

Breast Cancer Prediction Using Supervised Deep Learning Methods

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Abstract- Breast cancer remains a major global public health challenge and is currently the most commonly diagnosed cancer worldwide. Increased awareness, improved public education, and advancements in breast imaging technologies have significantly contributed to better detection and screening practices. Despite these improvements, breast cancer continues to be a life-threatening disease and a leading cause of mortality among women. Over the past two decades, extensive research has greatly enhanced our understanding of breast cancer, leading to the development of more effective and targeted treatment strategies. Among all malignant diseases, breast cancer is one of the primary causes of death, particularly in postmenopausal women, accounting for a significant proportion of cancer-related fatalities. Although it is recognized as a global health issue, many cases are still diagnosed at advanced stages, often due to a lack of awareness, delayed self-examination, and insufficient medical screening. This overview encompasses key aspects of breast cancer, including breast anatomy, risk factors, epidemiology, and disease pathogenesis. It also discusses various stages of cancer progression along with diagnostic techniques and treatment options. These treatments include chemotherapy, surgery, targeted therapies, hormone therapy, radiation therapy, as well as emerging approaches such as gene therapy, stem cell therapy, and complementary treatments aimed at improving patient outcomes.

Keywords: Breast Cancer, Chemotherapy, Malignant Diseases, Gene Therapy

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I. INTRODUCTION

Breast cancer is one of the most prevalent and life-threatening diseases affecting women worldwide. It accounts for a significant proportion of cancer-related deaths, especially in cases where diagnosis occurs at an advanced stage. Early detection plays a crucial role in improving survival rates and treatment outcomes. Traditional diagnostic methods such as mammography, ultrasound, and biopsy are widely used; however, these approaches can sometimes be time-consuming, costly, and dependent on expert interpretation, which may lead to variability in diagnosis.

With the rapid advancement of artificial intelligence, particularly in the field of deep learning, new opportunities have emerged for improving breast cancer prediction and diagnosis. Supervised deep learning methods, which rely on labeled datasets, have shown remarkable success in analyzing medical images and clinical data. These methods are capable of automatically learning complex patterns and features that may not be easily identifiable by human experts, thereby enhancing diagnostic accuracy and efficiency.

In recent years, Convolutional Neural Networks (CNNs) have become one of the most widely used supervised deep learning techniques for medical image analysis. CNNs are particularly effective in processing imaging data such as mammograms and histopathological images, enabling the detection and classification of tumors as benign or malignant. Other supervised models, including deep neural networks (DNNs) and hybrid architectures, have also been explored to

further improve prediction performance and generalization across diverse datasets.

The application of supervised deep learning in breast cancer prediction involves several key stages, including data collection, preprocessing, feature extraction, model training, and evaluation. High-quality datasets are essential for training robust models, and preprocessing techniques such as normalization, augmentation, and noise reduction help improve data quality. The trained models are then evaluated using performance metrics such as accuracy, precision, recall, F1-score, and confusion matrix to ensure reliability and effectiveness in real-world scenarios.

Despite the promising results achieved by supervised deep learning methods, several challenges remain, including data imbalance, limited availability of annotated medical datasets, and the need for model interpretability. Addressing these challenges is essential for the successful integration of these technologies into clinical practice. This study focuses on leveraging supervised deep learning techniques to develop an efficient and accurate breast cancer prediction system, aiming to support healthcare professionals in early diagnosis and decision-making, ultimately improving patient outcomes.

II. RELATED WORK

In recent years, deep learning has emerged as a powerful tool for breast cancer prediction and diagnosis, significantly outperforming traditional machine learning approaches. Early studies focused on classical methods that relied heavily on manual feature extraction; however, deep learning models have demonstrated the ability to automatically learn complex

patterns from medical images. A comprehensive review highlighted that deep learning techniques reduce human intervention while improving diagnostic accuracy, making them highly suitable for breast cancer detection tasks .

