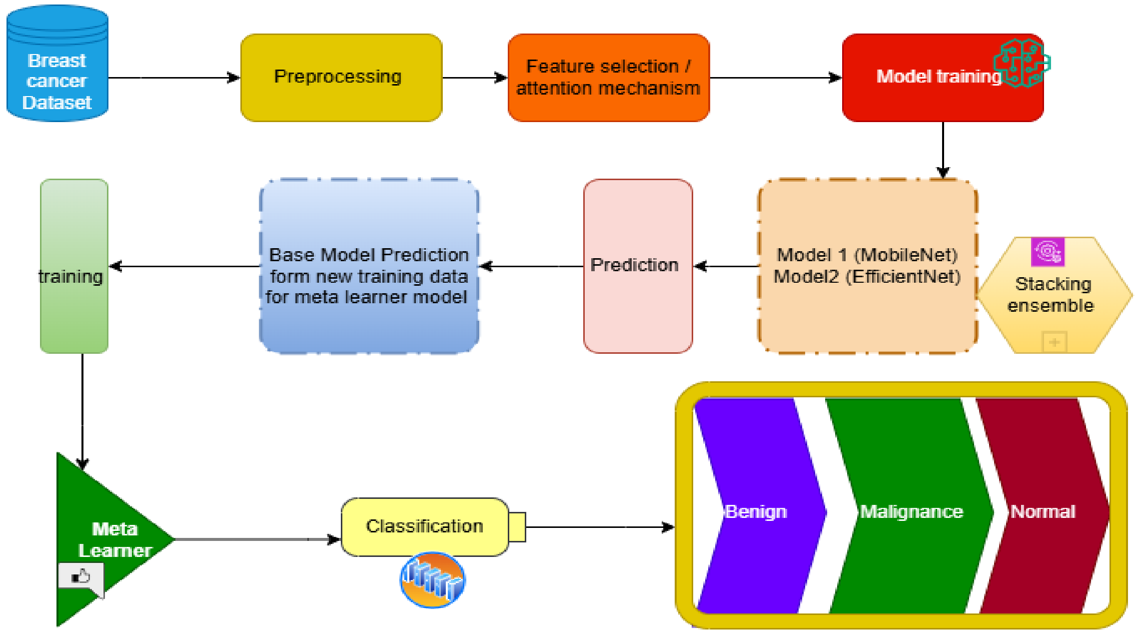


Figure 1: Proposed Model For Breast Cancer Classification

Dataset

The selected dataset is typically obtained from the Kaggle website (Breast Ultrasound Images Dataset(BUSI) (kaggle.com)), one of the most widely used resources for accessing datasets, particularly for projects involving data science, machine learning, and deep learning. 1683 histology images of the breast, categorized as benign, malignant, and normal, are included in the data. These photos are split into three sets with ratios of 80%, 10%, and 10% for training, validation, and testing, respectively.

Prepossessing

The CLAHE (Contrast Limited Adaptive Histogram Equalization) in specific plays a crucial role in enhancing the details in breast cancer ultrasound images since ultrasound images inherently have lower contrast compared to the traditional light-based images due to the sound wave phenomenon and thus have a monochromatic, flat appearance with little or no distinction in tissue intensity differences. Brightness of tumors, particularly the small or benign tumors, is quite comparable to that of the adjacent tissues, so that they may not be visible. Global histogram equalization tries to extend the intensity range over the whole image in an equal manner and is prone to cause over-brightening in parts, to enhance noise in the unnecessary areas, as well as ignoring small and local structures in which tumors often reside. CLAHE, on the contrary, can be used to enhance local contrast because it can split an image into small tiles and adjust the histogram of each tile separately. This local modification increases edge visibility, increases tumor edges, and efficiently enhances small lesions despite their occurrence occupying a small section of the picture. Further to that, CLAHE can incorporate a clip limit parameter to avoid over-bright pixels dominating the histogram, hence the trend towards an over-sharpened appearance and the inhibition of speckle noise magnification, typical of ultrasound imaging. The diagnostic benefit, in addition to visual improvement, is that CLAHE does equalize the contrast improvement across the images, preventing variability between scans and different imaging devices. This not only assists radiologists by automatically compensating for contractions that they would typically do manually, which makes input data easier to process with deep learning models, like CNN, thus increasing the accuracy of tumor detection and classification.

