RESEARCH PAPER

A Hybrid Deep Learning Approach Integrating Modified Vgg Features With Xgboost For Early Breast Cancer Diagnosis

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ABSTRACT
Early detection of breast cancer remains a major challenge due to subtle radiological variations and limited labeled medical data. This work presents an enhanced breast cancer classification model using hybrid deep learning framework that integrates modified VGG based feature extraction with an XGBoost classifier to improve diagnostic performance. The VGG architecture is enhanced through batch normalization, reduced filter redundancy, and dropout regularization to improve feature generalization. The modified VGG network is enhanced to capture discriminative spatial and textural patterns from mammographic images.These extracted features are then classified using XGBoost, a powerful gradient boosting algorithm, which enhances model accuracy by effectively handling complex patterns and variations in the data to improve classification robustness and mitigate overfitting. Extensive experiments on benchmark breast imaging datasets demonstrate that the proposed hybrid model outperforms conventional machine learning approaches. Performance metrics such as accuracy, F1 score, sensitivity, specificity, and AUC show consistent improvements, confirming the effectiveness of integrating modified VGG features with the XGBoost classifier. The findings indicate that combining deep spatial representations with gradient boosted decision trees provides an effective strategy for early breast cancer diagnosis.
Keywords: Breast cancer, Extreme Gradient Boosting, Visual Geometry Group architecture,
Contrast Limited Adaptive Histogram Equalization, Deep learning
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INTRODUCTION

Breast cancer results from the abnormal proliferation of cells in breast tissue, leading to the formation of tumors that spread to other parts of the body. Common symptoms include breast thickening or the presence of lumps which can be identified by, routine screening procedures such as mammography to facilitate early detection. Breast cancer most often begins in the cells that line the ducts, which carry milk from the glands to the nipple. This type is called **ductal carcinoma**. It can also start in the cells of the lobules, the glands that produce milk.This type of cancer is called lobular carcinoma [1].

Nearly 230,000 new cases of breast cancer are reported annually by the National Cancer Registry Programme (NCRP), and this number is expected to rise significantly in the coming years. Contributing factors include an increase in cases among younger women, limited awareness of screening methods, and lifestyle factors such as pollution, obesity, and the use of alcohol and tobacco, all of which worsen the burden of the disease. The earliest indication of breast cancer is often an abnormality detected on a mammogram, before it can be felt by a healthcare provider. As the disease progresses, physical signs may become apparent, including a breast lump or tenderness, skin irritation or dimpling, nipple discharge or pain, and changes such as scaliness, ulceration, or retraction. Breast pain alone is typically not an initial sign of breast cancer and is more commonly associated with benign conditions.Breast cancer is diagnosed through a combination of tests and procedures, following an abnormal finding on a physical examination or a screening test such as mammography [2].

The diagnostic process often employs the triple test strategy, which consists of a clinical breast examination, multiple imaging studies, and a confirmatory biopsy. Initially, a healthcare practitioner obtains a detailed medical history and performs a physical examination to detect any palpable lumps or skin abnormalities. If clinical concerns arise, imaging studies are conducted to further evaluate the findings. These include **diagnostic mammography** for

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detailed X-ray visualization, **breast ultrasound** to differentiate between solid masses and fluid filled cysts, and in certain cases, **breast MRI** for patients with dense breast tissue or those at high risk.
A biopsy is the only certain way to confirm malignancy, in volving the collection and examination of a tissue sample by a pathologist. Following a positive diagnosis, the tissue specimen undergoes additional laboratory testing to determine specific characteristics, such as **HER2** (Human Epidermal Growth Factor Receptor and **hormone receptor status (ER/PR),** which are important for guiding treatment decisions and assessing the potential effectiveness of targeted therapies.
Mammography remains the most effective technique for the early detection of breast cancer. Mammographic images have the drawback of being highly complex. Thus, tumor detection by radiologists can be enhanced through image processing and feature extraction techniques. By extracting features from suspicious regions in mammographic images, clinicians can identify tumors in real time, thereby expediting diagnosis and facilitating timely treatment. Since breast cancer represents a group of related diseases rather than a single disorder, its detection can be challenging.There are numerous factors that contribute to the challenges of automatic breast cancer detection. The region of interest (ROI) may be extremely small, increasing the risk of misidentification. Mammograms often contain microcalcifications of varying sizes, shapes, and distributions, making sample matching nearly impossible. In some cases, the ROI exhibits low contrast, further complicating detection.
Moreover, dense breast tissue and skin thickening, particularly common in younger women can obscure suspicious regions, rendering them almost invisible. Dense tissue is often mistaken for calcifications, leading to a high rate of false positive detections. Microcalcifications often appear as white pixels on mammograms, making them difficult to detect in dense breast tissue, which is associated with a higher rate of false positive results. Masses and microcalcifications often indicate potential malignancy. Detecting masses is more challenging than identifying microcalcifications, as masses often exhibit low contrast and display a wide range of sizes and shapes. In breast cancer diagnosis, the use of hierarchical or grouping frameworks in classification and pattern recognition systems is rapidly expanding. A key component of these systems is the evaluation process and machine learning based decision making for medical diagnosis. Intelligent classification algorithms enable clinicians to identify cancer signs that could otherwise remain undetected.
Recent advancements in research methodologies and innovative analytical techniques have significantly improved the identification of cancerous cells and the development of effective treatment strategies for cancer patients. Among these, Clustered Regularly Interspaced Short Palindromic Repeats (CRISPR) technology has emerged as a valuable tool. CRISPR is a precise and powerful gene editing system that enables researchers to modify genetic material with high efficiency. Through genetic engineering, scientists can now screen and evaluate drugs more effectively to specifically target cancer cells [3]. When imaging or screening tests suggest a potential malignancy, a biopsy is performed to obtain a sample of abnormal tissue. This sample is examined microscopically by a pathologist, serving as the standard for cancer diagnosis and for determining the specific type and grade of the cancer.
Breast cancer detection methods primarily involve imaging tests, physical examinations and in some cases, genetic or molecular testing. The goal is to detect cancer at an early stage when it is most treatable. Among the primary screening methods, mammography is the most common and effective test for women at average risk. It uses low dose X-rays to identify changes in breast tissue that are too small to be felt during a physical examination. Digital breast tomosynthesis (3D mammography) captures images from multiple angles to create a three dimensional view of the breast, which helps reduce false positives and is especially beneficial for women with dense breast tissue. In breast magnetic resonance imaging (MRI), magnets and radio waves are used to produce detailed images [4]. It is a highly sensitive test, typically reserved for women at high risk such as those with breast cancer gene mutations or a strong family history and is used in addition to mammography. Considerable research has been conducted in the field of image processing for cancer detection but still, there remains a gap in achieving the highest possible accuracy.

