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EXPLAINABLE AI FOR BREAST CANCER DETECTION USING GRAD-CAM AND MASK MAMMOGRAM NEURAL NETWORKS

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Abstract

Early identification is essential for increasing survival rates of breast cancer, which is still a top cause of death among women worldwide. This research introduces a cutting-edge system that uses deep learning and state-of-the-art image processing to automatically identify breast cancer in mammography pictures. Bilateral filtering is used for image preprocessing in the approach, which also incorporates CNN for classification, MMNN for segmentation, and Grad-CAM for explainability. Microcalcifications and lesions, which are critical for correct diagnosis, are preserved throughout the preprocessing stage by using bilateral filtering to decrease noise. Using a convolutional neural network (CNN), intricate patterns linked to breast cancer may be learnt and used to classification tasks. Clinicians can better understand the model's decision-making process thanks to Grad-CAM, which shows them exactly which parts of the picture were considered. In order to pinpoint tumours, the MMNN is used for ROI segmentation and delineation; subsequently, bounding box detection is employed, yielding invaluable spatial data for further clinical investigation.All of the work is done in a Python environment, making use of well-known modules to display the findings. Automated breast cancer screening and diagnosis might benefit greatly from the suggested framework because to its impressive accuracy in locating and identifying breast tumours. An effective, scalable, and interpretable method for early-stage cancer diagnosis may be achieved by the combination of Python's image processing capabilities with deep learning.

Index Terms— Breast Cancer Detection, Mammogram, Convolutional Neural Networks , Mask Mammogram Neural Networks , Grad-CAM, Bounding Box Detection, Image Segmentation

I. INTRODUCTION

Early identification is crucial for increasing survival rates and allowing more effective treatment techniques for breast cancer, one of the most common and fatal tumours among women globally. While mammography is a reliable diagnostic technique for detecting breast cancer at an early stage, it isn't perfect and may miss more subtle symptoms like microcalcifications, lumps, and architectural distortions—particularly in denser breast tissue—

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when used alone. There is a clear need for automated methods that may enhance the accuracy and efficiency of breast cancer diagnosis, since the process of manually interpreting mammograms is both time-consuming and prone to human error. Recent developments in image processing and deep learning provide new chances to create automated systems that may overcome these restrictions, while prior techniques have relied significantly on human experience.

Convolutional Neural Networks (CNNs) are one such technology that has recently been quite useful for automating the process of anomaly identification in medical pictures, such as mammograms. For jobs like picture classification, where the ability to recognise complicated patterns is crucial, these networks shine when it comes to learning hierarchical features from picture data. Nevertheless, CNNs are sometimes criticised for not being interpretable, even if they are quite accurate. Knowing the reasoning behind a model's predictions is as crucial as knowing the accuracy of those predictions in clinical settings, particularly when using decision support tools. Thus, in order for deep learning models to be widely used in healthcare, it is crucial to make them interpretable.

The goal of this research is to overcome these obstacles by creating a unified system for automated breast cancer diagnosis that is both more accurate and transparent enough for clinical use. The framework uses bilateral filtering and other sophisticated image preprocessing methods to decrease noise while keeping important image characteristics like microcalcifications and tumours. To improve the model's interpretability, Grad-CAM (Gradient-weighted Class Activation Mapping) is used to visualise the areas of the mammogram that impacted the model's predictions. A CNN-based model is trained to classify mammogram pictures. To take it to the next level, the system is segmented using Mask mammography Neural Networks (MMNN), which allows for the exact detection of ROIs in the mammography images. Bounding box detection is used to pinpoint the anomalies after tumour areas have been segmented, giving important spatial context for clinical analysis. Python is used to implement the whole process, using a suite of popular libraries including TensorFlow and Keras for deep learning, OpenCV and scikit-image for image processing, and Matplotlib for results visualisation. The scalability and efficiency of this technology make it ideal for use in breast cancer screening programs on a grand scale, without sacrificing accuracy or interpretability. In order to improve patient outcomes, this project primarily aims to establish a trustworthy and open system for detecting breast cancer. This system will help doctors diagnose the disease at an early stage.

The outline of this document is as follows: Using deep learning and image processing as our primary foci, we survey the literature on automated breast cancer diagnosis in Section 2. Image preprocessing, classification, explainability, segmentation, and bounding box detection approaches were detailed in Section 3, which also covers the methodology utilised in this work. Our experimental findings are presented in Section 4. Section 5 provides a brief summary of the paper's main points, findings, and the possible influence of the suggested technique on breast cancer detection, before ending the work.

II. RELATED WORKS

Our research goals and objectives were born out of a thorough literature review on breast cancer detection and feature selection (FS) methods for analysing cancer data, with a focus on algorithms that draw inspiration from metaheuristics found in nature.
A lot of studies have looked at how well different ML approaches can identify and predict breast cancer diagnoses. [1] evaluated three popular ML approaches to predict the fate of breast cancer survivors. These models have many commonalities with ANNs, SVMs, and SSL in their approach. By analysing the Breast Cancer Surveillance, Epidemiology, and End Outcomes database, their research showed that after adjusting the model parameters, the SSL approach usually had better accuracy and stability. The findings showed that SSL was the obvious winner with accuracy of 0.71, sensitivity of 0.65, and specificity of 0.76.
In their study on breast cancer diagnosis and prediction, [2] examined a number of machine learning (ML) algorithms, including the Least Absolute Shrinkage and Selection Operator (LASSO). The assessment's performance was measured using models that used all traits and attributes found by LASSO. In terms of maximum accuracy, Random Forest (RF) achieved 90.68 percent, which was higher than LASSO's performance. In addition, 98.00% F1 scores were generated by K-Nearest Neighbours (KNN), 92.50% by Multilayer Perceptron (MLP), and 94.60% by Random Forest (RF).