Feature selection (Attention mechanism)

An attention mechanism does not perform classical feature selection (as filter-based approaches). Instead:

- It estimates weights of each feature (or pixel, patch or channel in images).
- These weights can imply features that are more important towards classification.
- Effectively, low-attention-valued features have less weight and may be termed as candidates of pruning.

Data splitting

During this stage, the dataset is divided into three sections:

(i) Training data, (ii) validation data, and (iii) testing data.

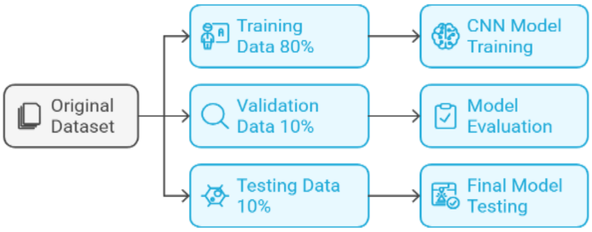


Figure 2: Splitting of Original Dataset

Training Data: The CNN-based different transfer learning models use 80% of the training data, though this ratio may vary depending on the project's requirements. The training dataset includes both the input and the desired output.

Validation Data: The validation data, which accounts for 10% of the original dataset, is used to assess the performance of various CNN-based transfer learning models during training. The information obtained from this validation method can be used to change the model's hyper parameters and configurations. To prevent over-fitting, we divided the dataset into a validation set.

Testing Data: The CNN-based transfer learning models are tested on new data.

Ensemble Model

In machine learning, ensemble methods provide a very effective method to enhance the stability and accuracy of models. Stacking is a form of ensemble learning in which outputs of several base models (also called level-0 models) are fed into a meta-model (also called a level-1 model) to produce the final prediction. Under this method, the meta-model can learn what the optimal combination of the predictions of the base models is; it may encompass complex relationships as well as run the base models together to perform better. The study targets a combination of MobileNet and EfficientNetV2, which are among the well-known convolutional neural networks (CNNs) with various architectural properties in the form of a stacking ensemble. MobileNet is characterized by its efficiency and applicability to mobile and embedded systems, whereas DenseNet is highly efficient at repeating features and could even attain top-notch accuracy in image recognition assignments.

Model Architecture

The ensemble stacking model is made up of the following:

Base Models (Level-0):

MobileNet: A lightweight CNN that replaces convolution with depth-wise separable convolutions to decrease the number of parameters and computational needs.

EfficientNetV2: EfficientNetV2 is a CNN architecture in which every layer is linked to every other one in a feed-forward manner, which facilitates the reuse of features and decreases the vanishing gradient.

Level-1 Model (Meta-Model):

A binary classification model, e.g., Logistic Regression, where the input gets predictions of all of the Level-0 models, and as output, the overall prediction is produced.

The figure below shows the ensemble-level architecture.

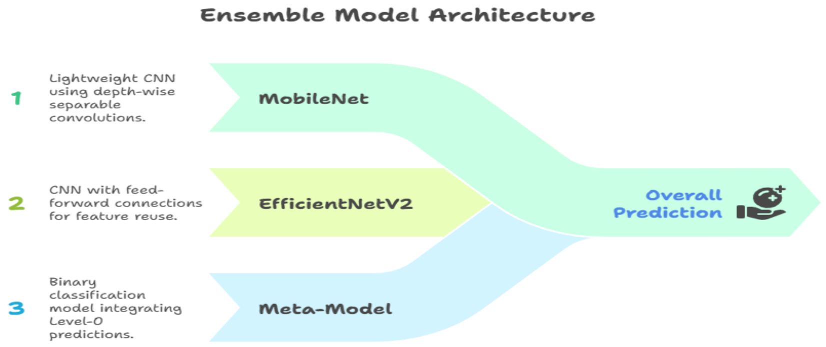


Figure 3: Ensemble Model Architecture

Mathematical Formulation

So, first, we will fix a definition of the following:

- x: Image to be input. Questions Answers
- M(x): MobileNet model, which returns a probability of size 1 where the number of classes is C.
- D (x): DenseNet model, returns the probability vector of C size.
- M(x)_i: The i-th probability vector of the output of the MobileNet that indicates the possibility of the input image falling in category i.
- D(x)_i: The component i of the output probability vector of DenseNet, where it denotes the probability among all the classes that the input images belong to the classes.

