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An ensemble-based approach for breast cancer identification using mammography

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ABSTRACT

Breast cancer is among the most common cancers in women worldwide; timely detection is vitally important for improving chances of survival. The present study examines an innovative machine learning technique for the diagnosis of breast cancer using the breast cancer Wisconsin (diagnostic) dataset from Kaggle. The dataset includes 569 instances, and each instance has 30 attributes derived from digitized fine needle aspiration (FNA) images of masses found in the breast. We will present an ensemble deep learning (DL) model fusing a convolutional neural network (CNN) and LRAlexNet architectures to increase the accuracy and robustness of this type of cancer diagnosis. CNN models are well-known for their power to capture spatial hierarchies in image data, and LRAlexNet is a specialized deep CNN that excels at image classification due to its depth and parameter optimization. In this work, we use the ability to extract features of CNNs along with the superior classification performance of LRAlexNet to distinguish between benign and malignant cancers. The model will be trained and validated on the curated breast imaging subset of the digital database for screening mammography (CBIS-DDSM) dataset, and performance will be evaluated using sensitivity, accuracy, specificity, and the area under the curve (AUC) for the receiver operating characteristic. The results show that the ensemble CNN-LRAlexNet model achieved superior accuracy for breast cancer prediction when compared to traditional machine learning methods.

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1. INTRODUCTION

Breast cancer is among the most common cancers in women around the world. It is essential to detect and treatment of breast cancer at early is crucial to increasing survival with breast cancer and decreasing the burden of disease. Traditional screening modalities, such as mammography, ultrasound, magnetic resonance imaging (MRI), and biopsy, are still useful in the identification of malignant tissues, but each of these imaging studies has limitations regarding their sensitivity, specificity, and overall accuracy [1]–[3]. For example, mammography may miss malignant tumors or yield a false positive that results in an unnecessary intervention. Moreover, the interpretation of imaging studies requires a trained specialist, is often very slow, is subjective, and is open to human error. Deep learning (DL), a type of artificial intelligence (AI), has demonstrated to be a valid and reliable tool for implicating and identifying breast cancer. Using large datasets, DL algorithms can identify patterns and features that may not be prominent when viewed by a human observer to improve detection accuracy while decreasing the time required for diagnosis. As a result, DL approaches are entering the breast cancer detection system space to assist in the advancement of improvements and, in some cases, exceeding traditional approaches. If breast cancer is identified at earlier times and stages, the breast cancer survival rates and treatment prior to cancer metastasis [4].

DL algorithms trained on large datasets of mammograms and other imaging modalities have great promise for resolving these challenges, lowering false-positive rates, and improving diagnostic accuracy [5]–[8]. For breast cancer diagnosis, convolutional neural networks (CNNs) are generally trained on large datasets of mammograms, MRIs, or ultrasound images. The ensemble CNN-LRAlexNet model is developed to be user-friendly and robust for real-life practice and trained on the curated breast imaging subset of the digital database for screening mammography (CBIS-DDSM) cancer dataset from Kaggle, which was created using digitized fine needle aspiration (FNA) features that are widely used in clinical practice.

The contributions from the current proposed work in the article are:

i) The proposed method combines improvements in advanced feature extraction (CNN) and classification (LRAlexNet), with an emphasis on binary distinction (benign/malignant), which is important for clinical decision-making across different types of tissue and sample collections.
ii) The proposed architecture performs very well, achieving an accuracy of 96.4% using a relatively standardized dataset, and shows promise for use in more situations with less dependence on large, annotated image datasets.
iii) Data preprocessing, augmentation, and hyperparameter optimization ensure the model is resilient against overfitting and potentially adaptable to different population imaging scenarios.
iv) The model advances practical application and early screening in less-resourced settings to make automated breast cancer detection more accessible and reliable than specific DL models.

The breast cancer images with cancerous tissues highlighted in red are shown in Figure 1. The main reason for conducting the current model experimentation is the urgent need to find a better identification model for breast cancer segmentation and classification. A disease that has a huge effect on the health and financial stability of many women around the world. Even though medical technology has become more advanced, it is still very important to identify patients at an early age or stage to improve their chances of survival and the way they are treated. Still, the existing methods of diagnosing breast cancer often aren't very accurate or effective, which can lead to missed or late diagnoses [9]–[11].