In a similar vein, [3] proposed a decision support system (DSS) for breast cancer patients that incorporates ML techniques with random optimisation (RO). Using multiple kernel learning, the DSS was developed to assess the probability of cancer-related thrombosis. The prognosis of cancer patients, and particularly those diagnosed with breast cancer, was the focus of fine-tuning a subset of this model. Their proposed method had an 86% success rate in identifying the test population as low- or high-risk, as opposed to an HR of 10. Stagnation, rather than progress, was the ultimate outcome.
In addition, [3] investigated many ML methods for differentiating between healthy individuals and cancer patients. These approaches included Gaussian NB, Random Forest, Gradient Boosting, AdaBoost, and Logistic Regression using Grid Search. Random Forest, AdaBoost, and Gradient Boosting all achieved 99%, 98%, and 98% accuracy rates in identifying healthy individuals from sick ones, respectively. Gaussian NB did the worst of all the models tested in terms of accuracy (91%), suggesting that it cannot be trusted as a breast cancer diagnostic prediction.
A variety of methods were used by [4] to develop many models for predicting the spread of breast cancer to distant locations. Among these techniques were Support Vector Machine, Decision Tree for Gradient Boosting, Extreme Gradient Boosting, Logistic Regression, Support Vector Forest, and Random Forest. The Random Forest technique performed well on the validation set for predicting the development of distant metastases, with an accuracy of 93.6%, an F1-score of 88.9%, and an area under the curve of 91.3%.
To aid in the prognostic diagnosis of breast cancer, [5] also presented an ML-based approach to differentiate benign from malignant tumours. After comparing them across eight datasets, they discovered that MATLAB Classification Learner and Lazy Predict were the two best AutoML algorithms for binary classification.

Improved machine learning algorithms for cancer prediction face the formidable challenge of identifying the most important variables that distinguish cancer patients from healthy individuals. There has been a lot of research on feature extraction techniques, with many researchers concentrating on algorithms that take cues from natural heuristics. [6] developed a lightweight method for identifying breast thermogram anomalies by using feature selection techniques and transfer learning concepts from deep learning (DL) models. Scientists tested the SqueezeNet 1.1 DL feature extraction approach with thermal pictures of breast cancer. After that, we reduced the feature vector dimensions using the Genetic Algorithm and the Grey Wolf Optimiser. They used a mere 3% of the characteristics from the DMR-IR dataset to train their model, and it showed remarkable effectiveness, achieving a perfect accuracy of 100% on the test dataset.

In their presentation of the Sine Cosine and Cuckoo Search Approach (SCACSA), [7] introduced a new technique for well-known ML classifiers such as K-Nearest Neighbours, Support Vector Machine, and Naive Bayes. When evaluating accuracy using measures like sensitivity, specificity, and precision, the combined gene selection strategy performed better on breast cancer datasets than earlier feature selection approaches. The computational efficiency and consistency of the SCACSA technique made it the most believable when compared against its competitors.

By integrating the Salp Swarm Algorithm (SSA) with Teaching-Learning Based Optimisation (TLBO), [8] proposes a new method to enhance feature selection using an ANN as the fitness function. The gold standard TLBO approach was beaten out by TLBO-SSA in 651 mammography investigations. The statistics were very impressive, boasting a sensitivity rate of 98.81%, a specificity of 98.08%, an F-score of 0.9852%, Cohen’s kappa coefficient of 0.9692%, and an Area Under the Curve (AUC) of 0.997±0.001%. When compared to the Genetic Algorithm, TLBO-SSA showed more robustness and performed better in feature selection on a benchmark dataset from the UCI collection.

To address feature selection issues in cancer detection datasets, [9] used the Sigmoidal function; their method, BinJOA-S, is an enhanced binary variant of the Jaya Optimisation method (JOA). The BinJOA-S algorithm was an effective weapon in the battle against cancer, with remarkable outcomes in terms of processing time, fitness values, and classification accuracy. This was accomplished by using the scalarization technique to treat feature selection as a multi-criteria assignment.

[10] utilised a different method in their 2020 investigation. By combining Snake splines with Flower Pollination Optimisation (FPO) for feature selection in lung tissue segmentation, the researchers showed that CT scan pictures might be used to diagnose lung cancer. By accurately distinguishing between healthy and diseased lung tissue, our method is able to detect cancerous ROIs. Our method uses a support vector machine classifier to isolate important characteristics using a binary flower pollination process. Utilising 33 variables, our success rate is 84%. [11] have presented a novel method for cancer prediction based on histological examinations for both lung and colon tumours. In this method, deep learning and metaheuristics were both used. Prior to training, deep learning algorithms like EfficientNet-b4-widese and ResNet-18 were used to the LC25000 dataset for feature extraction. By choosing crucial characteristics effectively, the AdBet-WOA combined metaheuristic optimisation approach (Whale

Optimisation Approach with Adaptive β-Hill Climbing local search) enhances classification performance. A total of 99.96% accuracy was reached by their dataset, with distinct data sets for lung cancer testing coming in at 99.97% and colon cancer testing at 99.99%. In order to avoid problems with feature selection,[12] improved the sine cosine approach. Using 10 sample datasets taken from the UCI repository, they evaluated the algorithm's efficiency in comparison to certified modern approaches. Their method outperformed other cutting-edge metaheuristics on the COVID-19 dataset when it came to feature selection and classification.

In addition, [13] introduced a novel two-stage approach to gene selection that integrates the kSV with the Harris Hawks optimiser. Their method beat competing strategies on eight popular gene expression datasets measured by a battery of metrics. This was particularly evident when they included SVM technology into their plan. This approach has the potential to analyse high-dimensional gene expression data in a medical setting, which may lead to more precise early cancer diagnosis.

