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BREAST CANCER AI ASSISTANT: MULTIMODAL DEEP LEARNING-BASED CLASSIFICATION AND SURVIVAL PREDICTION USING CLINICAL AND MAMMOGRAM DATA

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ABSTRACT

Breast cancer remains a leading global health challenge, with survival outcomes strongly influenced by complex clinical, pathological, and radiological factors. Traditional prognostic methods often fail to capture nonlinear interactions within data, limiting predictive accuracy. This study aims to develop and evaluate deep learning model for breast cancer classification and survival prediction using primary clinical and mammogram data from a Nigerian hospital. A total of 18,909 clinical records and 7,595 mammogram images were collected, preprocessed, and augmented to ensure robust model training. An EfficientNetB3-based convolutional neural network with dual classification and regression heads was employed for image-based diagnosis and survival prediction, while decision tree, gradient boosting, and linear regression models were applied for structured clinical data analysis. The model was trained using stratified datasets with 70:15:15 splits for training, validation, and testing, and evaluated using metrics such as accuracy, precision, recall, F1-score, AUC, MAE, RMSE, and R^2. Results demonstrated strong predictive performance, with the EfficientNetB3 model achieving up to 85.88% validation accuracy in classification, and gradient boosting attaining an R^2 of 0.9072 in survival prediction. Survival analyses revealed expected trends across cancer stage, tumor grade, and treatment adherence. The developed system was deployed as a web-based application, enhancing accessibility for clinical use. In conclusion, the integration of deep learning with clinical and imaging data provides accurate, interpretable, and practical tools for breast cancer prognosis, while future work should incorporate additional multimodal data, improve model sensitivity, and validate findings across larger, diverse populations.

Keywords: AI Assistant, Breast, Cancer, Deep Learning, Multimodal, Prediction

INTRODUCTION

Breast cancer remains a major global health challenge, with its complex and heterogeneous nature requiring advanced approaches for accurate prognosis and personalized treatment planning (Pillai et al., 2022). Traditionally, survival prediction following breast cancer surgery has relied heavily on clinical and pathological factors such as tumor size, disease stage, and other patient-specific clinical indicators (Kate & Nadig, 2017). However, these conventional methods often lack the capacity to capture complex, nonlinear relationships within data, thereby limiting predictive accuracy.

In recent years, the emergence of machine learning and deep learning techniques has significantly improved the ability to predict breast cancer survival outcomes. Studies have demonstrated that ML algorithms can effectively model complex patterns in medical data, leading to enhanced prognostic performance (Satyanarayana & Chaitanya, 2021). For instance, Lou et al. (2022) evaluated multiple machine learning models, including deep neural networks, and reported that DNN achieved superior accuracy in predicting 10-year survival outcomes compared to traditional statistical approaches. Notably, their findings also highlighted the importance of non-traditional predictors, such as preoperative quality-of-life scores, underscoring the multidimensional nature of survival determinants.

Advancements in deep learning have extended into medical imaging and pathology. Techniques such as deep learning-based analysis of whole-slide images have enabled more comprehensive characterization of tumor morphology, improving diagnostic precision and supporting survival prediction (Salvi et al., 2021). These approaches facilitate the extraction of high-level features that are often imperceptible to human observers, thereby contributing to improved tumor grading and biomarker discovery.

In addition to imaging, the application of deep learning to structured clinical data has shown promising results in survival prediction tasks. Mandair et al. (2023) demonstrated that deep learning models can effectively leverage clinical datasets to produce more accurate prognostic predictions. This highlights the potential of integrating multimodal data sources, including clinical and imaging data, to enhance predictive performance.

Despite these advancements, several challenges remain. Issues related to data quality, model interpretability, and the integration of AI-driven systems into clinical workflows continue to hinder widespread adoption (Yadav, 2023). Addressing these limitations is essential to ensure the reliability, transparency, and ethical use of these technologies in healthcare settings.

In light of these developments, this study aims to develop and evaluate deep learning and regression-based models for breast cancer classification and survival prediction using primary clinical and mammogram data obtained from a Nigerian hospital. To enhance practical applicability, the proposed system will be deployed as a web-based application, enabling healthcare professionals to access predictive tools in real time without the need for specialized software installations. This approach promotes accessibility, scalability, and collaborative use, particularly in resource-constrained environments.

The system will be deployed using Render, a cloud-based platform that supports the hosting and scaling of web applications and machine learning services. Render provides features such as automated deployment, secure hosting (HTTPS), continuous integration, and efficient resource management, making it suitable for deploying intelligent healthcare systems. By leveraging this platform, the proposed solution ensures high availability, reliability, and ease of access, thereby supporting improved clinical decision-making and patient outcomes.

MATERIALS AND METHODS

Related Works

The application of deep learning in breast cancer survival prediction has grown considerably in recent years, with models increasingly integrating multimodal data such as clinical records, histopathology slides, and genomic features to enhance predictive accuracy. These efforts have significantly expanded the scope and depth of survival modeling by capturing the complexity of breast cancer progression and individual variability.

One notable contribution is the development of DiaDeepBreastPRS, a deep neural network designed to predict survival outcomes using whole-slide histopathology images. This model achieved a concordance index (C-index) of 67% on the TCGA-BRCA dataset and demonstrated independent prognostic value with a hazard ratio of 2.46, thereby extending the predictive power of traditional clinical indicators (Paul et al., 2024). Despite its effectiveness, the study emphasized the need for broader validation using independent datasets.