- z: Vector of MobileNet and DenseNet concatenated prediction, z = [M(x), D(x)]. Z has the size of 2C.
- Meta(z): The meta-model is the concatenated input into which the vector z is fed, and the final prediction is outputted.

The last forecast may be formulated as:
Final Prediction = Meta([M(x), D(x)])
If the meta-model is a judgmental model, i.e., a Logistic Regression model:
Meta(z) = sigmoid(w^T z + b)
Where:

- w is a 2C dimensional weight vector.
- b is the bias.
- sigmoid(x) = 1 / (1 + exp(- x))

The last prediction is a number ranging between 0 and 1, displaying the likelihood that a given input image will fall into a particular class (regarding binary classification). In multi-class classification, the meta-model may be a softmax activation on behalf of a softmax activation on a concatenated prediction.

Experimental Result

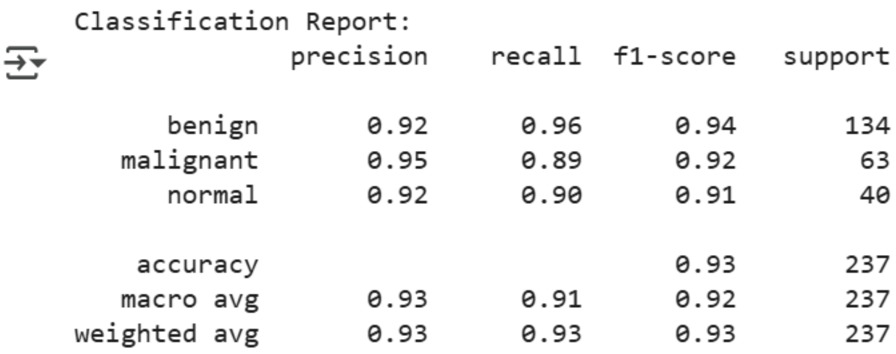
Our study's findings, which focused on classifying breast cancer histopathological images using the BUSI dataset, demonstrated the dependability and efficacy of the chosen Transfer learning ensemble model, MobileNetV2, and DeseNet. The evaluation metrics used to assess the model's performance provided a comprehensive view of its potential.

The Kaggle dataset, which comprises 1675 photos classified into three distinct classes—Benign, Malignant, and Normal—was utilized by the authors to simulate the suggested methods. The distribution of data images concerning classes and their description is shown in table 4.1.

Table 2: Dataset Description

Dataset Name	Total images	Benign	Malignant	Normal
BUSI	1683	891	421	371

After data splitting, the ensemble model will be implemented. We combine two transfer learning models (MobileNetV2, Denset) to make a single ensemble model, revealing a key milestone: In the 15th epoch, the test data achieved an amazing accuracy of 93%. The epochs continued between 83 and 585 seconds, indicating that CPU resources were efficiently utilized, as shown in Fig.

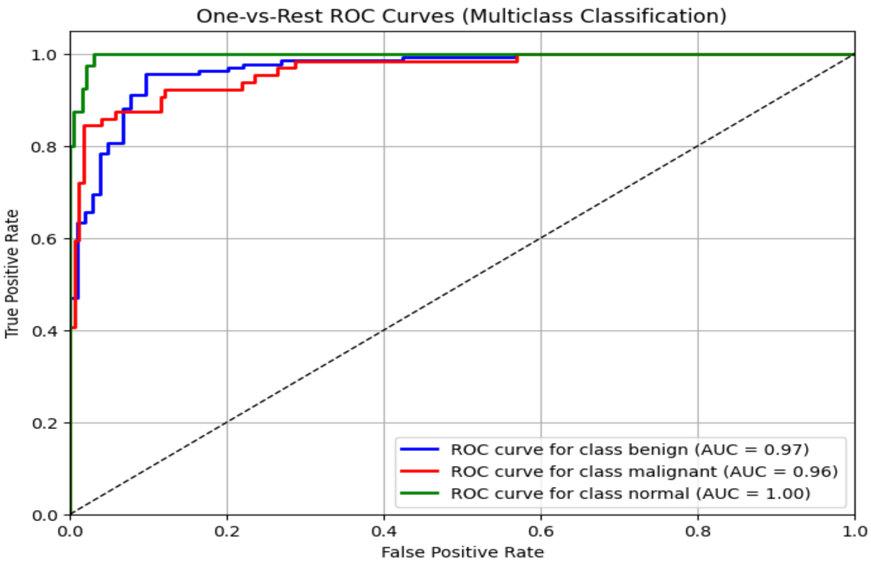


```
Classification Report:
              precision    recall  f1-score   support

      benign       0.92      0.96      0.94       134
   malignant       0.95      0.89      0.92        63
      normal       0.92      0.90      0.91        40

    accuracy                           0.93       237
   macro avg       0.93      0.91      0.92       237
weighted avg       0.93      0.93      0.93       237
```