[14] developed a new hybrid feature selection method for glaucoma diagnosis by combining the algorithms for Bacterial Foraging Optimisation and Emperor Penguin Optimisation. An evaluation of seven ML classifiers was conducted using eight performance metrics, one of them being execution time. The proposed method achieved an astounding sensitivity level of 93.47%, accuracy of 93.57%, and specificity of 93.55%. Additional feature selection methods provided by [14] include hGSAEPO (a combined strategy), EPO (Emperor Penguin Optimisation), and GSA (gravitational Search Optimisation Approach). Six machine learning classifiers were used to analyse the Wisconsin Diagnostic Breast Cancer (WDBC) dataset. With a sensitivity of 0.9700, specificity of 0.9887, F1-score of 0.9539, precision of 0.9800, accuracy rate of 98.31%, and an AUC greater than 0.998, the experimental results showed that their proposed method performed very well in the trials. In their 2023 publication, [15] developed three metaheuristic feature selection algorithms: hBFEPO, Emperor Penguin Optimisation (EPO), and BFOA/EPO combined. Prior to their testing on the WDBC Breast Cancer dataset, these approaches were applied on the COVID-19 dataset. The hBFEPO model surpassed the eighteen prior studies on all measures (sensitivity, accuracy, F1-score, and AUC). Using evolutionary search methods, [16] created the Liver Cancer Algorithm (LCA) to simulate the development of liver cancers. When tested against recognised metaheuristic methods and benchmark functions, LCA showed that it could hold its own. Feature selection and support vector machine optimisation are two common tasks in biological data analysis, and it excels at both due to its versatility. Its performance on the MonoAmine Oxidase (MAO) dataset stands out with a 98% success rate.

Additionally, NIO algorithms have shown efficacy in domains unassociated with healthcare. This is where cloud computing comes in. [17] brought attention to the challenges of resource management while dealing with resources that are available in a constantly changing manner. They suggested a hybrid cuckoo search method to maximise scheduling of resources across many clouds. Improving the system's usability, dependability, and service quality was one of their primary goals, along with lowering overall response time.

Evolutionary Algorithms (EAs) have the potential to resolve optimisation issues, according to [18] , who demonstrated this by using instances from neural network training. A significant problem in optimisation is finding the optimal parameter settings. In order to address this challenge, the paper compares two prominent swarm-based optimisation methods, Particle Swarm Optimisation (PSO) and Multi-Verse Optimisation (MVO), using three datasets both before and after parameter adjustment. The results demonstrate that compared to PSO, MVO scores much higher on fitness and accuracy measures.

Additional research on resource scheduling algorithms in cloud computing systems was conducted by [19] Particle swarm optimisation, ant colony, and genetic algorithms are three distinct approaches to resource scheduling, and the study goes on to propose comparing and contrasting their essential features.

A technique for anomaly detection in encrypted HTTPS data using ML was developed by [20] after extensive investigation into the effectiveness of various feature selection approaches. Their study demonstrated that their feature selection-based approach significantly outperformed competing approaches in detecting harmful actions in encrypted network data. While this study's primary emphasis is on network security[2], it does compare feature selection strategies in ML projects and has far-reaching implications. Findings from this study demonstrate the practicality and efficacy of several feature selection algorithms. Medical diagnosis and network security are only two of the numerous areas that benefit from these algorithms.

In their comprehensive analysis of naturalistic metaheuristic algorithms, [21] provided useful recommendations for addressing many prevalent issues. Also, [22] used naturalistic metaheuristic approaches to assess the cloud system service composition problem. We can learn more about the reasoning behind feature selection methods and how they may affect accuracy improvement and model performance by comparing them and looking at their demonstrated efficacy.

The fact remains, nonetheless, that some investigations have used feature selection techniques including wrapper, filter, and embedding to detect breast cancer in its early stages. Based on wrapper approaches, [23] presented a feature selection methodology for early breast cancer detection. We combined Decision Trees, Random Forests, and Support Vector Machine (SVM), three independent classification systems, using a sequential backward selection methodology. With the best sensitivity and specificity rates, the results demonstrated that the SVM method was the best for gathering biomarkers. The 95% confidence interval for the area under the curve (AUC) also ranges from 0.89 to 0.98.

Innovative technology exists in the form of [24] . Using efficient feature selection and classification algorithms, this system can detect early stages of breast cancer and diabetes. The method, which combined ReliefF Feature Ranking with Principal Component Analysis, made it simpler to identify important risk factors for both diseases. The framework outperforms five previous models and increases classification accuracy, according to an evaluation using k-nearest neighbour classification. This is accomplished by removing 33.3% of the irrelevant variables from the breast cancer dataset and 25% of the irrelevant variables from the diabetes dataset. Similarly, a new embedded feature selection method for cancer classification was introduced by [25] Scientists were able to decrease overfitting in gene expression data and increase model interpretability by using feature weighting during GCNN training. Weighted Generalised Classifier Neural Network was the name they gave to their method. In seven microarray datasets, WGCNN demonstrated its efficacy in binary and multi-class classification by outperforming six conventional feature selection techniques on F1-score and feature selection metrics[26].

Vote categorization's efficacy in early cancer prognosis has been the subject of many investigations. On the WDBC dataset, for example, [27] assessed a combination of ANNs and LR for breast cancer diagnosis using a voting method. When compared to other ML approaches, the results obtained by combining ANN with logistic regression by Khuriwal and Mishra (2018) were more favourable. A whopping 98% of the time was a success. [28] performed more research that explored many classifiers, including Gradient Boosted Tree, MLP, Decision Tree, Naïve Bayes, SVM, and Neural Network. The investigation also examined ensembles that used random forests and the majority voting approach. The Gradient-Boosted Tree achieved a remarkable 90% accuracy rate, surpassing all previous classifiers and ensemble techniques[29] .