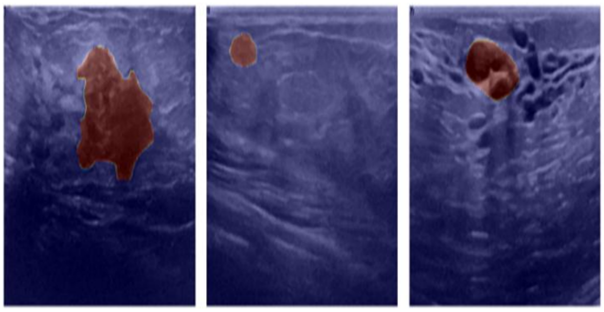


Figure 1. Breast cancer images with cancerous tissues highlighted in red

2. LITERATURE REVIEW

Research on breast cancer detection is particularly relevant since it is the most commonly diagnosed neoplasia worldwide, especially in women. Early detection greatly increases the efficacy of treatment outcomes and survival rates, thus justifying the necessity for more advanced screening methods [12], [13]. CNNs have proven to be very effective in detecting patterns in mammography, histopathology, and FNA images [14], [15]. Research utilizing CNN designs like ResNet, VGGNet, and LRAlexNet has shown enhanced diagnostic precision in breast cancer detection. Notwithstanding the progress in DL methodologies, obstacles persist in guaranteeing that models are generalized across varied populations and imaging apparatus [16]. Furthermore, the interpretability and trustworthiness of AI-driven diagnostic tools are becoming significant challenges, necessitating additional study to guarantee that models are transparent and dependable in clinical environments [17]. Table 1 provides details of earlier works and their details from 2020 to 2025.

Table 1. Earlier literature on ten current topics of the work

Authors	Methodology	Dataset (sample size)	Major contribution	Limitations of the work
El-Nabawy *et al.* [4]	Feature fusion of clinical, genomic, and histopathological data with DL	METABRIC	Improved subtype classification by integrating multi-source data	Fusion complexity, requirement of diverse datasets
Aggarwal *et al.* [2]	Meta-analysis of DL models in medical imaging	Various public datasets	Established a pooled accuracy benchmark for DL approaches	Heterogeneity in dataset quality, limited conclusion strength
Nassif *et al.* [5]	Systematic review of AI models for diagnosis	Various (not specified)	Outlined the strengths of AI methods for breast cancer diagnosis	Comparison across models/studies is challenging
Ahmad *et al.* [1]	Customized AlexNet and SVM applied to mammography	DDSM (not specified)	Demonstrated effectiveness of combining CNN and SVM	Limited generalization, dataset-specific optimization
Luo *et al.* [8]	Review of CNN, ensemble learning, and attention mechanisms	Multiple mammography datasets	Highlighted DL models outperformed conventional approaches	DL needs large, diverse data, issues with interpretability, and clinical uptake
Zhang *et al.* [9]	Advanced DL models for lymph node metastasis	Routine full-breast mammograms, sample size	Enabled lymph node metastasis prediction from mammograms	Lacks multi-center validation, exact dataset size not reported
Vijayalakshmi *et al.* [7]	Hybrid model with shearlet transform, feature extraction, bidirectional long short-term memory (BiLSTM)-CNN	Mammographic Image Analysis Society (MIAS), ~320 images	Achieved 97.14% accuracy, combining handcrafted and DL features for diagnosis	Reliant on single dataset, generalizability limited
Rabah *et al.* [10]	CNN-based multimodal DL combining mammography images + metadata	Chinese mammography database (CMMD): 4,056 images, 1,775 patients	Outperformed image-only models, area under the curve (AUC) 88.87% for multiclass lesion subtype classification	Dataset focused on Chinese cohort may not fully generalize
Melek *et al.* [12]	11 DL models (DenseNet, ResNet, VGG, ensembles, CNNs)	10,000 histopath images (6172IDC)	DenseNet201: 89.4% accuracy, 95.8% AUC for benign/malignant classification	Data imbalance, dependence on high-quality images

2.1. Research gap and proposed model

From the above, earlier existing works on mammogram analysis, the following gaps are identified for the current work. Prior studies demonstrate the strong accuracy of transfer learning, but many are limited by specialized datasets (e.g., MIAS and histopathology images) and lack broad generalizability to diverse, real-world clinical feature identification. Most published previous works report performance using single-modality data or focus on specific imaging types (e.g., mammography and histopathology), rather than integrating multi-source feature extraction for enhanced classification robustness. Several high-accuracy previous existing models depend on very large and annotated datasets, which are not always accessible, especially in resource-constrained or underprivileged healthcare contexts. Figure 2 illustrates the architecture of the proposed ensemble model and emphasizes its importance for a range of computer vision and medical research applications. The ensemble model's training and testing entail the use of datasets and validation procedures with the goal of creating a resilient breast cancer detection model. By employing the ensemble model, which is the integration of the LRAlexNet model into basic CNN model as the central architecture, along with the LeakyReLU activation function and Adam optimizer, the current study achieves an accuracy of 96.4% [18], [19].