This work proposes a hybrid diagnostic model that combines the robust classification capabilities of Extreme Gradient Boosting (XGBoost) with the deep feature extraction strengths of a modified Visual Geometry Group (VGG) architecture. The approach aims to enhance breast cancer detection accuracy, providing radiologists with a reliable and efficient tool for faster and more precise clinical evaluations.
The core contributions of this paper include:
An innovative hybrid framework for early breast cancer diagnosis that combines the Extreme Gradient Boosting (XGBoost) classifier with deep feature extraction using a modified VGG architecture.
A modified VGG network designed for enhanced feature extraction, capable of capturing high level discriminative features from breast imaging data and improving the quality of inputs for classification.
Robust and accurate classification achieved through the integration of VGG features with XGBoost, resulting in enhanced performance, reduced misdiagnosis, and increased reliability for clinical applications.

RELATED WORKS

A novel hybrid approach for breast cancer classification is proposed in [5] which integrates feature extraction techniques with the Antlion Optimization (ALO) algorithm. Furthermore, a new preprocessing technique is introduced to efficiently eliminate noise from mammography images by combining a Gaussian filter with Residual Pixel Removal (RPR). In [6], a multiscale cascaded convolution model for breast cancer classification is introduced. It facilitates the extraction of varied spatial semantic elements. In addition, a different residual attention based

network with a dual decoder is proposed for segmentation. The attention mechanism selectively processes parts of the mammography images, while the dual decoding technique captures the diverse spatial properties of the encoder pattern.

In [7], a deep learning model for breast cancer detection based on granular computing is proposed and evaluated using datasets of breast histopathology images. The proposed framework integrates granular computation, activation functions with learnable parameters, and an attention mechanism into the GoogleNet and ResNet architectures, in addition to several other architectural enhancements. Granular computing facilitates the extraction and emphasis of key image features prior to the training phase, thereby improving feature representation. Consequently, the model requires fewer training images compared to conventional approaches that do not employ granularity. In [8], a computer aided diagnostic (CAD) system for tumor identification is investigated using an image fusion technique combined with various image content representations and ensemble convolutional neural network (CNN) models. To enhance tumor feature representation and improve the diagnostic performance of the CAD system, a three channel fused image is generated from multiple input images.

In [9], a patch based deep learning approach using a Deep Belief Network (DBN) is proposed to identify and classify breast cancer in histopathological images. The network automatically extracts features from image patches, which are then classified using logistic regression. The patch based deep learning model receives the extracted features as input and outputs a probability matrix representing the predicted class. The proposed model demonstrated high accuracy when trained and tested on a histopathology image dataset that includes images from four distinct data cohorts. The analysis of breast cancer research in [10] demonstrated that feature selection techniques, when integrated with deep learning, can be employed to consolidate data from diverse sources for the early detection of breast cancer. It was further observed that predictive models must be evaluated using statistically robust measures to enable medical recommendation systems to accurately identify erroneous omission rates.

In [11], three state of the art transfer learning models, AlexNet, ResNet, and MobileNetV2 are integrated to develop an automated breast cancer detection system. System efficiency is enhanced through the use of an inverted residual bottleneck structure, depth wise separable convolutions, and residual learning. The framework addresses both the detection of abnormalities and the identification of malignancies. Output images are classified into three categories: normal, benign, or malignant, based on a three class classification approach.

In [12], various aspects of deep learning applications in breast cancer diagnosis were investigated, including algorithm types, analytical techniques, experimental designs, MRI image modalities, ground truth references, sample sizes, distributions of benign and malignant lesions, and performance metrics. The study highlights the challenges associated with the widespread adoption of these techniques in clinical practice and identifies potential directions for future research. Overall, the existing literature on deep learning based breast cancer diagnosis using magnetic resonance imaging (MRI) was comprehensively reviewed, providing valuable insights into current advancements and persisting limitations.