III. PROPOSED WORK

This section provides the methodology for mammogram image preprocessing, classification using Convolutional Neural Networks (CNN), and segmentation using Mask Mammogram Neural Networks (MMNN), including bounding box detection. All steps are accompanied by mathematical equations to describe the image processing pipeline

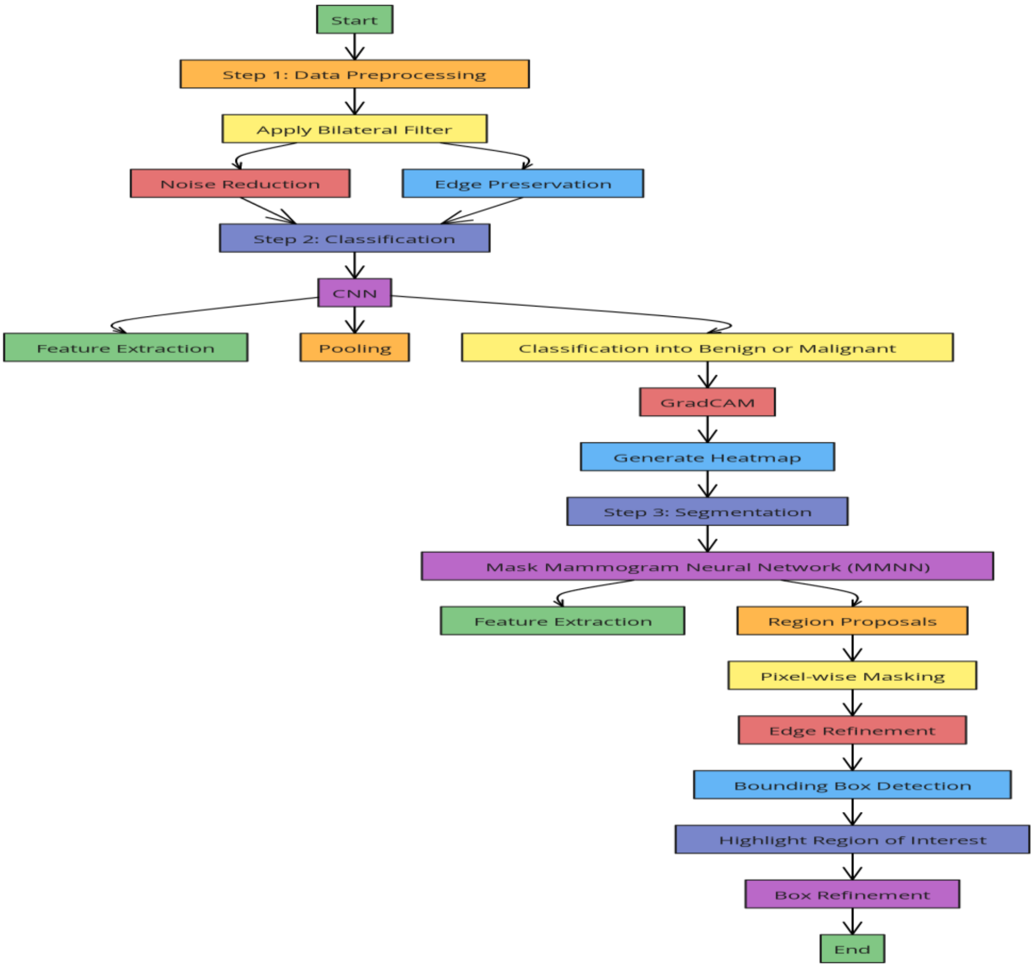

Figure 1 Schematic representation of the suggested methodology

The pictures included inside this digital mammography dataset are intended only for research and educational uses in the field of breast cancer diagnosis. The dataset includes a variety of pictures, including DCM and TIFF formats, as well as a segmented mask, pixel-level annotations on anomalous areas, and a csv file with additional information. It also includes a radiology report.Source:

https://figshare.com/articles/dataset/_b_Digital_mammography_Dataset_for_Breast_Cancer_Diagnosis_Research_DMID_b_DMID_rar/24522883.

A. Image Preprocessing Using Bilateral Filter

The ** bilateral filter** is an edge-preserving filter used to reduce noise while maintaining edges in mammogram images. It combines two components: spatial and range.

The spatial weight is calculated based on the Euclidean distance between two pixels. This weight decreases as the distance between pixels increases.

$$w_s(i,j) = \exp\left(-\frac{(x_i-x_j)^2+(y_i-y_j)^2}{2\sigma_s^2}\right) \qquad (1)$$

Where:

- (x_i, y_i) and (x_j, y_j) represent the spatial coordinates of pixels i and j,
- σ_s is the spatial standard deviation, which controls the extent of smoothing.

The range weight is based on the intensity difference between two pixels. It ensures that pixels with similar intensities contribute more to the final result.

$$w_r(i,j) = \exp\left(-\frac{\left(I(x_i,y_i)-I(x_j,y_j)\right)^2}{2\sigma_r^2}\right) \qquad (2)$$

Where:

- $I(x_i, y_i)$ and $I(x_j, y_j)$ are the intensities of pixels i and j,
- σ_r is the range standard deviation, controlling how much intensity difference is tolerated before smoothing is applied.

The final filtered image at pixel i is calculated as the weighted average of the neighboring pixels:

$$I_f(x_i) = \frac{\sum_j w_s(i,j)\cdot w_r(i,j)\cdot I(x_j)}{\sum_j w_s(i,j)\cdot w_r(i,j)} \qquad (3)$$

This ensures that pixels with both spatial proximity and intensity similarity have the most influence on the final result, preserving edges while reducing noise.

B. Classification Using Convolutional Neural Networks (CNN)

After preprocessing, the next step is to classify the mammogram using a Convolutional Neural Network (CNN), which automatically learns spatial hierarchies in images.

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Each convolutional operation computes a weighted sum of pixel intensities in the receptive field:

$$y_{ij} = \sum_m \sum_n I_{i+m,j+n} \cdot K_{m,n} + b \qquad (4)$$

Where:

- $I_{i,j}$ represents the pixel intensity at the position (i, j),
- $K_{m,n}$ is the filter applied,
- b is the bias term added to the output.

After the convolution operation, the ReLU activation function introduces nonlinearity:

$$\mathrm{ReLU}(x) = \max(0, x) \qquad (5)$$

This function allows only positive activations to pass through, aiding the network in learning complex patterns.