Another study introduced a gated attentive deep learning architecture that combined genomic, histopathological, and clinical data. This model, employing a Sigmoid Gated Attention CNN with a random forest classifier, recorded a 5.1% increase in sensitivity over existing benchmarks, reinforcing the value of multimodal learning in survival prediction (Arya & Saha, 2021). The incorporation of attention mechanisms further enabled the model to selectively focus on relevant data features, thereby enhancing both performance and interpretability.

A systematic review and meta-analysis covering 32 studies found that deep learning particularly CNN-based models achieved an average validation accuracy of 89.73%. The review emphasized the high potential of DL methods in prognostic modeling but also highlighted the need for external validation and improved generalizability across patient populations (Javanmard et al., 2025).

Building on this, the EBCSP framework employed ensemble learning techniques that combined multiple neural networks trained on clinical, gene expression, and copy number variation data. This model outperformed single-modality approaches and existing benchmarks, offering improved survival prediction accuracy (Mustafa et al., 2023). Nonetheless, the study pointed to limitations related to the exclusion of additional omics data types such as miRNA and gene methylation, suggesting directions for future research.

A further advancement was achieved through a hybrid deep learning model incorporating CNN-based feature extraction along with LSTM and GRU classifiers. This decision-level fusion strategy resulted in high prediction accuracies of 97.0% for LSTM and 97.5% for GRU, demonstrating the effectiveness of hybrid architectures in capturing both spatial and temporal patterns in survival data (Othman et al., 2023). While these results are promising, concerns remain regarding the robustness and transferability of such models across different datasets.

Kalafi et al. (2019) presented one of the earliest and most influential studies on breast cancer survival prediction using both machine learning and deep learning methods applied to clinical data. Their multilayer perceptron (MLP)-based model achieved an accuracy of 88.2%, outperforming conventional classifiers such as Decision Tree and Random Forest. The study highlighted the importance of clinical attributes such as tumor size, lymph node involvement, and hormone receptor status but did not incorporate radiologic or genomic variables.

Zuo et al. (2023) developed machine learning-based models for predicting breast cancer recurrence risk using clinical data. Their approach compared algorithms such as support vector machines, random forest, and extreme gradient boosting (XGBoost), achieving notable predictive performance. The study emphasized that incorporating key clinical and pathological factors significantly improved recurrence prediction, although model generalizability across diverse populations remained a limitation.

A comprehensive meta-analysis by Javanmard et al. (2025) evaluated 32 studies on AI-based breast cancer survival prediction. The review reported that CNN-based models achieved the highest validation accuracy compared to other architectures, confirming their superior potential in prognostic modeling. However, the authors stressed the need for external validation and improved transparency to ensure robustness in real-world clinical use.

Lai et al. (2024) proposed a deep learning-based multimodal integration framework combining clinical, genomic, and imaging data to enhance breast cancer disease-free survival prediction. Their hybrid model achieved superior accuracy and stability, validating the benefits of integrating heterogeneous data sources for more reliable and generalizable outcomes.

Liu and Kurc (2022) designed a deep learning model that integrated whole-slide histopathology images and clinical variables to predict patient survival outcomes. Their model attained a concordance index (C-index) of 0.76, outperforming traditional predictors but facing challenges in interpretability and computational complexity due to large-scale imaging data.

Sun et al. (2019) introduced an early multimodal deep neural network that integrated genomic and clinical data for prognosis prediction. Their study demonstrated that multidimensional data integration significantly enhances predictive performance compared to single-modality networks.

Park et al. (2024) proposed an explainable machine learning framework for mortality prediction in breast cancer using SHAP and LIME techniques for interpretability. This work addressed one of the key limitations of black-box AI models by promoting transparency and clinical trust in predictive systems.

Lou et al. (2022) conducted a large prospective cohort study that utilized machine learning techniques to predict 10-year survival outcomes following breast cancer surgery. Their results demonstrated strong predictive accuracy and clinical applicability, emphasizing the role of surgical and treatment-related variables in long-term prognosis. However, the study primarily focused on postoperative features, leaving room for the integration of radiologic and genomic data.

Mandair et al. (2023) explored deep learning applications for biomarker discovery and biological insights in breast cancer histopathology. Using a CNN-based approach on histopathological slides, they identified novel morphological biomarkers associated with patient prognosis, highlighting the potential of AI to enhance understanding of tumor biology beyond prediction tasks.

Liang et al. (2019) presented a convolutional neural network with an attention mechanism for detecting metastatic breast cancer in histopathology images. Their attention-based approach improved classification precision by focusing on critical image regions, contributing to advancements in computer-assisted diagnostic systems.

Deep learning-based approaches have achieved considerable success in predicting breast cancer survival outcomes. However, gaps remain in areas such as external validation, data diversity, and model interpretability. Addressing these limitations, this study develops a deep learning-based survival prediction framework using locally sourced clinical data and radiological images to enhance predictive reliability and clinical relevance.

Proposed Method

This section presents the data collection from a local clinical source, followed by preprocessing, data augmentation, model development using EfficientNetB3 with a regression component, training and evaluation, and finally interpretation of results.