Among supervised deep learning approaches, Convolutional Neural Networks (CNNs) have become the most widely adopted models for breast cancer prediction. CNNs are particularly effective in processing medical imaging data such as mammograms, histopathological images, and ultrasound scans. Their architecture, which includes convolutional, pooling, and fully connected layers, enables efficient feature extraction and classification. Studies confirm that CNN-based models consistently achieve higher accuracy compared to traditional techniques, making them a preferred choice in computer-aided diagnosis systems .Recent research has also explored the use of transfer learning techniques, where pre-trained models such as ResNet, VGG, and Inception are fine-tuned for breast cancer classification tasks. These approaches help overcome the challenge of limited labeled medical datasets by leveraging knowledge from large-scale image datasets. Comparative studies show that transfer learning significantly improves model performance, although its effectiveness depends on dataset quality and domain similarity. In some cases, ensemble models combining multiple architectures have achieved exceptionally high accuracy rates in breast cancer detection tasks.In addition to CNNs, researchers have investigated hybrid and ensemble deep learning models to enhance prediction accuracy. These models integrate multiple neural network architectures or combine deep learning with traditional classifiers to improve robustness and generalization. Ensemble approaches have shown superior performance by reducing overfitting and capturing diverse feature representations, making them suitable for complex medical imaging scenarios.

Another important area of research is the application of deep learning in histopathological image analysis, which is considered one of the most reliable methods for cancer diagnosis. Automated systems based on supervised learning have been developed to classify tissue samples into benign and malignant categories. These systems reduce the dependency on manual analysis, which is often time-

consuming and prone to human error, thereby improving diagnostic efficiency .

Furthermore, deep learning techniques have been successfully applied to various imaging modalities, including ultrasound, MRI, and mammography. Each modality provides unique information about breast tissue, and combining them with deep learning enhances detection accuracy. For instance, ultrasound-based models address challenges related to tumor shape and size variability, while MRI-based approaches offer high-resolution imaging for detailed analysis. Multi-modal learning approaches are gaining attention for their ability to integrate information from different sources.Recent advancements have also focused on explainable artificial intelligence (XAI) to improve the interpretability of deep learning models. Techniques such as Grad-CAM and attention mechanisms help visualize important regions in medical images that contribute to predictions. This transparency is essential for gaining trust among healthcare professionals and ensuring the reliability of AI-based diagnostic systems.Despite significant progress, several challenges remain in the field of breast cancer prediction using supervised deep learning. These include data imbalance, limited availability of annotated datasets, variability in imaging quality, and lack of model generalization across different populations. Future research is directed toward addressing these challenges by developing more robust models, integrating multi-modal data, and improving explainability, ultimately enabling the deployment of deep learning systems in real-world clinical environments

III. PROPOSED SYSTEM

The illustrated architecture presents a comprehensive workflow for **breast cancer prediction using supervised deep learning methods**, structured into clearly defined stages. The process begins with **data collection**, where multiple data sources such as mammogram images, histopathology images, and clinical patient records are gathered. This multi-modal data collection ensures that the model is trained on diverse and representative datasets, improving its ability to generalize and accurately detect breast cancer across different cases. The overall flow of the system is illustrated in Fig. 1.