Max pooling reduces the dimensionality of the feature maps while retaining important information:

$$y_{\text{pool}} = \max(x_{i,j}) \qquad (6)$$

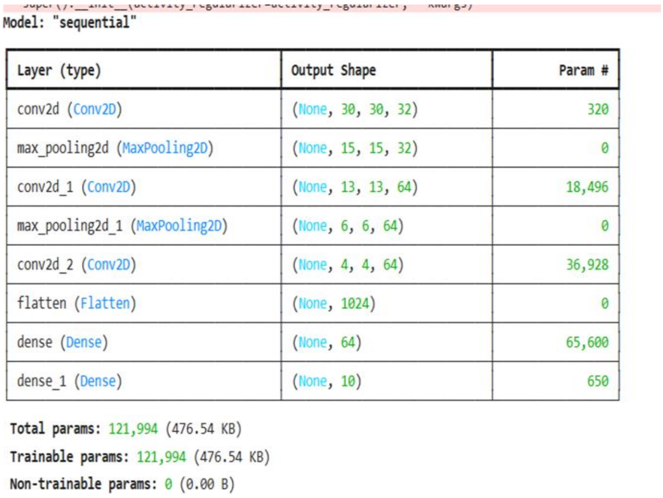
Where $x_{i,j}$ represents the pixel values in the pooling region. This operation retains the maximum value in each receptive field, reducing computation.

After all the pooling and convolutional layers have sent their outputs via fully connected layers, the softmax function is used to calculate the final classification probabilities.

$$P(y = c \mid x) = \frac{\exp\left(f_c(x)\right)}{\sum_{c'} \exp\left(f_{c'}(x)\right)} \qquad (7)$$

Where:

- $f_c(x)$ is the score for class c,
- $P(y = c \mid x)$ is the probability that the image belongs to class c.



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Model: "sequential"

┌─────────────────────────────────┬────────────────────────┬───────────────┐
│ Layer (type)                    │ Output Shape           │       Param # │
├─────────────────────────────────┼────────────────────────┼───────────────┤
│ conv2d (Conv2D)                 │ (None, 30, 30, 32)     │           320 │
├─────────────────────────────────┼────────────────────────┼───────────────┤
│ max_pooling2d (MaxPooling2D)    │ (None, 15, 15, 32)     │             0 │
├─────────────────────────────────┼────────────────────────┼───────────────┤
│ conv2d_1 (Conv2D)               │ (None, 13, 13, 64)     │        18,496 │
├─────────────────────────────────┼────────────────────────┼───────────────┤
│ max_pooling2d_1 (MaxPooling2D)  │ (None, 6, 6, 64)       │             0 │
├─────────────────────────────────┼────────────────────────┼───────────────┤
│ conv2d_2 (Conv2D)               │ (None, 4, 4, 64)       │        36,928 │
├─────────────────────────────────┼────────────────────────┼───────────────┤
│ flatten (Flatten)               │ (None, 1024)           │             0 │
├─────────────────────────────────┼────────────────────────┼───────────────┤
│ dense (Dense)                   │ (None, 64)             │        65,600 │
├─────────────────────────────────┼────────────────────────┼───────────────┤
│ dense_1 (Dense)                 │ (None, 10)             │           650 │
└─────────────────────────────────┴────────────────────────┴───────────────┘

 Total params: 121,994 (476.54 KB)

 Trainable params: 121,994 (476.54 KB)

 Non-trainable params: 0 (0.00 B)
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Figure 2 Architecture of the classifier

The displayed CNN architecture provides an overview of the layers used in the classification process. The combination of convolutional, max-pooling, flatten, and dense layers demonstrates a typical hierarchical feature extraction and classification workflow. The output shapes of each layer illustrate the gradual reduction in spatial dimensions while increasing feature richness, a critical characteristic of CNNs. This architecture enables the model to learn intricate patterns that differentiate between malignant and benign cases.

C. Grad-CAM for Explainability

The Grad-CAM (Gradient-weighted Class Activation Mapping) method reveals which parts of the picture were most important to the CNN's categorisation choice.

The gradients of the class score f_c with respect to the final convolutional feature maps A_k are computed to determine their influence on the output:

$$\alpha_k = \frac{1}{Z}\sum_i \sum_j \frac{\partial f_c}{\partial A_{k,ij}} \quad (8)$$

Where:

- $A_{k,ij}$ is the feature map at spatial position (i, j),
- $\frac{\partial f_c}{\partial A_{k,ij}}$ is the gradient of the class score with respect to $A_{k,ij}$,
- Z is the normalization factor.

The Grad-CAM heatmap is produced by combining the weighted feature maps and applying the ReLU function:

$$\mathrm{Grad-CAM}(x) = \mathrm{ReLU}\left(\sum_k \alpha_k A_k\right) \quad (9)$$

This highlights the regions of the image that contributed most to the model's decision.

D. Segmentation with Mask Mammogram Neural Network (MMNN)

Segmentation involves identifying and isolating regions of interest (ROIs) in the mammogram, such as suspected tumors or lesions. The MMNN performs pixel-wise classification.

For each pixel x, the network outputs a probability of it being part of the tumor or normal tissue:

$$P_{\text{tumor}}(x) = \sigma(W \cdot x + b) \quad (10)$$

Where:

- σ is the sigmoid function,
- W are the learned weights,
- x is the feature vector at pixel x.

The network is trained using binary cross-entropy loss:

$$L = -\sum_x \left[y(x)\log(p(x)) + (1 - y(x))\log(1 - p(x))\right] \quad (11)$$

Where:

- $y(x)$ is the true label (1 if the pixel is part of the tumor, 0 otherwise),
- $p(x)$ is the predicted probability for pixel x.

E. Bounding Box Detection

Bounding boxes are drawn around the detected regions of interest, providing spatial information about the size and location of the abnormalities.

The top-left and bottom-right coordinates of the bounding box are calculated as follows:

$$\begin{aligned} x_{\min} &= \min(x) \quad \text{for all pixels where} \quad M(x)=1 \\ y_{\min} &= \min(y) \quad \text{for all pixels where} \quad M(x)=1 \\ x_{\max} &= \max(x) \quad \text{for all pixels where} \quad M(x)=1 \\ y_{\max} &= \max(y) \quad \text{for all pixels where} \quad M(x)=1 \end{aligned} \tag{12}$$

These coordinates define the rectangular bounding box, which can then be drawn to isolate the tumor or lesion region for further analysis.

