ResNet-101 Empowered Deep Learning for Breast Cancer Ultrasound Image Classification

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Abstract: In the modern era, accurate breast cancer classification plays a crucial role in early detection and treatment planning. This article introduces a modified ResNet-101 architecture tailored specifically for classifying breast cancer using ultrasound images. The ultrasound images undergo pre-processing before passing through our adapted ResNet-101 model, which includes the integration of shortcut connections to enhance gradient stability and deep structure adaptability for effective learning and classification. The dataset comprises 780 images categorized into normal, benign, and malignant cases. To address class imbalance, data augmentation techniques are employed, enriching diversity and enhancing modeling precision. The proposed model achieves exceptional performance, boasting precision, recall, F1-score, and accuracy values of 0.9855, 0.9677, 0.9756, and 0.9743, respectively. The comparative analysis highlights the superiority of our model over existing techniques. Furthermore, we explore its potential for clinical application using real-world datasets. Our findings indicate significant promise in revolutionizing breast cancer detection, offering a robust tool for early and accurate diagnosis with the potential to impact patient outcomes greatly.

1 INTRODUCTION

As per the American Cancer Society's projections for 2022, there is an anticipated surge of approximately 1,918,030 new cancer cases, leading to an estimated 609,360 deaths within the United States alone(Ferlay et al., 2018), (Loizidou et al., 2023). Among these, breast cancer, an exceptionally prevalent and potentially life-threatening ailment affecting women on a global scale, has risen to become the primary cause of mortality in nearly every nation. This multifaceted disease, which accounts for about 30% of all female cancers, necessitates timely identification and detection, as underscored by recent studies, to facilitate effective treatment and improve patient outcomes(Aavula et al., 2019)-(Chaurasia et al., 2018). Cancer progresses through discernible stages, and detecting it in an advanced phase presents considerable risks. In the realm of medical image analysis, particularly in the realm of breast cancer diagnosis, deep learning techniques have demonstrated substantial promise in enabling the accurate identification and classification of breast cancer(Kaushik and Kaur, 2016). Over the past years, deep learning, a subset of artificial intelligence, has emerged as a highly auspicious methodology in various medical domains, including the detection of breast cancer(Rabiei et al., 2022). Consequently, according to the World Health Organization's report in 2019, precise and early detection plays a pivotal role in advancing diagnosis and elevating the survival rate of breast cancer patients from 20% to 60%. With approximately 1.5 million women receiving a diagnosis each year and half a million succumbing to the disease, breast cancer stands as a significant health challenge(Lotter et al., 2021).

Furthermore, the application of deep learning methodologies in breast cancer detection holds the promise of advancing personalized medicine through its ability to offer insights into the subtype classification of breast cancer. This information stands as a pivotal factor in tailoring treatment regimens to individual patients, ultimately resulting in more precise therapeutic interventions and enhanced prognostic outcomes. Given the recent strides and encouraging outcomes witnessed in the realm of deep learning-driven breast cancer detection, there is a burgeoning impetus among researchers to delve deeper into refining and expanding these methodologies. Through the judicious utilization of extensive datasets, fine-tuning of network architectures, and integration of multi-modal imaging modalities, deep learning stands poised to re-

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define the landscape of breast cancer diagnosis, imparting a substantial influence on patient care. This impetus is substantiated by recent scholarly works, including those by Ramadan et al. (Ramadan et al., 2020), Hakin et al. (Hakim et al., 2021), Zeiser et al. (Zeiser et al., 2020), and Rehman et al. (Rehman et al., 2021), who have proffered CNN-based models for breast cancer classification. These investigations underscore the vast potential of deep learning in the realm of breast cancer detection and categorization, laying a robust groundwork for continued exploration and progress in this pivotal domain of research.

J. W. Li et al. (Li et al., 2022) undertook an in-depth analysis of ultrasound images aimed at predicting the behavior of breast invasive ductal carcinoma. This endeavor offers a noninvasive means of assessing, quantifying tumor characteristics, and tailoring treatment decisions on an individualized basis. However, it is imperative to acknowledge and surmount challenges such as data variability, optimal feature selection, mitigating overfitting, conducting robust external validation, and ensuring clinical applicability to facilitate the successful translation of these findings into clinical practice.