According to the research analysis in [13-14], a screening procedure that employed artificial intelligence (AI) as detection support in mammography screening, and used AI to triage screening examinations for single or double reading, resulted in a significant 29% increase in cancer detection compared to standard double reading without AI. This improvement was achieved with a similar false positive rate and a substantial reduction in the screen reading workload. The majority of the additional detections were small, invasive, lymph node negative tumors. The types and stages of the detected malignancies, as well as early screening performance metrics, provide early indications of the potential clinical impact of AI supported screening. When AI supported screening was implemented instead of standard double reading, more invasive tumors of the nonluminal molecular subtype, including triple negative malignancies, were identified.

In contrast to the existing works, the suggested hybrid deep learning approach divides the two stages using an XGBoost classifier for final decision making and a modified VGG network for deep feature extraction. A modified VGG network that improves feature selection and decreases redundancy in deep layers is one of the benefits of employing a hybrid model. The proposed XGBoost classifier uses parallelized boosting to facilitate quicker training, regularization to prevent overfitting, and handling of intricate feature interactions. The modified VGG architecture is designed to detect small and specific patterns, like aberrant tissue architectures and microcalcifications linked to breast cancer. In the proposed framework, multiple significant feature representations extracted from the Modified VGG network are integrated through feature level fusion prior to classification by the XGBoost model.

MATERIALS AND METHODS

This section presents the detailed architecture and workflow of the proposed hybrid deep learning approach, which integrates a modified VGG based feature extraction with an XGBoost classifier for efficient and accurate early breast cancer diagnosis. The framework combines the feature learning capability of deep convolutional neural networks (CNNs) with the robust decision making power of ensemble learning, thereby enhancing the diagnostic accuracy and interpretability of breast cancer detection systems.

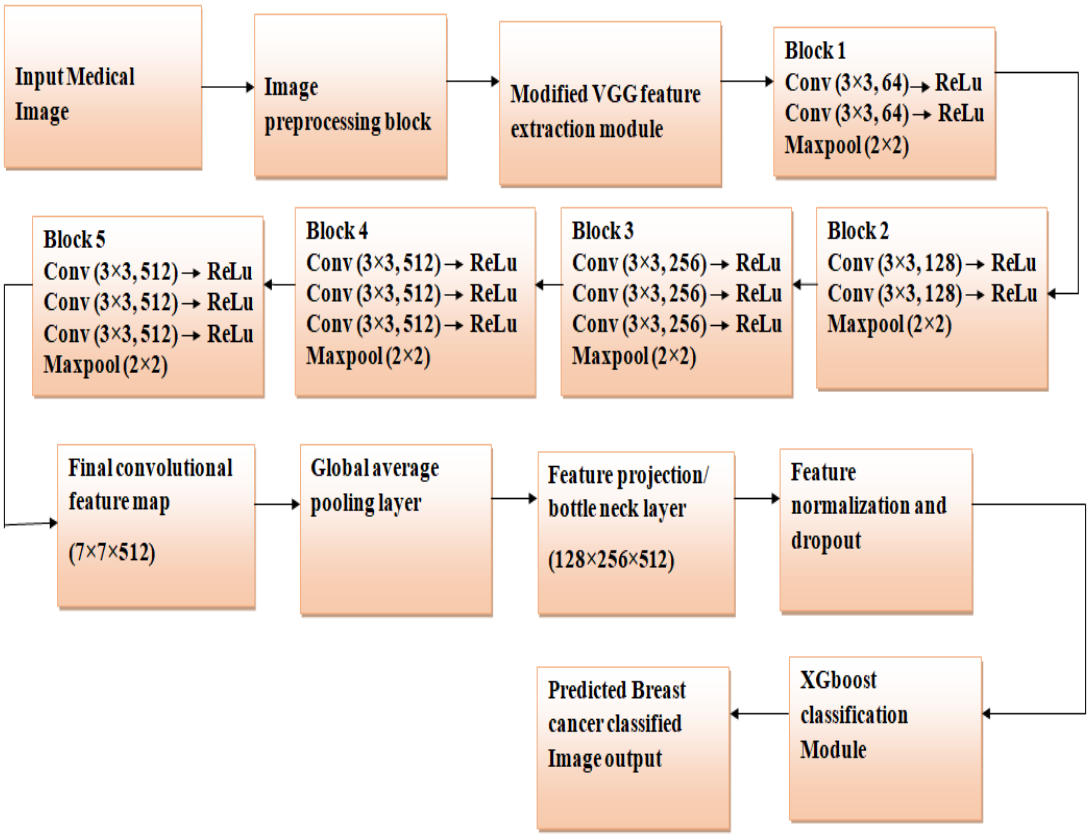

Figure.1. Block Diagram of the proposed work

The proposed system in Figure.1 adopts a two stage hybrid architecture comprising feature extraction and classification modules. In the feature extraction stage, a modified VGG network is employed to derive high dimensional, multiscale feature representations from mammographic images. In the classification stage, the XGBoost algorithm is utilized to discriminate the fused deep features into benign and malignant categories. By decoupling the feature extraction and classification processes, the proposed framework enhances flexibility, generalization capability, and robustness, particularly when addressing the challenges associated with imbalanced medical imaging datasets.