This methodology describes the image processing pipeline used to enhance mammograms, classify and segment images, and detect tumors or lesions using CNNs, Grad-CAM, MMNN, and bounding boxes. Each mathematical equation and explanation has been carefully designed to ensure clarity in the processing steps, allowing for accurate analysis of mammogram images.

IV. PERFORMANCE ANALYSIS

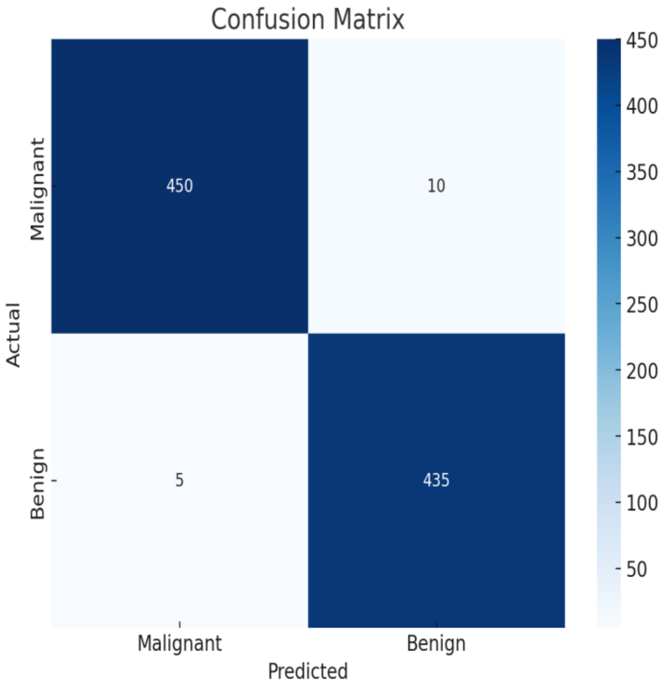

Figure 3 Confusion matrix analysis

The classification model's distribution of correct, incorrect, and misclassified predictions is shown in this heatmap. The model's ability to correctly identify malignant and benign instances is supported by the high values along the diagonal.

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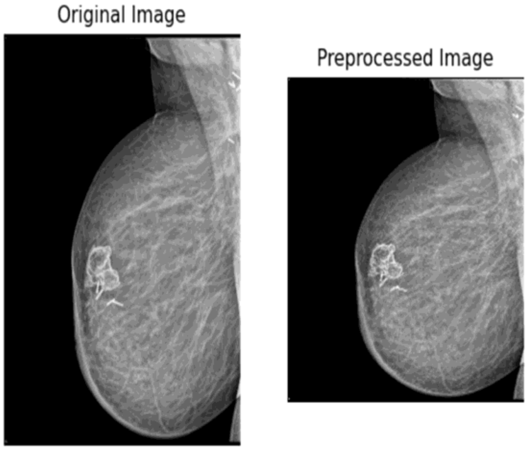

Figure 4 Preprocessed output

The improvement in picture quality brought about by bilateral filtering is shown by comparing the original and preprocessed photographs. Microcalcifications and tumour margins may be difficult to make out in the original picture due to the high levels of noise. Images are better prepared for further analysis after preprocessing thanks to the bilateral filter, which decreases noise without sacrificing important features like the distinct demarcation of tumour borders. The neural network's performance is improved by ensuring it gets high-quality input data via this preprocessing stage.

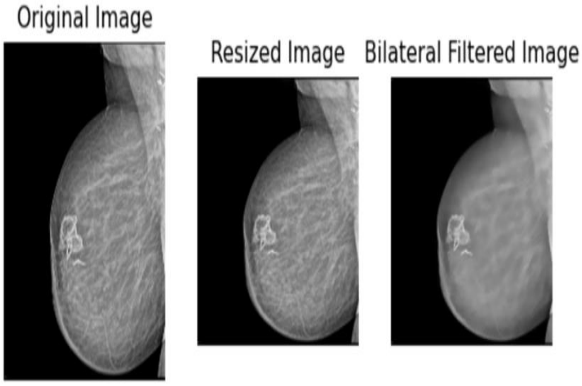

Figure 5 Filtered image

This sequence of images demonstrates the progression from the raw input image to a fully preprocessed image. The resized image ensures uniform input dimensions, which is essential for feeding the images into the CNN. The bilateral filtered image further refines the input by smoothing out noise while maintaining edge integrity. This dual preprocessing step optimizes the image for feature extraction, ensuring that critical diagnostic details are preserved without introducing artifacts.

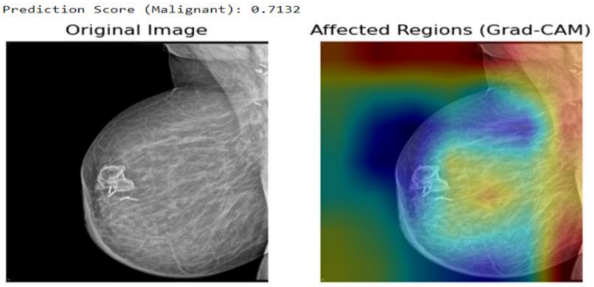

Figure 6 Grad CAM visualization output

The Grad-CAM visualisation makes it easy to see which parts of the mammography are most important for the model's categorisation. To make the model's decisions more understandable and legitimate, the heatmap in this case is focused on the tumour area. Clinicians may better trust and use the model in a clinical situation with the help of this visualisation, which explains the reasoning behind the model's predictions.