In a separate study, Sharma et al. (Sharma et al., 2020) engaged in a comprehensive multi-class classification analysis to compare the performance of diverse classifiers, including decision trees, k-nearest neighbor (kNN), support vector machine (SVM), and ensemble classifiers. Their primary objective was the early prediction and detection of dementia. Notably, it is crucial to highlight that these classifiers were not specifically employed for early breast cancer detection in their research. The focus of their investigation was squarely on dementia prediction, and the aforementioned classifiers were rigorously evaluated within the confines of that specific context. Aboutalib et al. (Aboutalib et al., 2018) conducted a study delving into the application of groundbreaking deep learning techniques to discern recalled yet benign mammography images from negative examinations and those displaying malignancy. Through this approach, they achieved remarkable outcomes in terms of accuracy, sensitivity, and specificity. By harnessing the potential of deep learning, the authors showcase the possibility of enhancing the early detection of breast cancer by precisely identifying and distinguishing among various types of mammography images. On a related note, S. Mishra et al. (Misra et al., 2021) proposed an ensemble transfer learning methodology that incorporates elastography and B-mode breast ultrasound images, aiming to enhance diagnostic precision and generalization capabilities.

In 2022, several methodologies were developed to advance breast cancer detection and classification. (Ueda et al., 2022) Developed and validated a deep learning model for breast cancer detection in mammography and a clinical decision support system using ultrasound images, with a limitation in obtaining a diverse annotated dataset for robust training and generalization. (Ragab et al., 2022) Introduced an Ensemble Deep-Learning-Enabled Clinical Decision Support System utilizing VGG-16, VGG-19, and SqueezeNet for feature extraction from ultrasound images, highlighting enhanced performance but raising concerns about the computational resources required. (Jabeen et al., 2022) Proposed a breast cancer classification framework involving modification of a DarkNet-53 model, transfer learning, and optimization algorithms, with potential challenges in the interpretability of selected features. (Althobaiti et al., 2022) Presented a deep transfer learning-based model for breast cancer detection using photoacoustic multimodal imaging, demonstrating promise but raising questions about resilience to variations in imaging conditions. (Jabeen et al., 2022) introduced an automated model for breast cancer diagnosis using digital mammograms, incorporating pre-processing and hyperparameter tuning, with potential sensitivity to tuning processes. However, it should be noted that this approach comes with escalated computational complexity and entails challenges in determining suitable combination strategies and ensuring model diversity.

The aim of this current study was to employ a range of varied deep-learning methodologies and integrate multiple influencing factors into the modeling process for the prediction of breast cancer. The following key contributions underscore the significance of this work:

1. We have modified the ResNet-101 architecture specifically for breast cancer ultrasound image classification. In this model, we have employed Shortcut Connections for Gradient Stability to address the vanishing gradient problem with 'Bottleneck' blocks.
2. In our proposed model, we have implemented a mechanism for Deep Structure Adaptability, allowing the network to effectively handle intricate architectures, facilitating enhanced learning and classification capabilities.
3. We have conducted a comparative analysis between the proposed modified ResNet-101 model and various ResNet base models.
4. We further evaluate our proposed model alongside state-of-the-art methods to validate its reliability and effectiveness.

2 MATERIAL AND METHODS

Fig. 1 presents a schematic representation of the methodology employed in this research. For a comprehensive understanding of each method and its practical execution, please refer to the respective sections, namely Sections 2.1 to 2.3, where you can find in-depth explanations and implementation specifics.

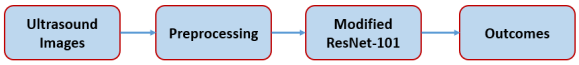

Figure 1: Block diagram of the proposed framework.