The Curated Breast Imaging Subset of the Digital Database for Screening Mammography (CBIS-DDSM) was used to evaluate the proposed work. This is a standardized dataset widely utilized for research in computer aided breast cancer detection. The dataset comprises 891 mass cases and 753 calcification cases, categorized according to the type of abnormality present, with a total of approximately 10,239 images. The sample images from the data set are shown in Figure 2. Each mammographic study includes both the Mediolateral Oblique (MLO) and Craniocaudal (CC) views for each breast. To ensure balanced class representation and reliable performance evaluation of the proposed hybrid architecture, the dataset was preprocessed and divided into training, validation, and testing subsets. The dataset was split into training and testing sets, comprising 70% and 30% of the data, respectively.An image enhancement method called Contrast Limited Adaptive Histogram Equalization (CLAHE) enhances local contrast while amplifying noise, which makes it ideal for detecting breast cancer.

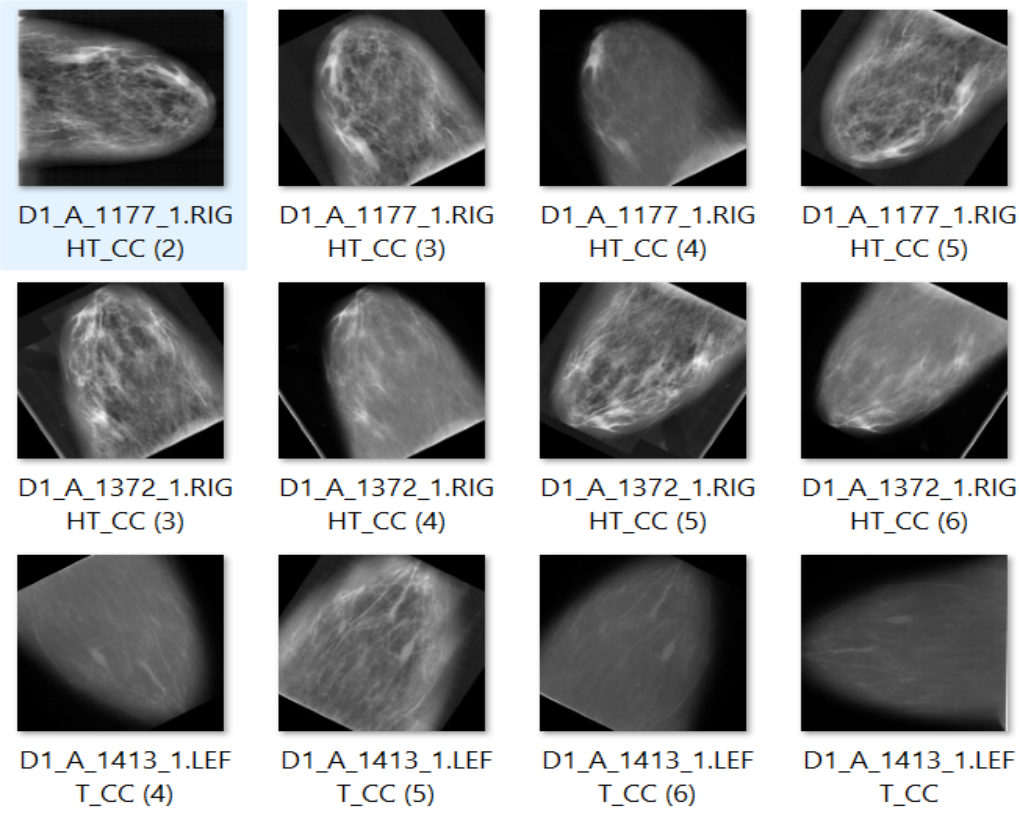

Figure 2: Sample images from the Data set

3.1 CONTRAST LIMITED ADAPTIVE HISTOGRAM EQUALIZATION

Contrast Limited Adaptive Histogram Equalization (CLAHE), an image enhancement technique, is ideal for detecting breast cancer since it intensifies noise while enhancing local contrast [15]. The input image I(x, y) is divided into nonoverlapping rectangular sub regions known as tiles in the CLAHE algorithm [16-17]. For every tile, a histogram value is calculated. The histogram $h_T(i)$ for tile T represents the frequency of each gray level i. $h_T(k)$ = Number of pixels in tile T with intensity level k where I ϵ {0, 1… L-1} and L is the total number of gray level.CLAHE sets a clip limit (T_{clip}) to prevent noise from being amplified excessively in homogeneous areas. The clip limit is expressed as in equation 1