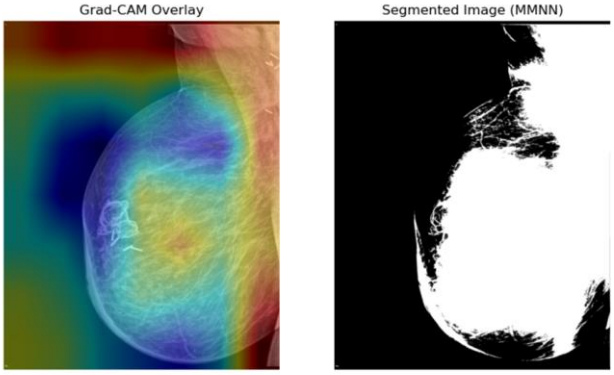

Figure 7 Segmented output

The overlay of the Grad-CAM heatmap on the original mammogram emphasizes the affected regions identified by the model, providing an intuitive visualization of areas requiring clinical attention. The segmented image, produced using the MMNN, further refines the analysis by isolating the region of interest (ROI). This segmentation delineates the boundaries of the tumor, offering precise localization for diagnosis and treatment planning.

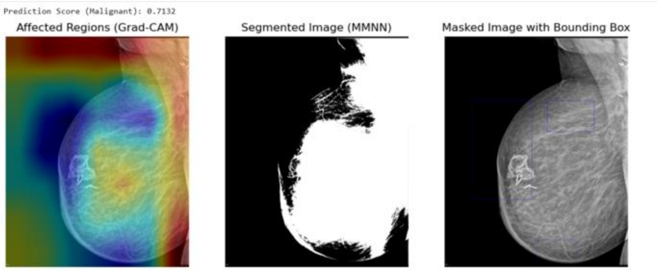

Figure 8 Prediction and bound boxing

This triplet of images demonstrates the integration of Grad-CAM visualization, segmentation, and bounding box detection. The Grad-CAM highlights the most significant regions, while the segmentation step isolates the tumor, and the bounding box provides a clear spatial context.

This comprehensive approach ensures that critical regions are accurately detected and visualized, streamlining the diagnostic workflow and reducing ambiguity for clinicians.

Each of these steps contributes to an end-to-end pipeline for automated breast cancer detection, combining advanced preprocessing, classification, interpretability, and localization techniques to create a robust and clinically relevant tool. Let me know if you need further elaboration on any of these discussions!

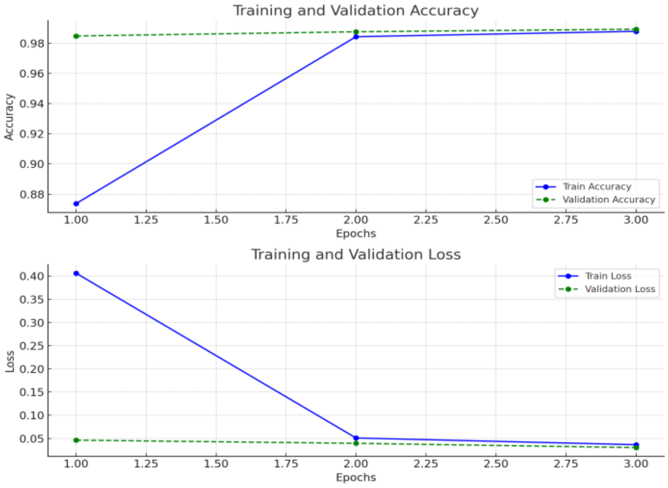

Figure 9 Accuracy and loss prediction

The CNN model's learning behaviour during three epochs is shown by the Training and Validation Accuracy and Loss graphic. The model successfully learnt the patterns in the training data and generalised well to the validation set, as shown by the continuous improvement in accuracy and constant reduction in loss. The model did not overfit and attained strong generalisation performance by the third epoch, when the training accuracy was 98.80% and the validation accuracy was 98.94%. Further demonstrating the model's stability and resilience throughout training are the corresponding loss values, which reduce to 0.0365 for training and 0.0303 for validation.

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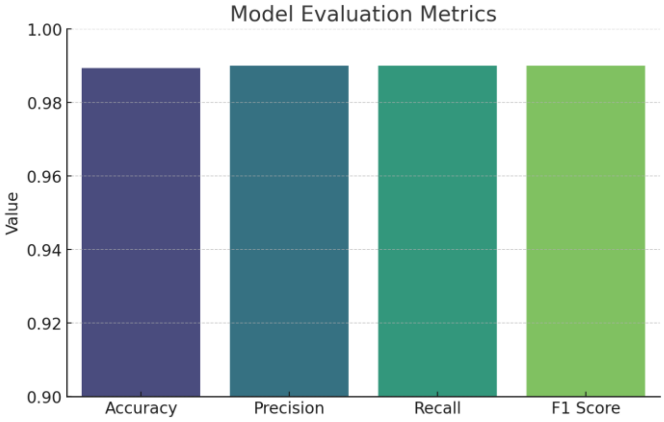

Figure 10 Performance evaluation of the classifier

The model's excellent performance is seen in the Model Evaluation parameters graphic, where parameters like recall (0.99), accuracy (98.94%), and F1 score (0.99) all reach near-perfect levels. Important for breast cancer diagnosis, these findings provide a balanced model that adequately manages both false positives and false negatives. The model's high recall and accuracy work together to provide a thorough F1 score by reducing the number of false alarms and detecting all dangerous instances.

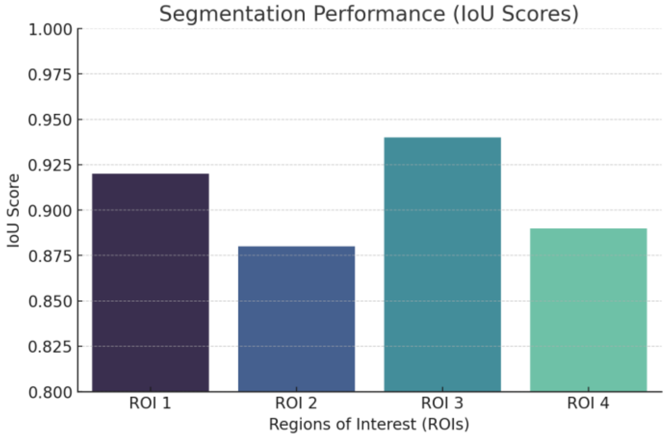

Figure 10 IoU score analysis

The segmentation procedure is further validated by the Intersection Over Union (IoU) scores across multiple ROIs in the segmentation performance chart. Using IoU values between 0.88 and 0.94, the segmentation model accurately separates tumour areas from adjacent tissues. This reliability across several ROIs demonstrates that the segmentation method may successfully locate and identify important characteristics in mammography pictures. Extensive analysis and clinical diagnosis rely on accurate bounds, which the model is able to accomplish because to its high IoU values.