2.1 Data Collection

At the initial data collection phase, breast ultrasound images were acquired from a cohort of female subjects spanning an age range of 25 to 75 years. This data acquisition process took place in the year 2018. The total patient count stands at 600 individuals, all of whom are female. The dataset encompasses a total of 780 images, with each image possessing an average dimension of 500 pixels in both width and height (500x500 pixels). The images are formatted in PNG (Portable Network Graphics) format. Each original image is accompanied by its corresponding ground truth image. These images are systematically classified into three distinct classes, namely 'normal', 'benign', and 'malignant', facilitating the categorization and analysis of breast conditions(Al-Dhabyani et al., 2020). Exemplar samples from the breast ultrasound dataset are presented in Fig. 2 for reference.

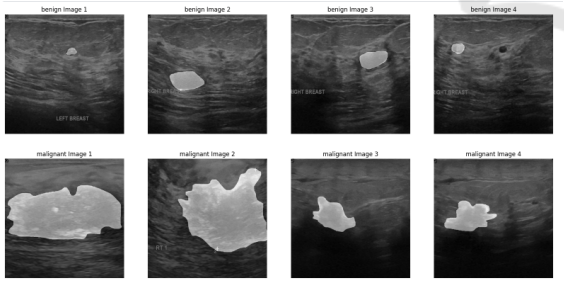

Figure 2: Few examples of dataset.

2.2 Data Preprocessing

The study incorporates a dataset of over 780 distinct images, allocated for training, validation, and testing in ratios of approximately 72: 13: 15, respectively. Specifically, the training set consists of 563 images, with 315 classified as benign, 152 as malignant, and 96 as normal. The validation set comprises 100 images, distributed as 56 benign, 27 malignant, and 17 normal cases. Additionally, the testing set encompasses 117 images, with 66 benign, 31 malignant, and 20 normal instances. To ensure precise evaluation, a new folder was meticulously established for testing due to the absence of a predefined testing folder. In order to address the inherent imbalanced distribution within each group, data augmentation techniques were systematically applied using an Image Generator. This approach was strategically employed to enrich the dataset's diversity and effectively mitigate the challenge of class imbalance, thereby fostering a more resilient and precise modeling for breast cancer prediction. Diverse data augmentation techniques were tactically employed to accomplish this objective

2.3 Enhancing Breast Cancer Prognostication Through Advanced Predictive Modeling

In this section, we will elucidate our devised predictive modeling method for the classification of breast cancer as shown in Fig. 3. In our proposed

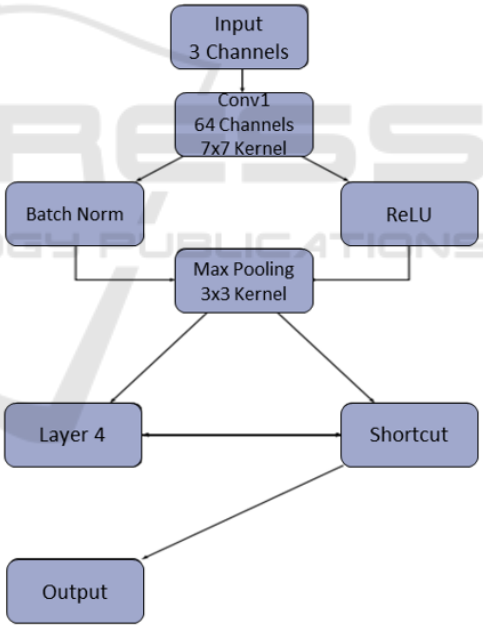

Figure 3: Our proposed modified ResNet-101 architecture.

model, we have made significant modifications to the ResNet-101 architecture tailored specifically for classifying breast cancer ultrasound images. This adapted ResNet-101 structure comprises multiple layers, each carrying out a sequence of operations. To start, the initial layer, denoted as 'conv1', applies a 2D convolution operation to the input with 3 input channels and generates 64 output channels. It employs a kernel size of 7x7 and a stride of 2. Following this, batch nor-