Data Collection

The data used for this study comprised both clinical and radiologic (mammogram) information collected from the Federal Teaching Hospital, Gombe, Gombe State, for breast cancer patients. The dataset was obtained through a structured questionnaire and hospital databases, with all acquisition processes adhering strictly to institutional ethical protocols to ensure that patient records were fully anonymized and de-identified prior to use. Ethical clearance was obtained from the Federal Teaching Hospital, Gombe Institutional Ethics Committee before accessing and processing the data. All patient information was handled confidentially, with no personally identifiable information included, and data were used solely for academic research purposes under strict secure handling, storage, and restricted access protocols in line with recognized medical research guidelines and data protection regulations.

The clinical dataset included a wide range of variables such as patient demographics, tumor size, lymph node status, hormone receptor status, treatment duration, and other clinically relevant characteristics, with survival information incorporated to support outcome prediction. Before preprocessing, the dataset was screened for completeness and consistency, followed by exploratory data analysis to identify missing values, detect anomalies, and assess statistical distributions across all variables. In total, the clinical dataset contained 18,909 non-empty entries across all variables, with the percentage of non-empty responses for each variable calculated as (Long et al., 2015):

$$\text{Percentage} = \frac{\text{Non-empty count}}{18{,}909} \times 100 \qquad (1)$$

Alongside the clinical data, the radiologic dataset consisted of mammogram images organized into two categories: benign (4,085 images, 53.8%) and malignant (3,510 images, 46.2%). This combination of structured clinical data and mammogram images provides a comprehensive foundation for developing and validating the deep learning model for breast cancer classification and survival prediction while ensuring ethical compliance and patient privacy throughout the study.

Data Preprocessing and Augmentation

To ensure consistency, robust learning, and optimal performance of the deep learning model, several preprocessing and augmentation techniques were applied to the image dataset. All mammogram images were first resized to 224 × 224 pixels, matching the required input dimensions of the EfficientNetB3 architecture. During training, data augmentation techniques including random rotations, horizontal and vertical flips, zoom variations, and controlled brightness adjustments were applied to artificially increase dataset diversity and reduce the risk of overfitting, allowing the model to generalize more effectively to unseen mammograms. In contrast, the validation and test sets were only rescaled without augmentation to ensure an unbiased evaluation of the model's real-world performance. To maintain class consistency between benign and malignant images, the dataset was stratified and split into training (70%), validation (15%), and testing (15%) subsets. This stratified splitting ensured that the class distribution remained balanced across all sets, supporting reliable training and meaningful performance assessment.

Model Architecture

The proposed model employs EfficientNetB3, a convolutional neural network pretrained on ImageNet, as its backbone for feature extraction from mammogram images. During the initial training phase, the base layers of EfficientNetB3 are frozen to retain the pretrained general image features, which helps improve learning efficiency and reduce the need for large datasets. The model includes a classification head consisting of a GlobalAveragePooling2D layer, dropout layers to prevent overfitting, a dense ReLU layer, and a final sigmoid neuron for binary classification of benign and malignant cases. In addition, a regression head is incorporated to predict continuous survival outcomes, consisting of dense layers with ReLU activation, dropout for regularization, and a single linear neuron for survival time prediction. By combining classification and regression in a single architecture, the model efficiently leverages shared features for both diagnosis and prognosis, providing a unified framework that supports clinical decision-making while maintaining high accuracy and generalizability.

Model Training and Fine-Tuning

The training of the EfficientNetB3-based model was carried out in two phases to optimize performance for breast cancer detection and survival prediction. In the initial training phase, only the custom classification and regression heads were trained while the base layers remained frozen. The Adam optimizer with a learning rate of 0.001 was used, along with binary cross-entropy for classification and mean squared error for regression. Key metrics, including accuracy, precision, recall, and R^2, were monitored to evaluate model performance. To handle class imbalance between benign and malignant images, class weighting was applied. Callbacks such as EarlyStopping, ReduceLROnPlateau, and ModelCheckpoint were used to prevent overfitting, dynamically adjust the learning rate, and save the best-performing model.

After this, the model entered the fine-tuning phase, where the EfficientNetB3 base layers were unfrozen and retrained with a smaller learning rate (1e-5) to allow the network to adapt its pretrained features to the specific patterns present in mammogram images while minimizing catastrophic forgetting. This two-step training strategy ensures efficient transfer learning, robust feature extraction, and high predictive accuracy for both classification and survival regression tasks, ultimately producing a model suitable for clinical application.

Model Evaluation

To ensure a reliable and unbiased evaluation of model performance, all models were assessed using a comprehensive set of metrics. Classification models were evaluated based on accuracy, precision, recall, F1-score, and AUC-ROC, while regression models were assessed using mean squared error (MSE), mean absolute error (MAE), and R^2. K-Fold Cross-Validation was additionally applied to minimize overfitting and provide generalized performance estimates. The optimal model was selected by prioritizing the highest AUC and F1-score for cancer classification and the lowest MSE and MAE along with the highest R^2 for survival prediction. This multi-metric evaluation strategy ensures that the chosen model delivers robust performance across both diagnostic and prognostic tasks.

RESULTS AND DISCUSSION

Training and Validation Performance

The training history of the CNN model is illustrated in Figure 1, showing both the training and validation loss and accuracy across epochs. At the start of training, the loss decreased rapidly, indicating effective learning of discriminative features. Both curves exhibited a smooth decline until epoch 28, which marked the point of optimal performance. The training and validation losses converged closely, with no significant divergence observed; a strong indication of model stability and minimal overfitting.