2.2. Novelty of the proposed work

The novelty of the current article lies in its innovative integration of advanced DL strategies, specifically, the combination of a customized CNN with an LRAlexNet architecture to create an ensemble model that excels in the challenging task of breast cancer identification using FNA diagnostic features. The suggested method effectively merges the spatial feature extraction capabilities associated with CNNs and the efficient, parameter-effective classification presented by a refined method of AlexNet. With normalization and a standardized reduction process as well as incremental data augmentations, the model shows strong effectiveness on a small, publicly accessible dataset (CBIS-DDSM dataset) and without access to large medical imaging datasets. In this sense, accurate novelty is two-fold: it provides a contribution to the forefront of the technology via a thoroughly validated ensemble network structure in relation to cytological breast cancer screening, and it adds to the conglomeration of considerations towards the translation of technology into the practical part of paramedical routine work.

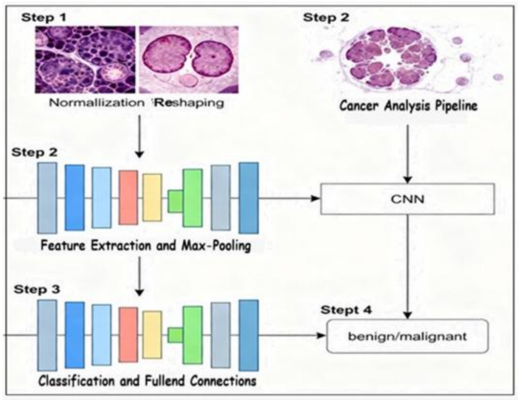


Figure 2. The architecture of the proposed model

3. METHOD

The study employs the CBIS-DDSM augmented dataset, which contains 569 observations and 30 numerical features extracted from digitally scanned images of breast tissue. The dataset is randomly divided into training and test sets at an 80:20 ratio for rigorous model validation. To overcome under-sampling and enhance generalizability, different augmentation techniques, including small geometric transformations and random perturbations, are used with the training database to mimic variability in clinical practice. The foundation of the model architecture is a DL ensemble of CNN and LRAlexNet modules. The CNN layers extract rich features and provide a sequence of convolution and max-pooling layers to capture spatial and structural features in the images, while LRAlexNet increases depth and allows efficient parameterization for high-level classification. After going through several convolution, activation, and pooling layers, the features are processed through fully connected layers into a final binary output (benign or malignant). Model training is conducted using the Adam optimizer with binary cross-entropy loss, and regularization techniques are implemented as needed to prevent overfitting.

3.1. Dataset, resources, and data normalization

The dataset comprises (CBIS-DDSM) characteristics derived from digitized pictures of breast masses, providing data for the classification of tumors as malignant or benign. The study used a dataset consisting of 569 samples. We classify the samples, obtained from reputable medical sources and libraries, into two separate categories: benign and malignant. They illustrate numerous clinical states pertinent to breast cancer identification. Their variations in texture, shape, and intensity of tissue illustrate the spectrum of breast conditions encountered in clinical environments [20], [21]. In the current work, data normalization is a key step in the preprocessing workflow to form consistency in all feature values obtained from the breast cancer diagnostic dataset. The process of data normalization removes the effect of different value ranges and/or degrees of intensity between individual samples for each feature, thereby avoiding the influence of distinguishing characteristics of an individual sample over influence settings in the training.

3.2. Data augmentation and hyperparameter tuning

To boost the robustness of the classification model and address potential limitations of a moderate dataset size, data augmentation techniques are incorporated during training. Augmenting the dataset involves generating additional, synthetically varied examples from the original features. Commonly employed augmentation strategies include slight rotation, flipping, scaling, and introducing minor random perturbations to the data, which reflect realistic variability seen in histopathological imaging. The breast cancer detection model had been trained using a sizable dataset of breast samples (x_train) and their corresponding labels (y_train). The training approach enabled iterative adjustments to the model parameters using a batch size of 32 and 100 epochs. Furthermore, a twenty percent validation split was used during training to track the model's performance on unknown data, thereby properly validating its generalization capabilities. The learning rate 0.02 is an essential hyperparameter that determines the number of parameter updates during optimization [22].