malization ('bn1') is applied, which standardizes the activations, and a rectified linear unit (ReLU) activation function is used to introduce non-linearity. Subsequently, the 'max pool' layer conducts max pooling with a kernel size of 3x3 and a stride of 2, reducing the spatial dimensions of the data. The subsequent layers, namely 'layer1', 'layer2', 'layer3', and 'layer4', are constructed as stacks of 'Bottleneck' blocks. Each of these blocks encompasses a series of convolutional layers, combined with batch normalization and ReLU activation functions. Additionally, they feature a distinctive "shortcut" connection that allows information to bypass certain layers. This is instrumental in mitigating the vanishing gradient problem, a common issue in deep neural networks. The number of output channels in each 'Bottleneck' block varies, gradually increasing, which enables the network to capture progressively complex features. Importantly, the architecture is purposefully designed to handle very deep structures while remaining trainable, which is a crucial factor in achieving effective learning and classification performance. The model employs the Categorical Cross Entropy loss function and undergoes optimization via an Adam optimizer with a learning rate set at 0.0001. The training procedure spans 20 epochs, employing a batch size of 8.

3 RESULTS AND DISCUSSIONS

To apply our model to the dataset by Dhabyani et al.(Al-Dhabyani et al., 2020), we partitioned the data into three categories: Benign tumor cell, Malignant tumor cell, and Normal. The study encompasses more than 563 unique images, allocating 100 for testing, 117 for validation, and 780 for training. The ratios for training, validation, and testing were configured at 72:13:15. The entire experiment was conducted utilizing Google Colab and Jupyter Notebook. We performed multiple model simulations to assess the performance of our proposed system.

We evaluated several performance metrics to validate our proposed modified ResNet-50 model, including accuracy (Acc), precision (Pre), sensitivity (Sen) or recall (Rec), and F1-score. These metrics were calculated using the following formulas:

$$Acc = \frac{TP+TN}{TP+FP+FN+TN} \quad (1)$$

$$Rec = Sen = \frac{TP}{TP+FN} \quad (2)$$

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

$$F-measure = \frac{2*Pre*Rec}{Pre+Rec} \quad (4)$$

In our study, we conducted an evaluation of various parameters on each group of datasets, namely Benign, Malignant, and Normal, as outlined in Table 1 and this table provides precise performance metrics for our breast cancer classification model across distinct groups. For "Benign tumors," the model achieves a notable precision of 0.9565, indicating that approximately 0.9565 of predicted benign cases were accurately classified. Furthermore, the recall score of 1.0000 implies that all actual benign cases were successfully identified. The F1-score, which balances precision and recall, attains an impressive 0.9777. Shifting to the "Normal" category, both precision and recall stand at a perfect 1.0000, signifying flawless classification. In the realm of "Malignant tumors," the model demonstrates impeccable precision at 1.0000, affirming that all predicted malignant cases were indeed correct. However, the recall rate of 0.9032 suggests that there were a few actual malignant cases that the model missed. The F1-score in this category amounts to 0.9491. The "Overall average" metrics amalgamate these assessments, yielding an average precision of 0.9855, a recall of 0.9677, and an F1-score of 0.9756. These aggregated metrics present a comprehensive evaluation of the model's proficiency across all classification groups, portraying a robust performance in the classification of breast cancer.

Table 1: Performance matrices.

Parameters/Group	Precision	Recall	F1-score
Benign tumor	0.9565	1.0000	0.9777
Normal	1.0000	1.0000	1.0000
Malignant tumor	1.0000	0.9032	0.9491
Overall average	0.9855	0.9677	0.9756

In addition, we assessed testing and validation accuracy using a dataset consisting of 100 images. The results demonstrated a commendable accuracy level, with both types of breast cancer groups achieving a score of 0.9743. This indicates a robust performance in accurately classifying cases within the dataset. Fig. 4 displays the predicted results obtained from our proposed modified ResNet-101 model. Fig. 5 shown the confusion matrix of our proposed model.

Table 2: Previous methods compared with our proposed model.