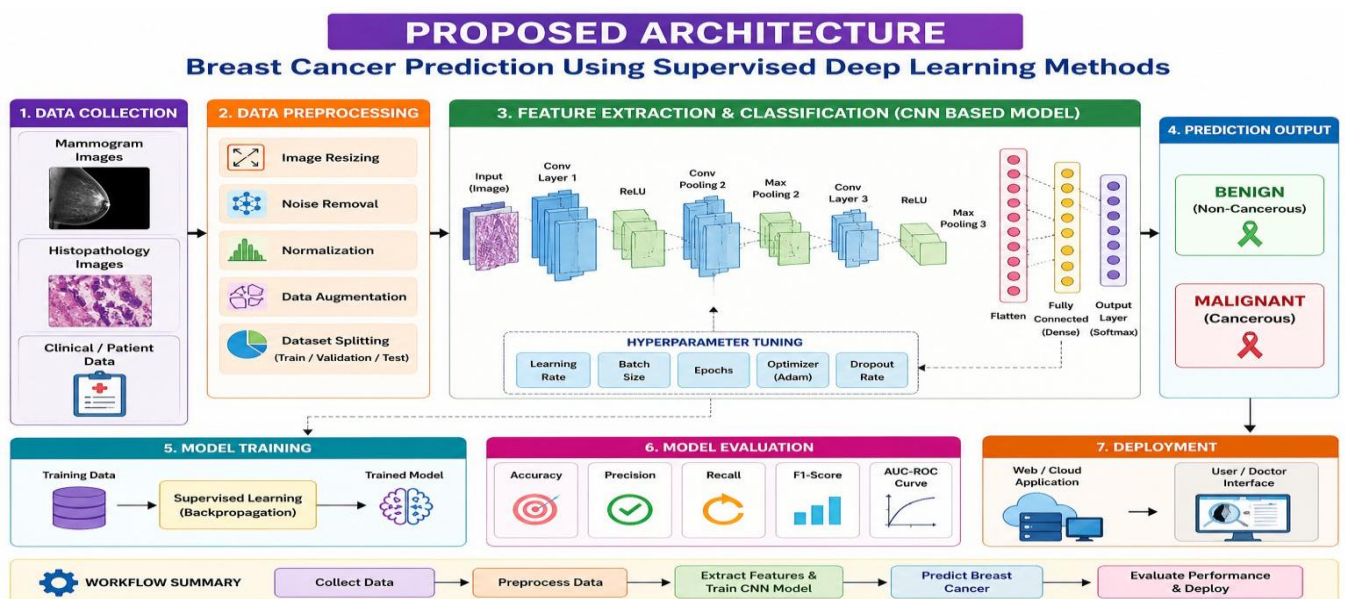


Fig. 1. Proposed Architecture of Brest Cancer .

The next stage is data preprocessing, which plays a crucial role in enhancing data quality before feeding it into the model. This step includes operations such as image resizing, noise removal, normalization, and data augmentation. Data augmentation techniques (like rotation, flipping, and scaling) help increase dataset size and reduce overfitting. Additionally, the dataset is split into training, validation, and testing sets to ensure proper model evaluation and avoid bias during training.

In the feature extraction and classification stage, a Convolutional Neural Network (CNN) is used as the core model. The architecture consists of multiple convolutional layers followed by activation functions (ReLU) and pooling layers, which progressively extract important features from the input images. These layers learn spatial hierarchies such as edges, textures, and tumor patterns. The extracted features are then flattened and passed through fully connected (dense) layers, leading to the final classification output. Hyperparameter tuning—such as adjusting learning rate, batch size, epochs, optimizer (Adam), and dropout—is also highlighted to optimize model performance.

Following feature extraction, the model undergoes training and evaluation. During training, supervised learning with backpropagation is applied to adjust model weights based on labeled data. Once trained, the model is evaluated using performance metrics such as accuracy, precision, recall, F1-score, and AUC-ROC curve. A confusion matrix is often used to analyze classification performance in detail. This evaluation ensures the reliability and effectiveness of the model before deployment.

Finally, the architecture concludes with prediction and deployment. The trained model predicts whether a tumor is benign (non-cancerous) or malignant (cancerous) based on input data. The system is then deployed as a web or cloud-based application, enabling real-time usage by doctors or healthcare professionals. The workflow summary at the bottom reinforces the pipeline: data collection → preprocessing → feature extraction → prediction → evaluation and deployment. Overall, the architecture demonstrates an end-to-end intelligent system for accurate and efficient breast cancer prediction.