3.3. Workflow of the proposed model

The proposed breast cancer detection technique starts by loading and preprocessing the dataset. The target labels, diagnosis, are encoded such that benign (B) is 0 and malignant (M) is 1. The dataset is split into a training set and test set in an 80:20 ratio using train_test_split with a random seed for reproducibility. The features are standardized by using a standard scalar in order to be on a similar scale. This part will help ensure that the model focuses on regions of interest in the images, which are necessary for accurate feature extraction and classification [23]–[25]. The samples are then passed through the LRAlexNet architecture, which is initialized with the segmented samples. In other words, the workflow of the proposed model is shown in Figure 3. Here, we are training the LRAlexNet model using samples and their features and identifying whether the patient has benign or malignant. To perform this, the Adam optimizer changes internal weights to decrease errors and achieve correct classifications.

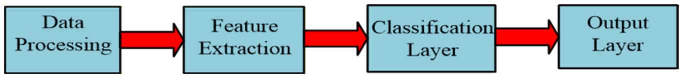


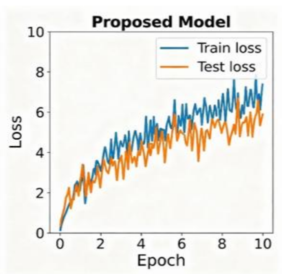
Figure 3. Workflow of the proposed ResNet101 model

4. VISUALIZATION OF RESULTS AND DISCUSSIONS

The performance of the proposed model Figure 2, showed a full picture of the model's structure, showing how the convolutional and pooling layers were arranged in a certain order, leading to dense layers for classification. Figure 4 shows that the model shows good performance over 15 epochs with excellent detailing on the training data (low training loss). But the test loss fluctuations suggest it may not generalize well, possibly due to over-fitting.

4.1. Experimental setup used for the implementation

The following specification units are utilized in each experiment: a 16 GB RAM module, 2.80 GHz Intel(R) Core (TM) i7-7700 central processor unit, and NVIDIA GTX 1050Ti graphics cards that were used for the experiments. For this investigation, the Python programming language is utilized, and more specifically, the ImageDataGenerator module from the Keras framework is utilized to compile sets of MRI pictures. Figures 4(a) and 4(b) show the loss of the model with respect to both training and testing for epochs like 10 and 15. The figures indicate that the model achieved low training loss, but the test loss fluctuated.



(a)

(b)

Figure 4. Training and testing loss of the model over 15 epochs of (a) epoch 10 and (b) epoch 15

Figure 5 illustrates the ROC curve displays the model's performance. This picture is crucial for comprehending the model's convergence and performance patterns during the training phase. Figure 6 displays the confusion matrix, which provides a comprehensive evaluation of the model's predictions on the test dataset. 68 number represents the number of data points that were correctly classified as benign (actual class) and were also predicted as benign by the model (predicted class).

The comparative results in Table 2 highlight the remarkable advancements seen in breast cancer detection using machine learning and DL algorithms over the last several years. The current study's proposed ensemble model (CNN-LRAlexNet) achieves an F1-score of 95.70, with sensitivity and specificity values of 96.50% and 96.10%, respectively, and an overall accuracy of 96.4%. From Figure 7, it is evident that ensemble and hybrid models, such as the proposed ensemble CNN-LRAlexNet and various CNN-long short-term memory (LSTM) or stacking approaches, consistently reach strong results across all six metrics.