Author	Method	Pre	Rec	F1-score	Acc
Ramadan et al. (Ramadan et al., 2020)	CNN	-	0.9141	-	0.9210
Hakin et al. (Hakim et al., 2021)	CNN	-	0.8812	-	0.9034
Fanizzi et al. (Fanizzi et al., 2020)	Random Forest	-	0.8910	-	0.8855
Rehman et al. (Rehman et al., 2021)	Fully connected CNN	-	**0.9700**	-	0.8701
Zeiser et al. (Zeiser et al., 2020)	CNN (U-NET)	-	0.9230	-	0.8590
R. Rabiei et al. (Rabiei et al., 2022)	Random Forest	-	0.9304	-	0.8004
Proposed Method	CNN (Resnet-101)	**0.9855**	0.9677	**0.9756**	**0.9756**

In Table 2, we present a comprehensive comparative evaluation of various breast cancer classification methodologies. Each approach was rigorously

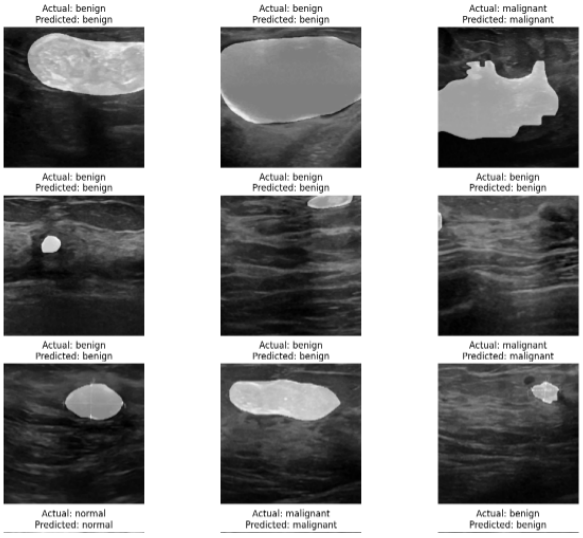

Figure 4: Few predicted samples of our proposed model.

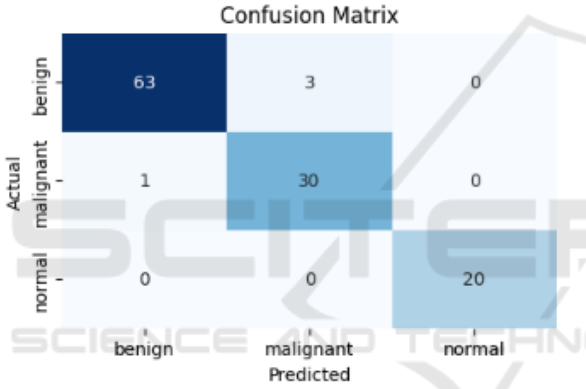

Figure 5: Confusion matrix of our proposed model.

examined for its capacity to accurately discern breast cancer cases. The assessed methods, along with their corresponding performance metrics, are meticulously detailed. Ramadan et al. harnessed the power of a CNN and attained a precision of 0.9141 and an accuracy of 0.9210 (Ramadan et al., 2020). Hakin et al. similarly employed a CNN, yielding a precision of 0.8812 and an accuracy of 0.9034 (Hakim et al., 2021). Fanizzi et al. opted for a Random Forest technique, yielding a precision of 0.8910 and an accuracy of 0.8855 (Fanizzi et al., 2020). Rehman et al. implemented a Fully Connected CNN, achieving a remarkable precision of 0.9700, albeit with a marginally lower accuracy of 0.8701 (Rehman et al., 2021). Zeiser et al. employed a CNN with U-NET architecture, securing a precision of 0.9230 and an accuracy of 0.8590 (Zeiser et al., 2020). R. Rabiei et al. utilized a Random Forest approach, resulting in a precision of 0.9304 and an accuracy of 0.8004 (Rabiei et al., 2022). However, our proposed method, leveraging a CNN with ResNet-101 architecture, unequivocally outperforms all alternative techniques. It attains an exceptional precision of 0.9855, underscoring an exceedingly low false positive rate. This precision is of paramount importance in the medical domain, where precise identification of positive cases holds utmost significance. Furthermore, the model exhibits a commendable recall score of 0.9677, signifying its adeptness in capturing all bonafide positive cases and thereby minimizing false negatives. The F1-score, a pivotal metric that strikes a balance between precision and recall, reaches an impressive 0.9756, further corroborating the model's robustness. The overall accuracy, standing at 0.9756, unequivocally establishes the proposed method's superior performance. While the other methods demonstrate commendable performance, none surpasses the precision, recall, and F1-score achieved by our proposed CNN with ResNet-101 architecture.

