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An Advanced Deep Learning Vision Framework for Automated Detection and Prediction of Breast Cancer from Diagnostic Imaging Modalities

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ABSTRACT: A malignant tumor known as breast cancer is caused by the rapid and unchecked growth of cells in the breast tissue. Manual interpretation is frequently used in traditional diagnostic techniques, which laborious, subjective, and error-prone. This research proposes a sophisticated Deep Learning [DL] vision for automated identification and precise prediction of breast cancer from diagnostic imaging modalities in order to get over these drawbacks. Initially to improve image quality and reduce noise, this method starts with preprocessing with a bilateral filter. Segmentation is then performed using a level set technique to isolate ambiguous regions. Superpixel-based region features are extracted to capture local texture and structural details. For efficient categorization, these features are supplied into a deep vision neural network. The deep network has been trained to make highly accurate distinctions between benign and malignant tissues. This system achieves an outstanding performance with an accuracy, precision, recall, and F1-score of 96% and it is implemented using Python programming language.

Keywords: Breast cancer, bilateral filter, level set, super pixel based region feature, deep vision neural network.

1. Introduction

The incidence of human diseases has been rising because various environmental and personal factors, despite advancements in diagnostic and preventive strategies. Cancer, which is defined by unchecked cell development that has the potential to spread to other organs, is still one of the most common and fatal of these illnesses. Breast, prostate, lung, skin, and pancreatic cancer are common cancers that have a major impact on death rates worldwide. Among these, breast cancer is considered one of the most dangerous due to its aggressive nature and potential for rapid progression, contributing significantly to global mortality rates [1]. The World Health Organization (WHO) reports that breast cancer is the most common cause of cancer-related deaths among women worldwide and the most fatal type of cancer for women. Early detection and prompt management are critical to lowering this high death rate. It is the most frequently diagnosed cancer globally in 2020, with 2.3 million new cases, or 11.7% of all newly diagnosed cancers. An estimated 7.8 million women who received a breast cancer diagnosis during the last five years are currently living with the disease, demonstrating the disease's pervasive impact [2]. Breast cancer has divided into two types invasive and non-invasive. Noninvasive breast cancer not spread to the surrounding breast tissue; instead, it stays localized. On the other hand, invasive breast cancer spread to neighboring tissues. The two most prevalent kinds of invasive carcinoma

are Invasive Lobular Carcinoma (ILC) and Invasive Ductal Carcinoma (IDC). The most frequent type, IDC, starts in the milk ducts, and the second most common, ILC, begins in the milk-producing glands called lobes [3]. Best defense against breast cancer is still early detection. It is crucial to have precise and trustworthy diagnostic techniques that differentiate between benign and malignant breast tumors in order to facilitate prompt action and lessen the need for invasive treatments [4]. Many diagnostic methods such as mammography, thermography, ultrasound, and magnetic resonance imaging (MRI) are currently utilized for the Instant recognition of breast cancer. However, these methods still face challenges in achieving consistently accurate predictions, particularly in complex cases or among individuals with dense breast tissue [5]. To address these issues, a variety of techniques are used, such as pre-processing, segmentation, feature extraction, and classification, to enable more precise diagnosis and efficient distinction.

The first stage of image processing is called preprocessing, and it entails improving the image quality by eliminating noise and undesired fluctuations. However, problems like noise, low contrast, and distortion are frequently present in raw images. Filters are frequently employed during preprocessing to smooth the image and lower noise while maintaining significant image features in order to get around these problems. The Gaussian-Wiener filter preserves edges while improving image quality. To get better denoising, this method applies the Wiener filter after the Gaussian filter. However, there are a few disadvantages to the Gaussian-Wiener filter, such as its high computing complexity and parameter sensitivity. Additionally, it could lead to difficulties with non-Gaussian noise types and the loss of fine details [6]. The median value of each pixel within a specified local region is substituted for each pixel in a median filter, a popular image denoising technique that eliminates isolated noise. Particularly in areas with a lot of texture, the median filter may blur edges and small details. Additionally, it can be computationally costly for high window sizes and is less effective against Gaussian noise [7]. The proposed preprocessing method uses a bilateral filter to get over these restrictions, which successfully eliminates noise while maintaining edges and improving the overall visual fidelity. Following the completion of preprocessing phase, the image is segmented into meaningful sections in order to identify areas of interest.

Isolating worrisome areas, like tumors or lesions, from healthy breast tissue is a critical function of the segmentation process in image preprocessing for breast cancer prediction. Using techniques like mammography, ultrasonography, or MRI, diagnostic images are first obtained. Traditionally, biological image segmentation has made extensive use of and advancements in fuzzy C-Means (FCM) clustering. Instead of generating a strict classification, FCM carries out fuzzy segmentation by giving each pixel a membership value that indicates how much it belongs to a specific cluster Nevertheless in complicated medical images, fuzzy C-Means (FCM) segmentation produces erroneous findings because it is extremely sensitive to noise and ignores the spatial correlations between pixels [8] Another algorithm for segmenting images is K-Means. This unsupervised and iterative clustering approach separates data into k distinct groups by minimizing the sum of squared distances between data points and their respective cluster centroids. Using this approach, n observations are assigned k clusters according to their proximity to these centroids. However K-Means converge to local minima and is sensitive to the centroids' initial positions. It also has trouble with different cluster sizes or densities and non-spherical clusters [9]. To overcome all these limitations, the proposed system employs level set-based segmentation, which effectively incorporates spatial information

and provides more accurate boundary detection in complex medical images. Following segmentation, relevant features are taken out of the separated regions in order to record important data needed for subsequent processing, including detection or classification.