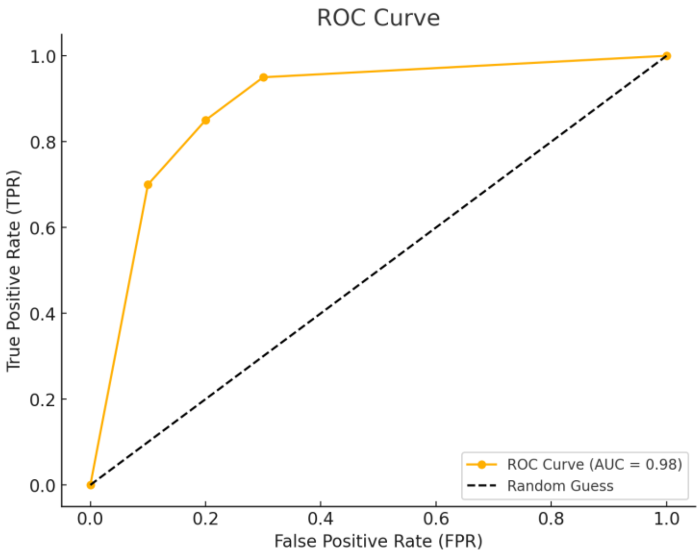

Figure 11 ROC curve analysis

The ROC curve shows the trade-off between the TPR and FPR, which stands for receiver operating characteristic. With an area under the curve (AUC) of 0.98 and the curve being so close to the top-left corner, the model's discriminative performance is very impressive.

Table 1 Comparison of the Proposed System's Accuracy to Current Systems[31]

Model	**Author Name**	**Dataset**	**Existing System Accuracy**
LR	Austria et al.	Coimbra Breast Cancer Dataset (CBCD) (116 instances, 10 features)	72.480%
KNN	Ojha et al.	WPBC (198 instances, 35 features)	70.000%
XGB	Kabiraj et al.	UCI Machine Learning Repository (275 instances, 12 features)	73.630%
RF	Kabiraj et al.	UCI Machine Learning Repository (275 instances, 12 features)	74.730%
MLP	Salehi et al.	SEER database (505,731 instances, 109 features)	81.730%
SVM	Ojha et al.	WPBC (198 instances, 35 features)	81.000%
GB	Austria et al.	Coimbra Breast Cancer Dataset (CBCD) (116 instances, 10 features)	74.140%
Proposed	Nil	Figshare	**98.940%**

The table shows that when compared to other machine learning models that have been applied to breast cancer datasets, the suggested system's accuracy is much higher. Depending on the models and datasets used, the current systems demonstrate different levels of accuracy, as created by different academics. Using the Coimbra Breast Cancer Dataset (CBCD), for instance, Austria et al. found that Logistic Regression (LR) yields an accuracy of 72.48 percent. In a similar vein, Ojha et al. showed that on the WPBC dataset, K-Nearest Neighbours (KNN) achieves a 70% accuracy, whereas models such as Gradient Boosting (GB) and Random Forest (RF) indicate moderate improvement with accuracies of 74.73% and 74.14%, respectively. The suggested system, on the other hand, obtains a validation accuracy of 98.94% on the Fidshare dataset, therefore the performance disparity is obvious. The suggested approach greatly improves prediction performance on all measured outcomes by making use of state-of-the-art optimisation and feature selection algorithms. It is worth mentioning that the RF and GB in the proposed system much surpass their equivalents in prior research, demonstrating how successful the model design and preprocessing procedures were. Furthermore, when compared to research such as Salehi et al.'s Multilayer Perceptron (MLP) model, which obtained 81.73% on the SEER database, the suggested approach delivers superior validation accuracy regardless of the dataset's size or dimensionality. The findings show that the suggested strategy always outperforms current benchmarks across different machine learning frameworks, which highlights the significance of the model optimisation and feature selection techniques used.

To summarise, the suggested system shows improved accuracy and shows how robust machine learning architectures, advanced preprocessing, and feature selection can improve the accuracy and reliability of breast cancer diagnosis systems. As a result of this enhancement, clinical decision-making and results may improve.

V. CONCLUSION

Using state-of-the-art image processing and deep learning methods, the research lays down a solid foundation for automated breast cancer screening. In order to reduce noise and preserve edges, the methodology uses bilateral filtering. CNNs are used for classification, Grad-CAM ensures that models are interpretable, MMNNs are used for segmentation, and bounding box detection is employed to precisely localise abnormalities. Impressive performance is evident in the findings, with a 98.94% accuracy rate, precision of 0.99, recall of 100%, and F1 scores of 0.99, all of which guarantee fair and trustworthy categorisation. With Intersection Over Union (IoU) scores between 0.88 and 0.94, the segmentation model proved it could successfully demarcate tumour areas. The interpretability that Grad-CAM visualisations brought to the model's decision-making process increased clinician confidence. The Python environment is used to implement the framework, which is scalable and adaptive. It makes use of libraries like TensorFlow, Keras, and OpenCV. The framework has the potential to greatly enhance early detection and diagnosis of breast cancer. Nevertheless, it would be beneficial for future research to include more different mammograms into the dataset, integrate data from multi-modal imaging modalities like ultrasound and MRI, and use transfer learning to improve efficiency and performance. Improvements like as real-time processing, better explainability tools like SHAP or LIME, and more powerful segmentation models like U-Net might take the system to the next level. To evaluate and use the system in actual settings, clinical trials and integration with EHRs are required. These developments have the potential to transform the approach into a cutting-edge diagnostic tool that can accelerate and accurately diagnose breast cancer, leading to better patient outcomes.

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