$T_{clip} = N_P/L \times$ clip factor (1)

where, N_P is the total number of pixels in the tile, L is the number of gray levels. The clip factor denotes a user defined parameter whose value is taken as 3 in the proposed work. Adaptive histogram equalization computes local histograms within contextual regions. For an image I(x, y), the histogram of a tile T is defined as in equation 2

$$h_T(k) = \sum_{(x,y)\in T} \begin{cases} 1, & if\ I(x,y) = k \\ 0, & Otherwise \end{cases} \quad (2)$$

where, k is the intensity level. The AHE transformation function for pixel intensity k is given by

$$I_{AHE}(x,y) = \frac{1}{|T|}\sum_{i=0}^{k} h_T(i)\ (L-1) \quad (3)$$

In equation 3, $|T|$ is the number of pixels in the tile .The transformation function for the pixel is given by equation 4 as

$$I_{CLAHE}(x,y) = (L-1)\ \frac{1}{|T|}\sum_{i=0}^{k} h_T(i) \quad (4)$$

To eliminate block artifacts, CLAHE applies bilinear interpolation across adjacent tiles. When a pixel falls within the area shared by four tiles, its final intensity is computed from the tile outputs Q_1, Q_2, Q_3, Q_4. Then the final output is expressed as in equation 5

$$I_{interp}(x,y) = w_1\ Q_{1+} w_2\ Q_{2+} w_3\ Q_{3+} w_4\ Q_4 \quad (5)$$

In equation 5, weights w_i depend on pixel distance from each tile centre.

CLAHE is used in preprocessing to enhance texture features and highlight dense breast tissue for improved segmentation. It also improves the visibility of microcalcifications since sharp gradients and textural signals are essential for deep learning models. CLAHE's enhancement of microtexture characteristics contributes to better overall system performance [14 –15].

3.2 MODIFIED VGG ARCHITECTURE

Breast imaging modalities produce gray scale images. Therefore the first convolutional layer of VGG is modified from 3×3×3 to 3×3×1 allowing direct processing of gray scale inputs. The modified architecture includes reduction in the number of fully connected layers to minimize over fitting [18]. The use of small convolutional kernels (3×3) and adaptive pooling in the proposed work preserve fine details of tumor and tissue structure. Integration of batch $F_{fused} = [F_1 // F_2 // F_3]$

The baseline VGG 19 architecture is proposed in [16].Repeated convolutional blocks with 3×3 stride kernels and one padding are the fundamental features. Following the convolutional blocks are 2x2 max pooling layers. Each convolutional and fully connected layer is followed by a $F_{i,j,m}^{(l)} = \sum_{u=1}^{k}\sum_{v=1}^{k}\sum_{c=1}^{c_{l-1}} w_{u,v,c,m}^{(l)} \cdot F_{i+u-1,j+v-1,c}^{(l-1)} + b_m^{(l)}$

In equation $w^{(l)}$are filter weights and $b_m^{(l)}$ is the bias for the m[th] filter. The ReLU activation function is given in equation 8

$$\widetilde{F^{(l)}} = \max(F^{(l)}, 0) \quad (8)$$

$$g_m = \frac{1}{h\times w}\sum_{i=1}^{n}\sum_{j=1}^{\omega}\widetilde{F^{(L)}}_{i,j,m}$$

where, L is the last convolutional layer.

A dense projection layer is applied after GAP to regulate the dimensionality of the retrieved features. A dropout is added after the projection layer to prevent overfitting on medical

$$\widehat{f_m'} = \frac{f_m' - \mu_m}{\sqrt{\sigma_m^2 + \varepsilon}}$$

and

$$y_m = \gamma_m \widehat{f_m'} + \beta_m$$

In equations 10 and 11 γ_m and β_m are learned scale and shift parameters and ε is a small constant for numerical stability. In the modified VGG architecture dropout rate of 0.3-0.5 is introduced to improve generalization on small medical datasets.

3.3 XGBOOST MODEL CONFIGURATION

Extreme Gradient Boosting (XGBoost) is a scalable, distributed gradient boosting framework engineered to optimize both computational efficiency and predictive performance. XGBoost functions as the final classification

$$\mathcal{L} = \sum_{i=1}^{n} l(y_i, \hat{y}_i) + \sum_{k=1}^{K} \vartheta(f_k)$$

Where $l(y_i, \hat{y}_i)$ is considered as logistic loss for binary cancer classification,$\vartheta(f_k)$ is a complex penalty that controls overfitting.

normalization and dropout layers improve stability and generalization [19–21]. The network learns to extract hierarchical features ranging from low level texture and edge details in the initial layers to high level semantic representation in deeper layers. If I represent the input image then the modified VGG network learns a mapping $F_i = \emptyset_i (I; \Theta)$, where F_i denote the feature map extracted from the i^{th} layer and Θ represent the network learnable parameter. The extracted deep features from several convolutional layers are subjected to feature level fusion. Each feature map F_i is flattened into a one dimensional vector and normalized using z score normalization as part of the fusion process. Equation 6 illustrates how the normalized features from chosen layers are concatenated to create a single feature vector.

(6)

ReLU activation function and three fully connected layers at the output. For each layer l, the input feature map is defined as in equation 7

(7)

A 2×2 max pooling with stride 2 is considered. The features from the intermediary layers are eliminated in the updated VGG architecture. This guarantees the high level representations of the retrieved features. In the global average pooling (GAP) layer the m[th] channel output is given as in equation 9

(9)

imaging datasets. The feature vector $\acute{F}$ is normalized in order to achieve feature standardization.