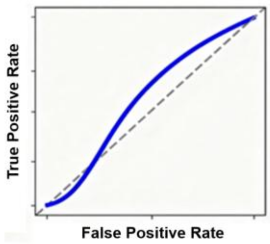


Figure 5. ROC curve for the proposed model

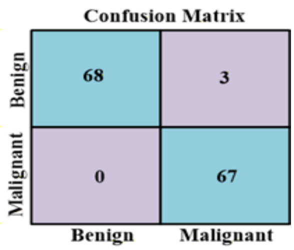


Figure 6. Confusion matrix

Table 2. Comparison of different models with their accuracies

Study	Model	F1-score	Sensitivity (%)	Specificity (%)	Precision (%)	AUC	Accuracy (%)
Nasir *et al*. [15]	CNN	91.14	92.31	95.60	90.00	94.62	94.62
Mapari *et al*. [16]	Early DL	96.20	96.51	not stated	95.92	not stated	96.21
Kaddes *et al*. [18] dataset 1	Hybrid CNN-LSTM	99.17	99.17	99.17	99.17	99.5	95.34
Kaddes et al. [18] dataset 2	Hybrid CNN-LSTM	99.80	99.90	99.90	99.80	100.0	99.17
Kwon *et al*. [20]	Stacking ensemble	100.0	100.0	99.9	100.0	100.0	89.4
Qasrawi *et al*. [21]	Hybrid ensemble	95.34	93.05	not stated	not stated	not stated	98
Alshayeji and Al-Buloushi [22]	CNN	99.13	99.59	99.53	98.71	not stated	99.13
Bhardwaj *et al*. [24]	Tree-based	96.77	not stated	not stated	not stated	not stated	99.1
Teoh *et al*. [25]	DL framework	97.35	not stated	not stated	98.79	not stated	86
Proposed model	Ensemble model	95.70	96.50	96.10	93.25	97.80	96.4

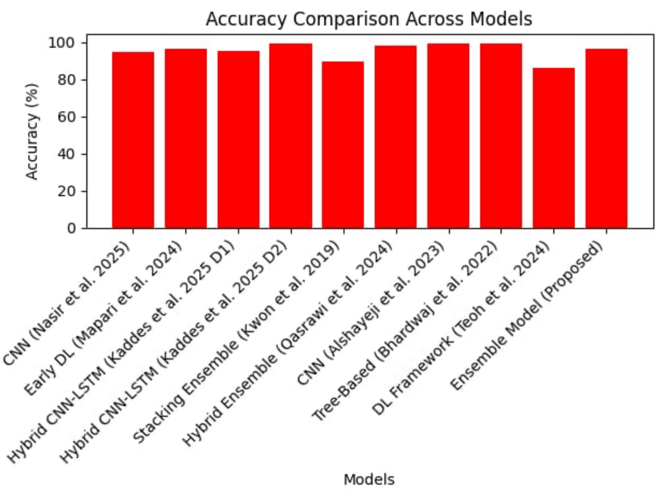


Figure 7. Comparison graph of the current model with other existing models

4.2. Clinical deployment and ethical AI contexts

The setting of clinical deployment and ethical AI considerations is crucial to fully understand their practical implications and to effectively address the serious barriers hindering the widespread adoption of machine learning models in healthcare settings. With AI-driven diagnostic tools, such as the ensemble CNN-LRAlexNet model presented in this study, demonstrating ever-improving accuracy and performance for breast cancer identification, the integration of AI into daily clinical practice has become increasingly tangible, feasible, and highly relevant for real-world medical workflows. Clinically, therefore, the model must successfully transition from its current laboratory-validated status to practical deployment, while demonstrating robust generalizability across diverse patient populations, various imaging devices, and different healthcare environments.

5. CONCLUSION

The current ensemble DL model achieves excellent accuracy and balanced performance metrics in relation to the CBIS-DDSM cancer dataset. Various potential limitations are important to consider when interpreting the results of AI models in the current AI tools and large language model (LLM)-enabled research environment. The model's evaluation is based on a relatively small and homogeneous dataset that may not fully represent the complexity and diversity that arises in clinical practice, raising concerns about generalizability and robustness beyond the current evaluation setting, all of which are common and essential aspects of evaluating most AI models in medical imaging. Like many AI models, the interpretability of the model's pathways of final decisions remains limited, commonly referred to as the "black box" issue, and could result in poor clinical trust and/or slow uptake of models based on the study's results and implications, particularly when explaining the models' results to clinicians or patients.

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AUTHOR CONTRIBUTIONS STATEMENT

This journal uses the Contributor Roles Taxonomy (CRediT) to recognize individual author contributions, reduce authorship disputes, and facilitate collaboration.

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Nakka Thirupathi Rao		✓				✓		✓	✓	✓	✓	✓		
Balakesava Reddy Parvathala		✓				✓		✓	✓	✓	✓	✓		
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C : **C**onceptualization
M : **M**ethodology
So : **So**ftware
Va : **Va**lidation
Fo : **Fo**rmal analysis
I : **I**nvestigation
R : **R**esources
D : **D**ata Curation
O : Writing - **O**riginal Draft
E : Writing - Review & **E**diting
Vi : **Vi**sualization
Su : **Su**pervision
P : **P**roject administration
Fu : **Fu**nding acquisition

CONFLICT OF INTEREST STATEMENT

The authors state that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper. The authors state no conflict of interest.

DATA AVAILABILITY

The authors confirm that the data supporting the findings of this study are available within the article.

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