Furthermore, the following image shows a ROC Curvefor amulticlass classification problemwith three classes: benign, malignant, and normal.



In class normal reparability is perfect (AUC=1.0), that is, predictions are error free. Both benign (0.97) and malignant (0.96) possess very strong performance as well, albeit not as strong as normal by a bit.

Performance evaluation metrics:

Accuracy, precision, recall, and F1-score are all distinct evaluation metrics.

Accuracy: It assesses the accuracy of the model's predictions. Accuracy is the ratio of accurately predicted observations to the total number of observations.

$$Accuracy = \frac{True\ Positive + True\ Negative}{True\ Positive + True\ Negative + False\ Posivite + False\ Negative}$$

Precision: Proportion of anticipated positives that are genuinely positive divided by the total number of predicted positives.

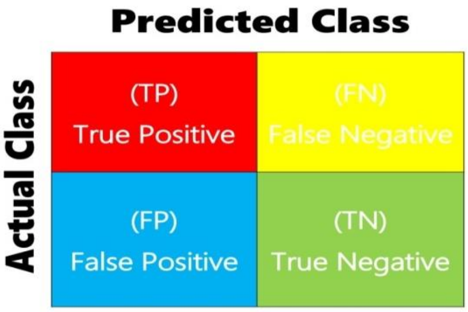
$$Precision = \frac{True\ Positive}{True\ Positive + False\ Positive}$$

Recall: The ratio of actual positive observations to the predicted number of positive observations.

$$Recall = \frac{True\ Positive}{True\ Positive + False\ Negative}$$

F1-Score: The weighted average of recall beside precision.

$$F1\text{-}Score = 2 \times \frac{Precision \times Recall}{Precision + Recall}$$



(TP) True Positive	(FN) False Negative
(FP) False Positive	(TN) True Negative

After the experiment using an ensemble model on the BUSI dataset to classify breast cancer images, we got the following classification metrics, as shown in Table 3.1.

Ensemble model table 3.1

Ensemble stacking	0.93	0.92	0.96	0.94	134	benign
		0.95	0.89	0.63	63	malignant
		0.92	0.90	0.91	40	Normal
Ensemble Voting	0.92	0.90	0.97	0.94	134	benign
		0.96	0.78	0.86	64	malignant
		0.90	0.95	0.93	40	Normal

In the same way the author further use ensemble model combine (Random forest , SVM) machine learning techniques using logistic regression as a meta classifier .

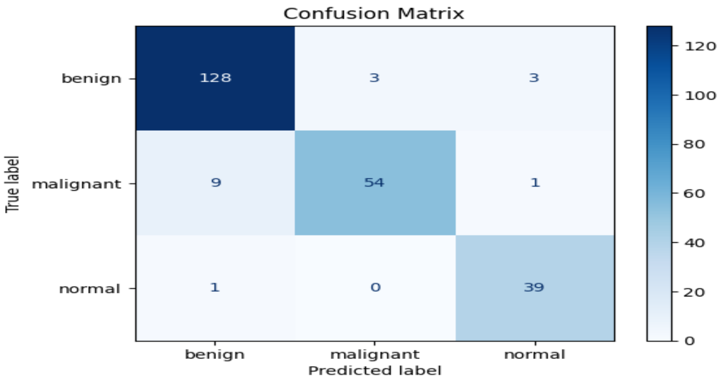
Ensemble model (Machine learning)table 3.2

Ensemble stacking (Machine learning)	0.92	0.91	0.96	0.93	134	benign
		0.94	0.78	0.85	63	malignant
		0.91	0.97	0.94	40	Normal

(III) Error Analysis Metrics

Confusion Matrix

- Provides a detailed breakdown of TP, TN, FP, and FN.