(10)

(11)

layer, utilizing high level deep representations extracted from the modified VGG feature encoder. XGBoost implements Gradient Boosted Decision Trees (GBDT) using an additive ensemble model [22]. The input feature matrix, where each sample consists of a ddimensional feature vector, is derived from the modified VGG network. XGBoost learns a strong classifier by sequentially constructing K regression trees [23]. XGBoost optimizes a regularized gradient boosting objective consisting of a differentiable loss term and a structural regularizer as in equation 12

(12)

$\vartheta(_{f_k}) = \gamma T + \frac{1}{2}\tau \sum_{j=1}^{T} w_j^2$, where T = number of leaves, w_j = weight of the j[th] leaf, γ = minimum loss reduction factor and τ = L_2 regularization term

This regularization technique is applied to reduce variance, particularly when deep CNN features yield representations that are highly discriminative but also high dimensional. At each boosting iteration t, the model fits a new decision tree using gradient and Hessian based optimization applied to the second order Taylor expansion of the loss function as defined in equation 13

$$\mathcal{L}^{(t)} \approx \sum_{i=1}^{n} \left[g_i \, f_t(x_i) + \frac{1}{2} h_i \, f_t^2(x_i) \right] + \vartheta(_{f_t}) \quad (13)$$

XGBoost computes the best split using gain metric using equation 14

$$\text{Gain} = \frac{1}{2}\left[\frac{{G_L}^2}{H_L + \tau} + \frac{{G_R}^2}{H_R + \tau} - \frac{(G_L + G_R)^2}{H_L + H_R + \tau} \right] \quad (14)$$

Split finding is a fundamental operation in XG Boost which determines how a decision tree partitions the feature space to maximize predictive performance.G_L , G_R and H_L , H_R are the sum of gradients and hessians for the adopted partitions. The representative tuned hyper parameters includes max depth = 6, learning rate = 0.1, subsample = 0.75, feature sampling fraction =0.65, minimum instance weight per leaf = 3. The parameters taken for L_2/L_1 regularization are 1 and 0.5. The class imbalance correction is based on the ratio of benign/malignant.

4. RESULTS AND DISCUSSION

The implementation uses Python 3.x and the Tensor Flow framework. A modified VGG architecture is utilized for feature extraction, and the XGBoost library is employed for the final classification task. The training strategy involves 5 fold cross validation with a batch size of 32. The key evaluation metrics are accuracy, recall, specificity, F1 score, and the Area under the ROC Curve (AUC). Recall is an important parameter that measures the ability to correctly identify malignant cases, thereby minimizing false negatives. The F1 score is used as a measure of the model's correctness, especially useful when dealing with imbalanced data. The Area under the Curve (AUC) is defined as the system's ability to discriminate between two classes across all possible classification thresholds.

In the proposed hybrid model, the CBIS-DDSM dataset is divided into 70% for training and 30% for testing. The modified VGG network is fine tuned using the Adam optimizer with a learning rate of 0.0005 and a dropout rate of 0.4. Deep features are extracted from both the Global Average Pooling (GAP) layer and the fully connected embedding layer. These features are then used to train an XGBoost classifier with tuned hyper parameters. The key optimized hyper parameters include a maximum depth of 6, a learning rate of 0.1, a subsample ratio of 0.75, a feature sampling fraction of 0.65, and a minimum instance weight per leaf of 3. The L2 and L1 regularization parameters are set to 1 and 0.5, respectively. Hyper parameter tuning is performed using fivefold cross validation. The classified images are shown in Figure.3