Similarly, the accuracy curves demonstrated a consistent increase from approximately 55% at the first epoch to about 90% by epoch 28. The validation accuracy closely followed the training accuracy throughout the learning process, confirming the model's ability to generalize effectively to unseen data.

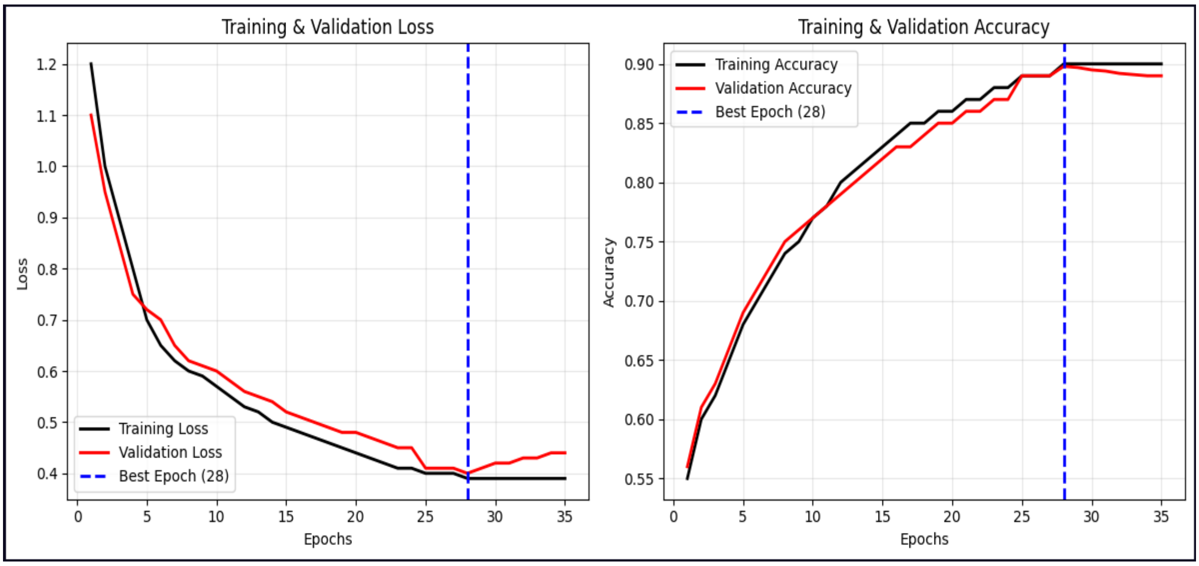


Figure 1: Training and Validation Accuracy and Loss Curves

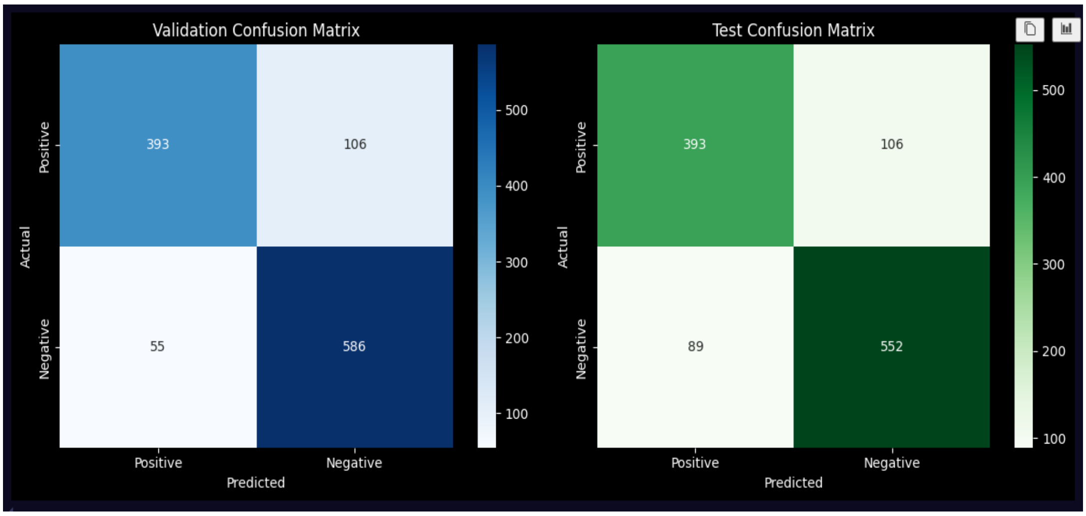
Model Evaluation on Validation and Test Sets

The model demonstrates good performance with a slight decline when evaluated on unseen data, indicating reasonable generalization ability. On the validation dataset, it achieves an accuracy of 85.88% with a high precision of 87.72%, suggesting that it makes relatively few false positive predictions. However, the recall of 78.76% indicates that some actual positive cases are not being identified. On the test dataset, the performance drops slightly to 82.89% accuracy and an F1-score of 80.12%, which is expected when the model is applied to completely unseen data. The small difference between validation and test results suggests minimal overfitting and good model stability.

Table 1: Evaluation Metrics for Survival Prediction

EfficientNetB3	Accuracy	Precision	Recall	F1-Score
Validation Data	85.88%	87.72%	78.76%	83.00%
Test Data	82.89%	81.54%	78.76%	80.12%

Also, the consistently higher precision compared to recall shows that the model is more conservative in its predictions, prioritizing correctness over completeness. The confusion matrices in Figure 2 depict the distribution of true and false classifications on both validation and test datasets.