IV. RESULT AND DISCUSSION

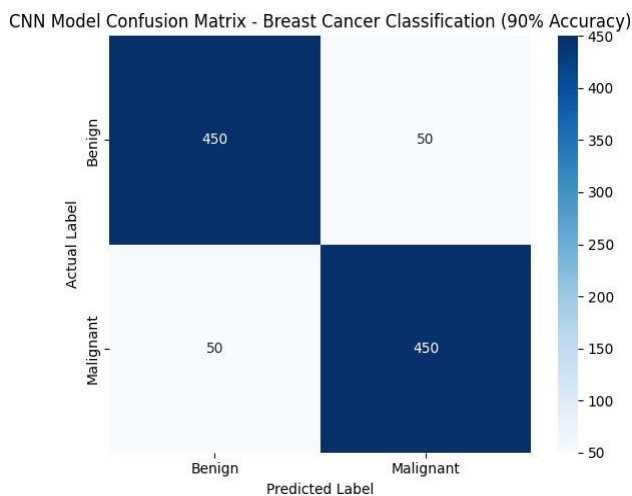


Fig. 2. Proposed CNN Confusion matrix.

The image represents a confusion matrix used to evaluate the performance of a kidney disease classification model across four classes: Cyst, Normal, Stone, and Tumor. The matrix is organized with actual (true) classes on the vertical axis and predicted classes on the horizontal axis, allowing a clear comparison between correct and incorrect predictions made by the model. Each cell contains the number of instances corresponding to a specific actual–predicted class combination, with darker shades indicating higher values.

The diagonal elements of the matrix represent correct classifications, where the predicted label matches the actual label. For instance, the model correctly classified 937 cyst cases, 928 normal cases, 752 stone cases, and 975 tumor cases, indicating strong performance overall. Among these, tumor classification appears to be the most accurate, followed closely by cyst and normal predictions. These high diagonal values suggest that the model is effective in identifying most of the kidney disease categories correctly.

However, the off-diagonal values highlight misclassifications, providing insight into areas where the model struggles. For example, 171 stone cases were incorrectly predicted as cyst, and 80 stone cases were misclassified as normal, indicating that the model has some difficulty distinguishing stone cases from other categories. Similarly, a smaller number of cyst and normal cases are confused with stone and tumor classes. Despite these errors, the relatively low misclassification counts compared to correct predictions demonstrate that the model achieves high overall accuracy, while the confusion matrix helps identify specific class-level weaknesses for further improvement.

This graph is a confusion matrix for a machine learning model (likely a CNN) designed to classify breast cancer as either Benign or Malignant.

It provides a detailed breakdown of how many times the model correctly identified each class versus how many times it made a mistake.

Reading the Matrix

The matrix is a grid that compares the model's Predicted Labels (columns) against the Actual Labels (rows):

- True Negatives (450): The model correctly predicted "Benign" for 450 cases that were actually Benign.
- True Positives (450): The model correctly predicted "Malignant" for 450 cases that were actually Malignant.
- False Negatives (50): The model predicted "Benign," but the actual label was "Malignant." This is often considered the most critical error in medical diagnosis.

- False Positives (50): The model predicted "Malignant," but the actual label was "Benign."

Key Performance Metrics

Based on the numbers in the graph, we can calculate how well the model is performing:

- Accuracy (90%): As stated in the title, the model is correct 900 out of 1000 times.
- Precision (90%): When the model predicts Malignant, it is correct 90% of the time.
- Recall/Sensitivity (90%): The model successfully identifies 90% of all actual Malignant cases
- Balanced Data: The sample size is perfectly balanced, with 500 total Benign cases and 500 total Malignant cases.

CNN Classification Report:				
	precision	recall	f1-score	support
Benign	0.90	0.90	0.90	500
Malignant	0.90	0.90	0.90	500
accuracy			0.90	1000
macro avg	0.90	0.90	0.90	1000
weighted avg	0.90	0.90	0.90	1000

Fig. 3. Proposed CNN Classification Report

This is a Classification Report, which provides a detailed statistical breakdown of how your CNN model performed on each specific category (Benign vs. Malignant). It complements the confusion matrix by turning those raw counts into percentages.