Confusion Matrix of the Proposed Model

Correct Predictions Values (Diagonal):

Benign was right: 128 Malignant got it right: 54

Normal was right: 39

These are your positive ones in each class.

Off Diagonal Values (Misclassifications):

Benign classified as Malignant: 3 Benign mislabeled Normal: 3

Malignant that are misclassified as Benign: 9

Malignant: False negative = 1

Normal wrongly classified Benign: 1

Normal labelled as Malignant: 0

Performance Insight: A majority of the benign samples are classified the right way. Malignant is more confused, particularly that it is expected to be benign (9 times).Normal-class has high accuracy of classification (39/40).The model is highly successful but shows a minor problem in the ability to differentiate between malignant and benign.

Comparison of our proposed model with the Benchmark study

We compared the results of our study to those of earlier research in the field to evaluate the efficacy of the suggested model. The main objective was to assess the model's performance in correctly identifying and categorizing specific features, like the distinction between "Benign," "Malignant," and "Normal" in a sizable set of photos depicting breast cancer. The outcomes showed that the recommended model completed this job with a very high degree of accuracy.

Model	Accuracy	Dataset	Reference Paper
Ensemble Model (Resent 50+Denset169)	92.5%	Breast Cancer Wisconsin	Reference Paper [9]

Alexnet	79%	(Mammography)Dataset	[21]
ShuffleNet	91.97%	Breast Cancer Wisconsin	[22]
Proposed Model (Denset + Mobile Net)	0.93%	BUSI	…….

Conclusion

The discussion section interprets the results, emphasizing the importance of deep transfer learning in breast cancer classification. The advantages of using ensemble models are highlighted, along with potential limitations and areas for future research in categorization systems. The suggested model demonstrated good accuracy in the categorization process, scoring 96.53%. The model can be modified using a different data augmentation approach. The success of this research will have important consequences for early breast cancer diagnosis and classification, potentially leading to improved patient outcomes, reduced false positives, and enhanced clinical decision-making. Furthermore, the built deep transfer learning ensemble model can serve as a significant tool for radiologists and pathologists, supporting them in making better-informed and quicker diagnoses.

Future Direction

- Integration of XAI (Explainable Artificial Intelligence) Methods: In the future, further research could explore explainable AI techniques, including SHAP (Shapley Additive Explanations) and Grad-CAM (Gradient-weighted Class Activation Mapping), to offer visual explanations for the classification of breast cancer images by deep learning models. These techniques can improve the transparency of the model, thereby facilitating the trust and comprehension of model decisions by clinicians.
- Enhancing Clinical Interpretability: Although present models accomplish high accuracy, the subsequent phase could concentrate on enhancing the interpretability of the outputs for healthcare professionals. This encompasses the creation of models that are capable of not only classifying images but also emphasizing the most critical regions within the image that impact the prediction.
- Future research could expand the classification models by incorporating supplementary patient-specific data (e.g., medical history and genetic markers) to develop a multi-modal XAI system. This would assist in the creation of more detailed and personalized explanations for individual predictions, providing insights not only from images but also from other pertinent data.
- Real-Time Explainable Models in Clinical Settings: The testing and deployment of explainable AI solutions in real-time clinical settings could be a valuable next step as models evolve. To guarantee the seamless adoption of XAI methods by medical practitioners, it would be necessary to resolve the challenges of speed, interpretability, and user-friendliness.
- Benchmarking Explainable Models: Additionally, research could be conducted to establish standardized benchmarks for explainable AI in medical imaging. In particular, this would entail a comparison of the efficacy of various XAI techniques about their simplicity of interpretation, reliability, and accuracy, particularly when applied to breast cancer classification.

Future research can guarantee that breast cancer classification models are not only accurate but also interpret-able by emphasizing explainable AI, thereby promoting improved patient outcomes and greater clinical adoption.

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