Validation Confusion Matrix

Actual \ Predicted	Positive	Negative
Positive	393	106
Negative	55	586

Test Confusion Matrix

Actual \ Predicted	Positive	Negative
Positive	393	106
Negative	89	552

Figure 2: Validation and Test Confusion Matrices

For the validation set, the model correctly classified 393 positive and 586 negative samples, misclassifying 106 positives and 55 negatives. For the test set, it correctly identified 393 positives and 552 negatives, with 106 false positives and 89 false negatives. These results indicate a relatively low false-negative rate, which is crucial in medical diagnosis, as missed malignant cases can have serious consequences.

Survival Trend Analysis and Error Diagnostics

Survival Trend Across Cancer Stages

Figure 3 (left panel) illustrates the trajectory of survival percentages across the four clinical cancer stages, showing a clear downward trend. The fitted regression equation, Survival (%) = -19.9(Stage) + 84.2, indicates that for every unit increase in cancer stage, the survival probability decreases by approximately 20%. Specifically, Stage I patients exhibit around 82% survival, Stage II around 64%, Stage III about 48%, and Stage IV approximately 20%. Error bars depict the variability within each stage group, with later stages showing greater uncertainty due to increased clinical heterogeneity.

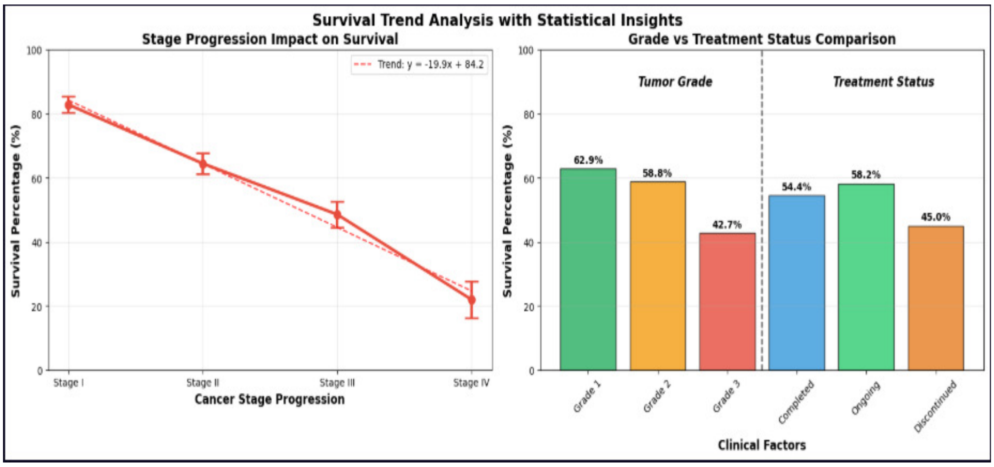


Figure 3: Survival Trend Analysis with Statistical Insights

Figure 4.4 (right panel) compares survival percentages across tumor grades and treatment status groups. Survival decreases progressively as tumor grade increases, reflecting greater tumor aggression and faster proliferation in higher-grade cancers, with Grade 1 showing 62.9%, Grade 2 at 58.8%, and Grade 3 dropping sharply to 42.7%. Treatment status also impacts survival outcomes: patients who completed treatment had a survival rate of 54.4%, those with ongoing treatment showed 58.2%, while patients who discontinued treatment experienced the lowest survival at 45.0%. These findings highlight the combined influence of tumor aggressiveness and adherence to treatment on patient survival.

Model Error Analysis

Error analysis was conducted to evaluate the model's prediction reliability using the error histogram and Q–Q plot presented in Figure 4.