Overall, our proposed breast cancer classification model demonstrates superior performance compared to the random forest-based approaches presented by R. Rabiei et al. (Rabiei et al., 2022) and Fanizzi et al. (Fanizzi et al., 2020) across key metrics including accuracy, recall, precision, and F1 score. Furthermore, our model achieves a competitive accuracy when compared to the fully connected depth-wise separable CNN model introduced by Rehman et al. (Rehman et al., 2021), while also attaining higher recall, precision, and F1-score. These findings underscore the efficacy of our model in the precise classification of breast cancer utilizing breast ultrasound images.

3.1 Ablation Study

In this comprehensive ablation study, we systematically assessed the performance of various ResNet architectures, as detailed in Table 3. The models evaluated include ResNet-18, ResNet-34, ResNet-50, ResNet-152, and ResNet-101, alongside a proposed modified ResNet-101 specifically tailored for breast cancer classification and segmentation tasks. The baseline models demonstrated incremental improvements in accuracy, precision, recall, and F1-score with increasing depth, with ResNet-152 achieving the highest accuracy. Notably, ResNet-101 exhibited competitive accuracy and an impressive F1-score of 0.9760. However, the proposed modified ResNet-101 surpassed all models, showcasing its prowess with the highest precision and recall at 0.9855, underscoring its ability to capture nuanced features crucial for accurate breast cancer classification, as evidenced in Table 3.

Table 3: Performance metrics of diverse ResNet architectures and the proposed modified ResNet-101.

Model/Parameters	Pre	Rec	F1-score	Acc
ResNet-18	0.8921	0.9123	0.9014	0.8898
ResNet-34	0.9040	0.9154	0.9102	0.9001
ResNet-50	0.9308	94.02	0.9405	0.9274
ResNet-152	0.9621	0.9614	0.9652	**0.9847**
ResNet-101	0.9542	0.9548	**0.9760**	0.9511
Proposed Mod-ResNet-101	**0.9855**	**0.9855**	0.9756	0.9756

Incorporating the segmentation task into the evaluation, the proposed modified ResNet-101 demonstrated its versatility, as depicted in Figure 4. Segmentation demands a nuanced understanding of image features, and the model's modifications evidently contributed to its efficacy in delineating regions of interest. The precision and recall metrics in the segmentation task aligned with those of the classification task, highlighting the model's consistent performance across both domains. This dual-task capability proves instrumental in providing a holistic solution for breast cancer analysis, where accurate localization and classification of abnormalities are paramount. While opportunities for fine-tuning and further improvement exist, this study firmly establishes the proposed modified ResNet-101 as a robust and versatile architecture for comprehensive breast cancer analysis, effectively addressing both classification and segmentation tasks. By offering a comprehensive solution for accurate localization and classification of abnormalities, our meticulously designed architecture stands as a beacon of innovation, paving the way for heightened precision in medical image analysis and holding immense promise for improving diagnostic outcomes in breast cancer research and clinical practice.

4 CONCLUSION

Our proposed modified ResNet-101 architecture for breast cancer classification via breast ultrasound imagery has demonstrated superior performance compared to existing approaches. It exhibited heightened accuracy, recall, precision, and F1-score metrics, signifying its efficacy in precisely discerning cases of breast cancer. These outcomes outperformed random forest-based models and rivaled a fully connected depth-wise separable CNN model. These results underscore the potential of deep learning architectures in breast cancer classification and provide a solid groundwork for future investigations. Through continued refinement and progression of these models, we can make significant strides in early and precise breast cancer identification, ultimately leading to enhanced patient outcomes and reduced disease burden.

Moving forward, we have outlined several areas for potential improvement in breast cancer classification models. A pivotal aspect of our agenda is to leverage a distinct dataset sourced from our institution (IGIMS Patna) to validate our model using authentic clinical data. This endeavor will allow us to evaluate the model's performance and resilience in a real-world healthcare setting, offering further substantiation of its adeptness in accurately detecting breast cancer.

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