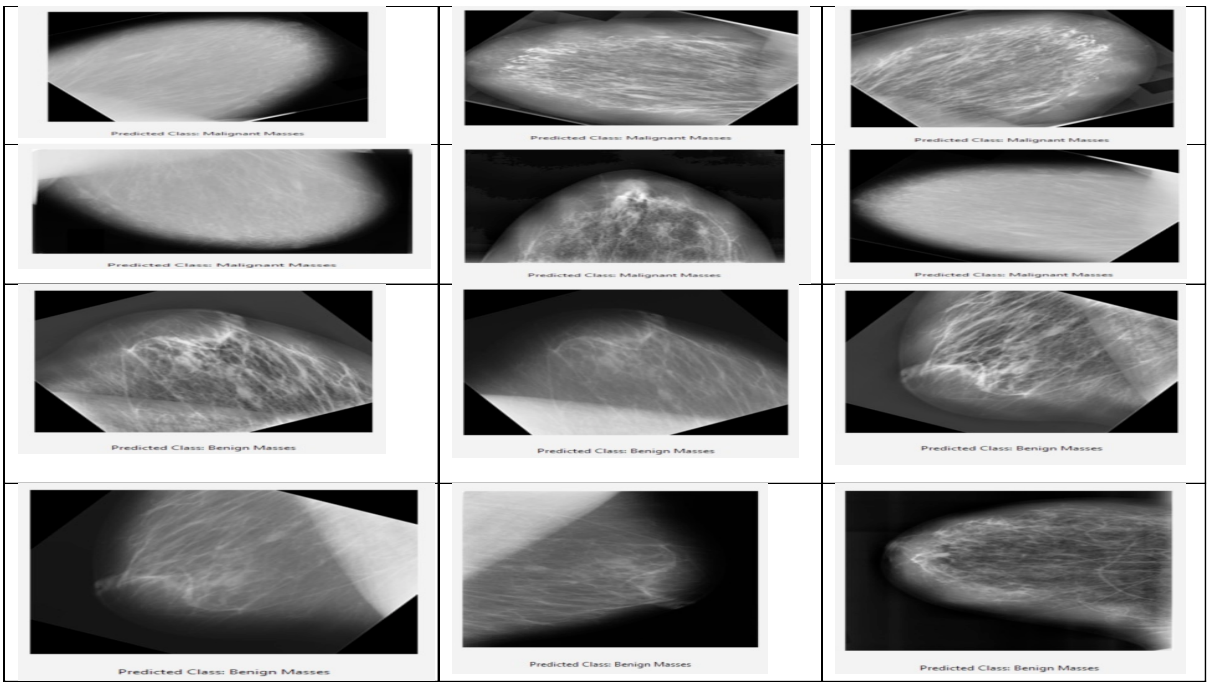

Figure.3. Classification results of the proposed work

To validate the advantages of the proposed hybrid architecture it is compared with other existing works like CNN [22], CNN+GRU [23], VGG19 [24], Inception V3 [25], ATEO – CNN [26], LBP+HOG+CNN [27] and proposed work. The hybrid model outperforms the other model with increase in all performance metrics.

Table 1: Performance comparison of the proposed work

Models	F1-Score	Accuracy	Precision	Recall
CNN [24]	89.46	84.43	87.76	82.18
CNN+GRU [25]	86.12	86.27	85.9	84.51
Fine tune VGG19 Ensemble Model [26]	95.21	95.29	95.46	95.20
Inception V3 [27]	92.02	91.23	85.05	96.01
ATEO – CNN[28]	97.31	95.31	95.24	96.11
LBP+HOG+CNN [29]	92.23	91.50	96.07	97.02
Proposed	97.2	96.8	96	96.05

The tree based ensemble modelling within the XGBoost classifier effectively captures nonlinear interactions present in the VGG feature space. This VGG feature space captures a subset of dimensions that are predictive for malignancy. The use of 5 folds cross validation yielded a standard deviation of ± 0.015 in the Area under the Curve (AUC) across all folds. This small deviation strongly indicates that the hybrid model is robust and is not overfitting to any particular data split. The high AUC value of 0.99 for malignant case detection reflects the system's efficient discrimination ability and the successful reduction in false negatives. The weight adjustment factor utilized in the XGBoost implementation is important in maintaining high sensitivity. The ROC curve (Figure.4) for malignant detection further confirms the high performance with an AUC of 0.99. The curve's steepness near high True Positive Rates (TPR) reflects the model's strong ability to detect malignancy. The resulting precision values highlight the model's robustness in handling class imbalance. Furthermore, the observed increase in accuracy confirms that the gradient boosting approach successfully captures nonlinear feature interactions more effectively than alternative methods.

The accuracy validation curve illustrates the convergence behaviour of the proposed model. During the initial epochs, both training and validation accuracy increase rapidly, reflecting the model's ability to learn discriminative representations from the preprocessed images. The close alignment between the training and validation accuracy curves indicates minimal overfitting. The upward trend observed in both training and testing accuracy further confirms that the model is effectively learning and improving its performance over the epochs. The loss validation curve provides critical insight into convergence stability. At the beginning of training, both training and validation loss decrease sharply, indicating that the model quickly adapts to the underlying data distribution. As training progresses, the loss curves exhibit a smooth, monotonic decline, reflecting the model's capacity to refine its internal representations