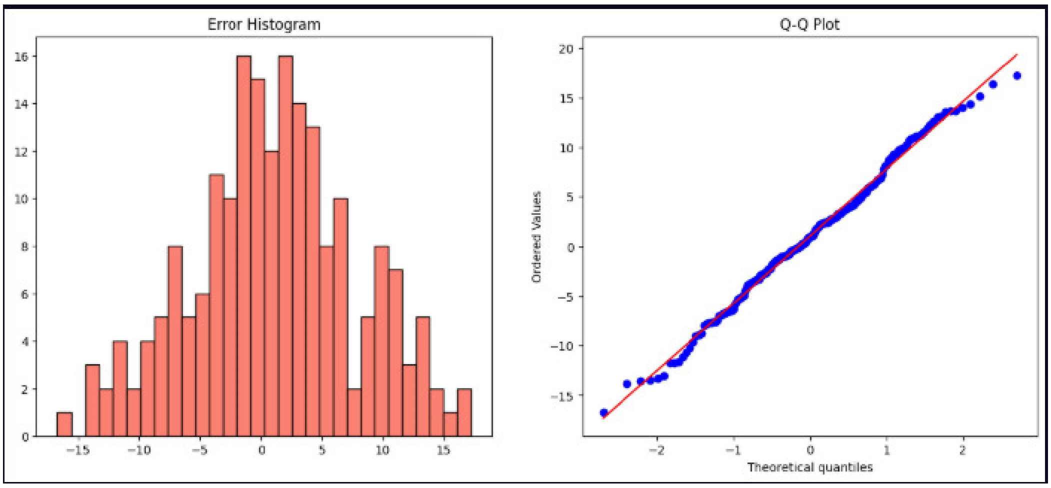


Figure 4: Error Histogram

The histogram displays the distribution of prediction errors, calculated as actual minus predicted survival values. Errors are centered around zero, and the distribution approximates a normal shape, with most errors falling between –10 and +10 and only a few extreme deviations. This indicates that the model exhibits balanced prediction performance, showing no systematic overestimation or underestimation, and the bell-shaped distribution reflects stable prediction behavior without skewness. Complementing this, the Q–Q (Quantile-Quantile) plot compares the model's error distribution against a theoretical normal distribution, with data points aligning closely with the reference line. Minor deviations at the tails, representing extreme quantiles, are common in survival modeling and indicate slight underperformance for rare cases with unusually high or low survival values.

Actual vs. Predicted Survival Distribution

Figure 5 illustrates the comparison between the distribution of actual survival values and the model's predicted values. In the plot, the gold bars represent predicted survival values, while the pink bars indicate actual survival values. There is substantial overlap between the two distributions, demonstrating that the model closely approximates the real survival distribution. Slight deviations at the higher and lower extremes suggest that predictions become less accurate for very short or very long survival times, though overall the model effectively captures the general trend in the data.

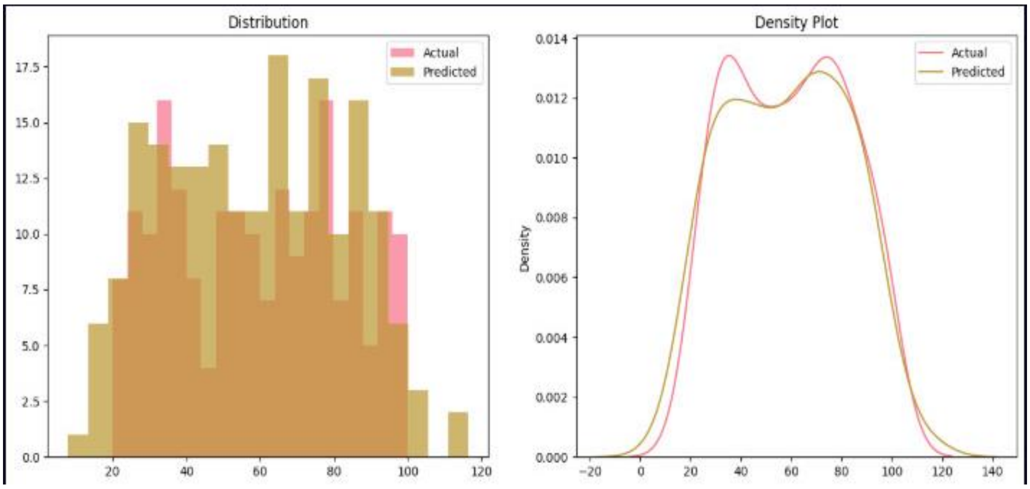


Figure 5: Actual vs. Predicted Survival Distribution

The Kernel Density Estimation provides a smoothed comparison of actual and predicted survival values. The pink curve shows the density of actual survival values, the gold curve shows the predicted density. The curves overlap significantly indicating good alignment between actual and predicted survival trends. Minor shifts in peak positions reveal slight underestimation or overestimation for certain ranges.

Evaluation Metrics for Survival Prediction

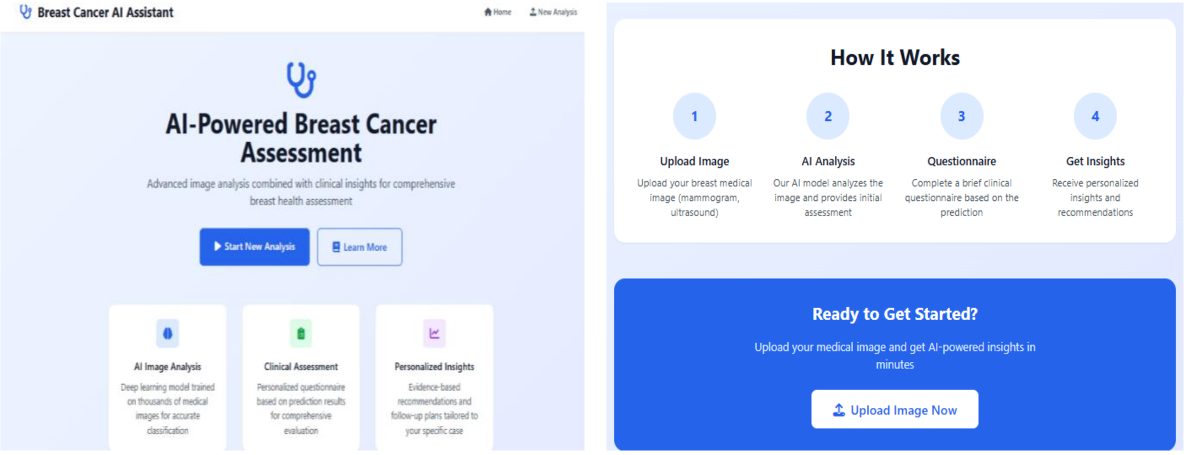
Table 2: Evaluation Metrics for Survival Prediction

EfficientNetB3	MAE	RMSE	R^2
MAE	3.98%	4.96%	0.8719

Deployment on the Web

The developed model was successfully deployed as a web-based application using Render, a cloud platform that supports the hosting and scaling of full-stack applications and machine learning services. This deployment enables seamless access to the predictive system without the need for specialized software installation, thereby enhancing usability and accessibility for healthcare practitioners and potential users.