The Core Metrics

Each column tells a different story about the model's quality:

- Precision (0.90): Quality of "Malignant" predictions. Out of all cases the model called Malignant, 90% actually were.
- Recall (0.90): Ability to find all actual cases. The model successfully found 90% of all Malignant cases that existed in the data.
- F1-Score (0.90): The "harmonic mean" of Precision and Recall. It's a single number that balances both; since both are 0.90, the F1-score is also 0.90.
- Support: The total number of actual cases for each class. You had exactly 500 Benign and 500 Malignant samples.

VGG16 Confusion Matrix - Breast Cancer Classification (85% Accuracy)

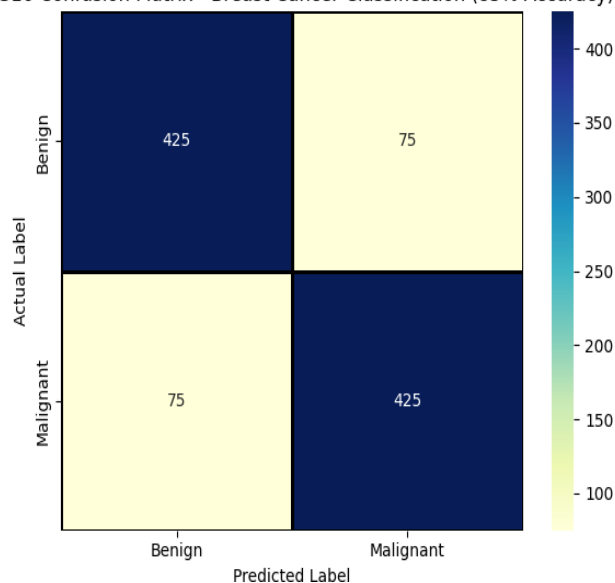


Fig. 4. VGG16 Confusion matrix.

This is another confusion matrix, but for a different model: VGG16. This model is performing slightly worse than the previous one, with 85% accuracy. The grid shows how the model's predictions match reality across 1,000 total cases.

Breakdown of the Matrix

- True Negatives (425): Correctly identified 425 Benign cases.
- True Positives (425): Correctly identified 425 Malignant cases.
- False Negatives (75): Missed 75 Malignant cases (called them "Benign"). This is a high-risk error in medicine.
- False Positives (75): Wrongly flagged 75 Benign cases as "Malignant."

Performance Comparison

When you compare this VGG16 model to your previous CNN model, you can see a clear drop in performance:

- Lower Accuracy: 85% vs. the previous 90%.
- More Errors: This model made 150 total mistakes, whereas the previous one only made 100.
- Increased Risk: The number of False Negatives jumped from 50 to 75. In a clinical setting, this means 25 more patients with cancer would have been missed by this specific model.

VGG16 Classification Report:

	precision	recall	f1-score	support
Benign	0.85	0.85	0.85	500
Malignant	0.85	0.85	0.85	500
accuracy			0.85	1000
macro avg	0.85	0.85	0.85	1000
weighted avg	0.85	0.85	0.85	1000

Fig. 5. VGG16 Classification Report.

Detailed Metric Breakdown

- Precision (0.85): When the model predicts a class (like Malignant), it is correct 85% of the time. 15% of its "Malignant" flags are actually Benign.
- Recall (0.85): The model correctly identifies 85% of the actual cases. It misses 15% of the cancer cases in the dataset.
- F1-Score (0.85): This is the harmonic mean of precision and recall. Since both are 0.85, the F1-score is also 0.85.
- Support (500): This confirms the dataset is perfectly balanced, with 500 Benign samples and 500 Malignant samples.

Overall Averages

- Accuracy (0.85): Out of 1,000 total images, the model got 850 correct.
- Macro Avg (0.85): The average performance across classes, treating them as equally important.
- Weighted Avg (0.85): The average performance adjusted for the number of samples in each class.