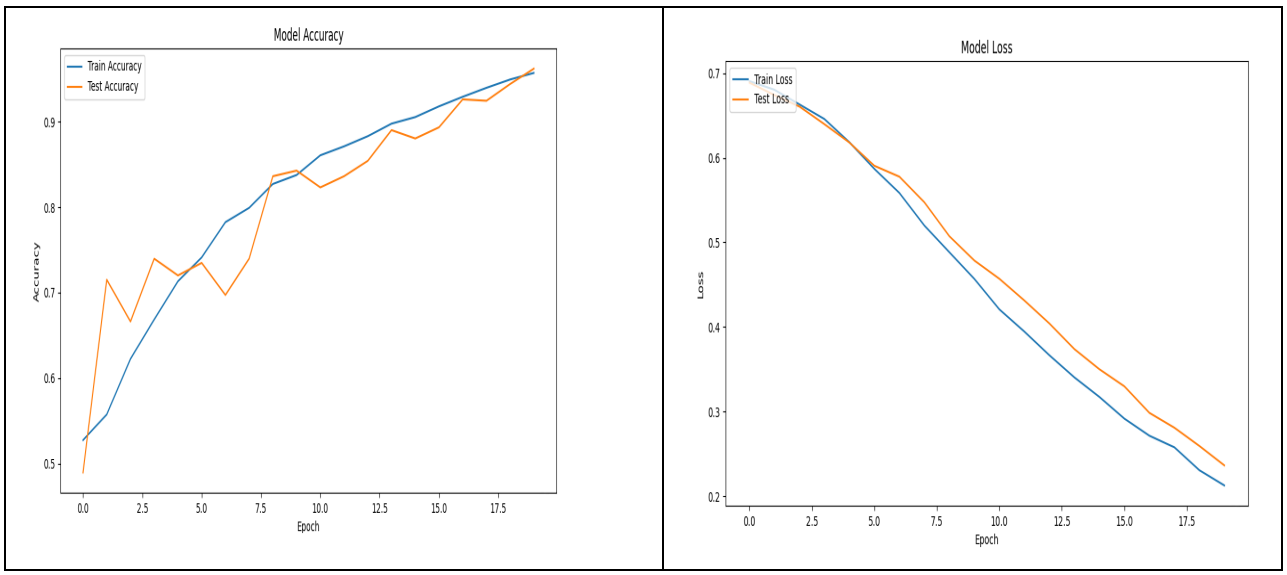

Figure.4: Accuracy validation curve and loss validation curve

without introducing excessive variance. The validation loss stabilizes after 19 epochs, reaching a minimum with negligible fluctuations.

The ROC curve (Figure.5) illustrates the true positive rate (TPR) against the false positive rate (FPR) across different decision thresholds. The proposed framework achieved an

AUC of 0.99, confirming its strong capability to distinguish between malignant and benign cases. To provide a more detailed evaluation of the model's performance, a confusion matrix was also employed. Analysis of the confusion matrix indicates that the hybrid model achieved a high proportion of true positive identifications, which is crucial for the early detection of breast cancer.

CONCLUSION

This study demonstrates that combining modified VGG deep feature extraction with the XGBoost classifier can significantly enhance the diagnostic accuracy of early breast cancer detection from mammographic images. The hybrid approach addresses key limitations in conventional computer mammographic images. The hybrid approach addresses key limitations in conventional computer aided diagnosis systems, particularly those related to overfitting, low contrast, and limited annotated data by improving the model's ability to identify subtle textural and structural abnormalities. The deep feature extraction produced by the modified network, when combined with XGBoost gradient boosting capabilities, result in a robust classification capable of modeling complex, nonlinear relationships within medical imaging data. The extracted features when used as input to XGBoost, has the ability to capture nonlinear correlations, apply tree level regularization, and mitigate sensitivity to imbalanced datasets. Experimental evaluation on the dataset indicates that the proposed model can effectively

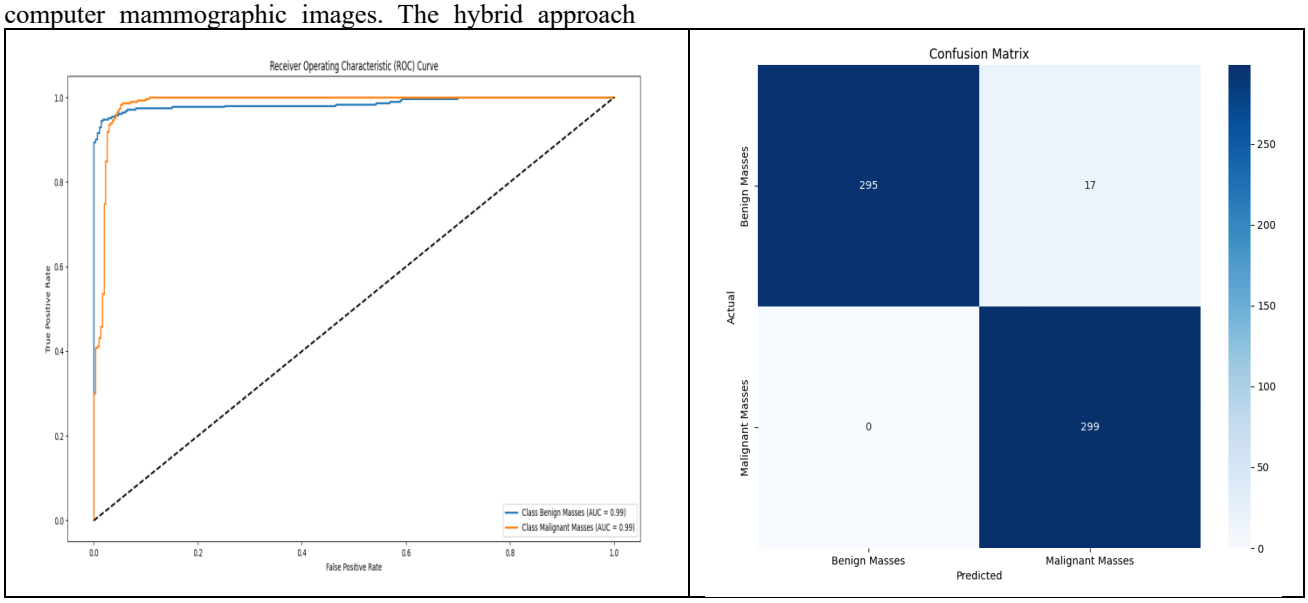

Figure.5: ROC of the model and confusion matrix

decrease missed diagnoses, lower false positive rates and reduce unnecessary biopsies. Future work may focus on expanding the model to multimodal imaging, incorporating attention mechanisms for improved lesion localization, and validating the approach on larger, more diverse datasets to further enhance its clinical applications.

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