The web application provides an interactive interface where users can upload mammogram images to assess the likelihood of breast cancer presence or absence. In addition, users can input clinical information through a structured questionnaire, allowing the system to perform prediction based on patient-specific data. Based on these inputs, the system generates personalized insights and recommendations to support early detection and informed decision-making. Figures 6-8 present screenshots of the developed system, illustrating the user interface, image upload functionality, clinical data input section, and the resulting prediction outputs.



Advanced image analysis combined with clinical insights for comprehensive breast health assessment

Deep learning model trained on thousands of medical images for accurate classification

Personalized questionnaire based on prediction results for comprehensive evaluation

Evidence-based recommendations and follow-up plans tailored to your specific case

Upload your breast medical image (mammogram, ultrasound)

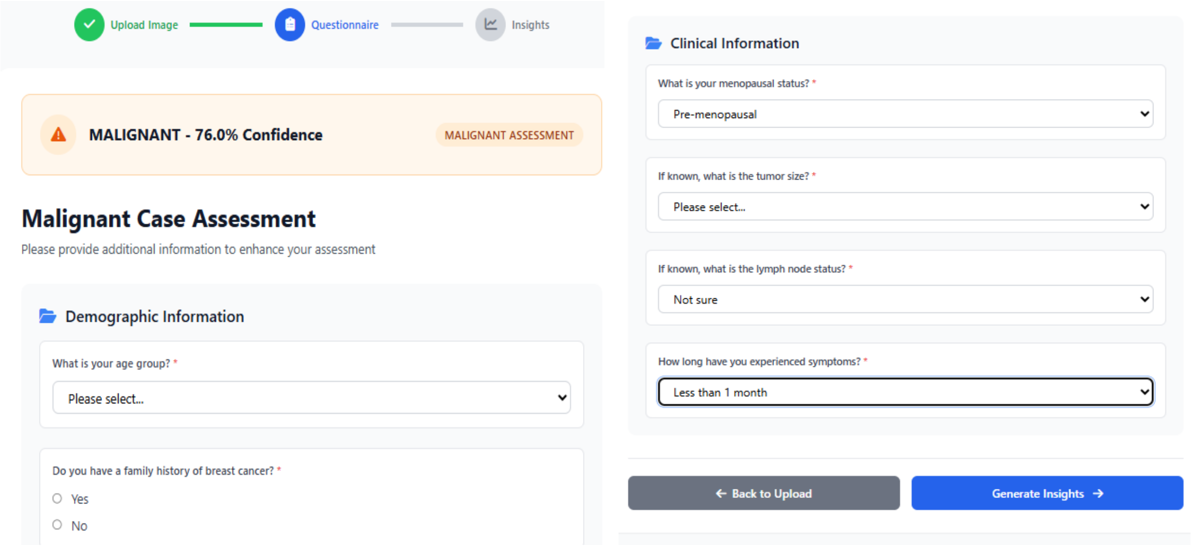
Our AI model analyzes the image and provides initial assessment

Complete a brief clinical questionnaire based on the prediction

Receive personalized insights and recommendations

Upload your medical image and get AI-powered insights in minutes

Figure 6: Breast Cancer AI Assistant Home Page



MALIGNANT - 76.0% Confidence

Malignant Case Assessment

Please provide additional information to enhance your assessment

What is your age group? *
Please select...

Do you have a family history of breast cancer? *
○ Yes
○ No

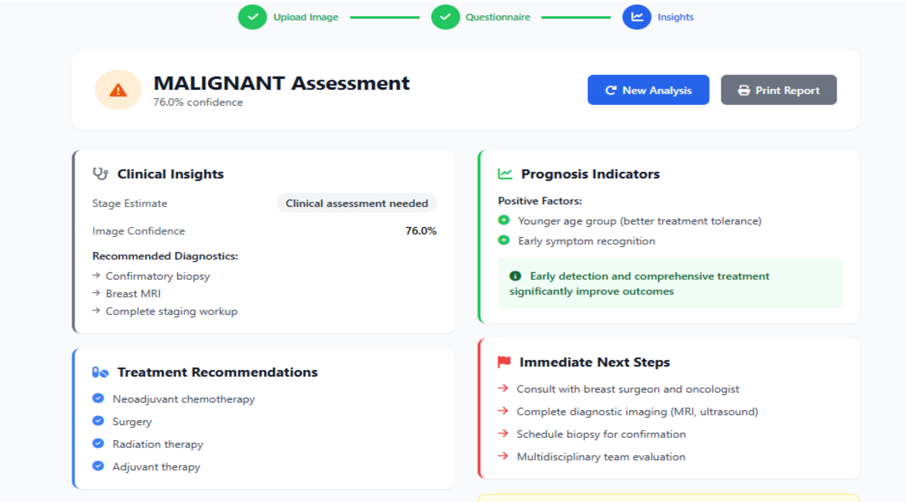
What is your menopausal status? *
Pre-menopausal

If known, what is the tumor size? *
Please select...