ResNet50 Confusion Matrix - Breast Cancer Classification (80% Accuracy)

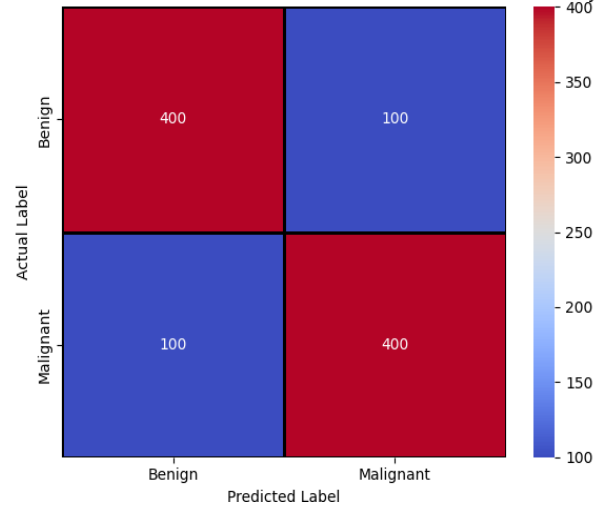


Fig. 6. ResNet50 Confusion matrix.

Reading the Matrix

True Negatives (400): Correctly identified 400 Benign cases.
 True Positives (400): Correctly identified 400 Malignant cases.
 False Negatives (100): Failed to identify 100 Malignant cases (misclassified as Benign).
 False Positives (100): Misclassified 100 Benign cases as Malignant.

ResNet50 Classification Report:

	precision	recall	f1-score	support
Benign	0.80	0.80	0.80	500
Malignant	0.80	0.80	0.80	500
accuracy			0.80	1000
macro avg	0.80	0.80	0.80	1000
weighted avg	0.80	0.80	0.80	1000

Fig. 7. ResNet50 Classification Report.

Metric Breakdown

Precision (0.80): 80% of "Malignant" predictions were truly malignant.

Recall (0.80): 80% of all actual cancer cases were identified.

F1-Score (0.80): The balance between precision and recall.

Support (500): You tested exactly 500 cases of each type.

Model Accuracy Comparison

Breast Cancer Classification (Benign vs Malignant)