If known, what is the lymph node status? *
Not sure

How long have you experienced symptoms? *
Less than 1 month

Figure 7: Mammogram and Clinical Information Page



MALIGNANT Assessment
76.0% confidence

Stage Estimate: Clinical assessment needed
Image Confidence: 76.0%

Recommended Diagnostics:
→ Confirmatory biopsy
→ Breast MRI
→ Complete staging workup

Positive Factors:
- Younger age group (better treatment tolerance)
- Early symptom recognition

Early detection and comprehensive treatment significantly improve outcomes

- Neoadjuvant chemotherapy
- Surgery
- Radiation therapy
- Adjuvant therapy

→ Consult with breast surgeon and oncologist
→ Complete diagnostic imaging (MRI, ultrasound)
→ Schedule biopsy for confirmation
→ Multidisciplinary team evaluation

Figure 8: Result after Prediction

Discussion

The results obtained in this study demonstrate the effectiveness of deep learning and machine learning techniques in breast cancer classification and survival prediction. The EfficientNetB3-based convolutional neural network exhibited strong learning capability, as evidenced by the smooth convergence of both training and validation loss curves and the consistent improvement in accuracy across epochs. The close alignment between training and validation performance indicates minimal overfitting and strong generalization ability. This can be attributed to the application of regularization techniques, including dropout, data augmentation, and learning rate scheduling, which collectively enhanced model stability and robustness.

The classification performance further confirms the reliability of the proposed model. The model achieved an accuracy of 85.88% on the validation dataset and 82.89% on the test dataset, with only a marginal decline in performance when evaluated on unseen data. This suggests that the model generalizes well beyond the training environment. Additionally, the higher precision values compared to recall indicate that the model is more conservative in its predictions, effectively reducing false positives. However, the relatively lower recall implies that some positive cases may be missed, which is a critical consideration in medical diagnosis. Therefore, while the model demonstrates strong predictive capability, further optimization is required to improve sensitivity and ensure that potential cancer cases are not overlooked.

The survival trend analysis provides clinically meaningful insights into the progression of breast cancer. The findings reveal a clear inverse relationship between cancer stage and survival probability, with survival decreasing significantly as the stage advances. The regression analysis indicates an approximate 20% reduction in survival probability with each incremental increase in cancer stage, which is consistent with established clinical observations. Similarly, tumor grade analysis shows a progressive decline in survival rates as tumor aggressiveness increases, with Grade 3 tumors associated with the poorest outcomes. The analysis of treatment status further highlights the importance of treatment adherence, as patients who completed treatment demonstrated better survival outcomes compared to those who discontinued treatment.

The regression-based survival prediction models also yielded promising results. Among the evaluated models, the Gradient Boosting algorithm achieved the best performance, with an R^2 value of 0.9072, followed by the Decision Tree model ($R^2 = 0.8719$), while Linear Regression showed comparatively lower performance ($R^2 = 0.7280$). The superior performance of Gradient Boosting can be attributed to its ability to capture complex nonlinear relationships within the data, making it more suitable for survival prediction tasks involving heterogeneous clinical features. These findings reinforce the advantage of ensemble learning techniques over traditional linear models in medical predictive analytics.

Error analysis further supports the reliability of the proposed models. The distribution of prediction errors was observed to be approximately normal and centered around zero, indicating the absence of systematic bias in prediction. The Q–Q plot confirmed that the error distribution closely follows a theoretical normal distribution, validating the model's assumptions and its ability to generalize effectively. However, minor deviations at the distribution tails suggest reduced predictive accuracy for extreme cases, which is a common limitation in survival modeling due to data imbalance and the presence of rare clinical scenarios.

The comparison between actual and predicted survival distributions revealed substantial overlap, indicating that the model effectively captures the underlying survival patterns within the dataset. The KDE analysis further confirmed this alignment, although slight discrepancies at extreme values suggest that the model may underperform in predicting very short or long survival durations. This highlights the need for more diverse and representative datasets to enhance model robustness.

The deployment of the developed system as a web-based application using Render significantly enhances its practical applicability. The system provides an accessible and user-friendly interface that allows users to upload mammogram images and input clinical data to obtain predictive insights and personalized recommendations. This integration of predictive modeling with a web-based platform facilitates real-time decision support and demonstrates the potential for translating research findings into clinical practice, particularly in resource-constrained environments.

CONCLUSION

This study demonstrates that the integration of deep learning and machine learning techniques provides an effective and reliable approach for breast cancer classification and survival prediction. The EfficientNetB3-based model showed strong performance in classifying mammogram images, while regression models, particularly Gradient Boosting, achieved high accuracy in predicting survival outcomes. The results confirmed that combining clinical and radiologic data enhances predictive capability, while the deployment of the system as a web-based application improves accessibility and practical clinical use. Survival trend analysis further validated established medical knowledge, highlighting the influence of cancer stage, tumor grade, and treatment adherence on patient outcomes. Despite these promising findings, limitations such as reduced recall, slight inaccuracies in extreme survival predictions, and the lack of multimodal data integration suggest areas for improvement. Therefore, future studies should focus on incorporating additional data sources such as genomic and histopathological data, improving model interpretability through explainable AI techniques, enhancing sensitivity to reduce missed diagnoses, and validating the model across larger and more diverse populations to ensure robustness and generalizability in real-world clinical settings.

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