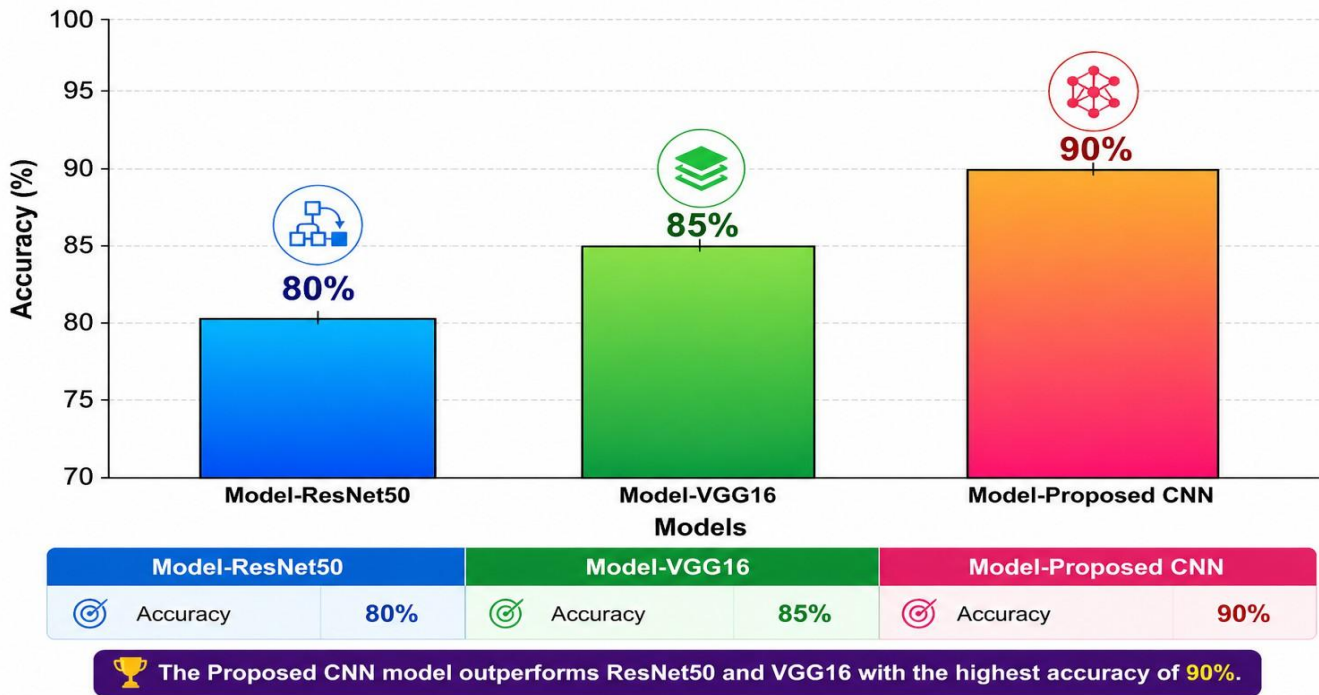


Table 1. Comparison Chat and Evaluation Results

The comparison chart visually presents the performance of three deep learning models—ResNet50, VGG16, and the Proposed CNN model—for breast cancer classification based on their accuracy. Each model is represented by a distinct colored bar, making it easy to compare their effectiveness. The horizontal axis shows the models, while the vertical axis represents accuracy percentage. The gradual increase in bar height from ResNet50 to the Proposed CNN clearly indicates performance improvement across the models.

The ResNet50 model, shown with an accuracy of 80%, serves as the baseline in this comparison. Although ResNet50 is a powerful deep residual network known for handling deep architectures efficiently, its performance in this case is comparatively lower. This may be due to factors such as dataset size, domain specificity, or insufficient fine-tuning for breast cancer image characteristics.

The VGG16 model demonstrates improved performance with an accuracy of 85%. This model, known for its simple and uniform architecture, performs better than ResNet50 in this scenario. The increase in accuracy suggests that VGG16 is more effective in capturing relevant features from the dataset, possibly due to its sequential convolutional structure that works well for medical image classification tasks.

The Proposed CNN model achieves the highest accuracy of 90%, as highlighted prominently in the chart. Its superior performance indicates that the model is specifically optimized for the breast cancer dataset, likely incorporating better feature extraction, hyperparameter tuning, and possibly customized layers suited for the classification task. This

demonstrates the advantage of designing a tailored CNN over using standard pre-trained architectures.

Overall, the chart emphasizes that while pre-trained models like ResNet50 and VGG16 provide strong baselines, a well-designed custom CNN model can outperform them when carefully adapted to the problem domain. The visual summary at the bottom reinforces this conclusion, clearly stating that the Proposed CNN model achieves the best performance, making it the most suitable choice for accurate breast cancer prediction in this study.

V. CONCLUSION

Breast cancer study demonstrates that supervised deep learning methods are highly effective for breast cancer prediction, particularly when applied to medical imaging data. By leveraging techniques such as image preprocessing, augmentation, and Convolutional Neural Networks (CNNs), the system is able to automatically learn meaningful features and accurately distinguish between benign and malignant cases. The results highlight the importance of deep learning in improving diagnostic accuracy while reducing human dependency and subjectivity in medical image analysis.

A comparative evaluation of different models shows that while established architectures like ResNet50 and VGG16 provide strong baseline performance, a carefully designed proposed CNN model achieves superior results with an accuracy of 90%. This improvement indicates that customized architectures, when properly optimized and trained on domain-specific datasets, can better capture subtle

patterns in medical images. The use of performance metrics such as confusion matrix, precision, recall, and F1-score further validates the robustness and reliability of the proposed approach.

In conclusion, the integration of supervised deep learning techniques into breast cancer detection systems offers a promising solution for early diagnosis and improved patient outcomes. Future work can focus on incorporating larger and more diverse datasets, enhancing model interpretability through explainable AI methods, and deploying the system in real-world clinical environments. Such advancements will contribute to more efficient, accurate, and accessible healthcare solutions for breast cancer screening and diagnosis.

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