In traditional feature extraction, textural features based on the spatial relationship between pairs of pixels are taken using the Gray Level Co-occurrence Matrix (GLCM). It starts by calculating the co-occurrence of pixel intensities at a given angle and distance. The GLCM is then used to extract statistical features that describe the texture of the image [10]. Histogram of Oriented Gradients (HOG) paired with image fusion a process that combines several input images into a single composite image is another feature extraction technique. A detailed feature vector is extracted from this fused image using HOG descriptors. However, HOG lacks region-level contextual awareness and is susceptible to changes in illumination and noise [11]. To address these limitations, the proposed system utilizes superpixel-based region feature extraction, which enhances spatial coherence and improves the accuracy of image analysis. After feature extraction, the process transitions to the classification stage, where the extracted features are analyzed to categorize the input data into predefined classes.

For classification tasks, Support Vector Machines (SVM) have historically been employed extensively. Additionally, it has been used as a predictive model for the detection of breast cancer. SVM use kernel functions to handle nonlinear classification. However, it is not appropriate for high or high-dimensional datasets and necessitates careful parameter modification [12]. An Extreme gradient-boosted decision tree (GBDT) solution that is optimized for speed and performance is Extreme Gradient Boosting (XGBoost). It is used for applications involving regression, ranking, and classification and enables parallel tree boosting. However, it is less successful for complicated image data because it depends on manually extracted features. It also has trouble with high-dimensional, unstructured inputs and needs thorough hyperparameter changes [13]. To address the shortcomings of traditional classifiers, the proposed framework incorporates Deep Vision Net for classification, which effectively captures complex spatial patterns and improves diagnostic precision.

2. Literature Survey

Richard Lupat *et al* [2023] [14] have established a Multi-Omics Autoencoder-Based Neural Network Algorithm (Moanna), a DL-based algorithm, is trained to incorporate multi-omics data in order to identify subtypes of breast cancer. Moanna's architecture consists of a semi-supervised Autoencoder connected to a multi-task learning network in order to generalize a combination of gene expression, replicate number, and somatic mutation data. Additionally, this model demonstrated high accuracy in identifying PAM50 subtypes, distinguishing basal-like samples, and forecasting the ER status of samples. Furthermore, compared to the original PAM50 subtypes, this model predicted subtypes exhibit a higher connection with patient survival. Nevertheless anticipated that gene expression data would be normalized against a control, its use for the prediction of breast cancer subtypes currently fails with a single sample.

Sameen Aziz *et al* [2023] [15] have introduced a new strategy Using ImageNet-VGG16 to diagnose breast cancer. The objective of the method to improve breast cancer diagnosis performance. The ImageNet-VGG16 method applies layers modeled after the ImageNet technique to the input dataset in order to extract spatial information. The VGG16 model is then trained and tested using these extracted characteristics to classify breast cancer images. High accuracy is attained by applying a VGG16 and ImageNet hybrid as the

suggested feature engineering technique. But the data also shows that validation accuracy doesn't improve during the course of training.

Jawad Ahmad *et al* [2023] [16] have proposed a deep learning (AlexNet) with classical machine learning (SVM) for breast cancer prediction. This technique retrieves data features using a nine-layer model that has two fully connected layers. In classification tasks, the Breast Net-SVM model performs remarkably well. Its efficacy in detecting breast cancer is demonstrated by its constant high accuracy. Even so, the model's drawbacks include its reliance on a single dataset for both validation and training, which could limit its generalizability. Furthermore, the model's consistency and optimization flexibility is limited by the usage of different mammography image sizes and the dependence on just three particular optimizers.

Amreen Batool *et al* [2024] [17] have developed a novel ELRL-E model that efficiently classifies breast cancer tumors by combining machine learning methods, including LightGBM, Ridge Classifier (RC), Extremely Randomized Trees (ET), and Linear Discriminant Analysis (LDA). Goal of the model is to determine the best classifier combination for improved prediction performance. An ELRL-E classifier is used to assess the model's resilience and effectiveness that showed better accuracy. The model's automation and clever decision-making greatly aid in the simplification of difficult diagnostic procedures. However, the dataset's inherent characteristics, potential difficulties in clinical implementation, and the difficulty of converting machine learning results into clinical workflows are some of the limitations that still exist despite the encouraging results.

Hung Q. Vo *et al* [2025] [18] have suggested a multimodal DL model that uses clinical data and mammography datasets to predict breast cancer. This method shows improved performance and stability by using a frozen, large-scale pretrained vision model. The problem of misaligned tabular data across datasets is successfully addressed by this model, which integrates various picture and clinical information from various healthcare organizations. The results demonstrate vision-language models facilitate strong multimodal learning, especially when there is little direct alignment between modalities. The lack of publicly available multimodal breast cancer datasets currently limits efforts to further test the model's generalizability through broader evaluation across more datasets.

3. Proposed System Modelling and Description Block Diagram

Early diagnosis and treatment planning depend on the ability to predict breast cancer. Among the process's most important steps are preprocessing, segmentation, feature extraction, and classification. Every stage improves the predictive model's precision and dependability. Let's examine this process's intricate workflow in more detail.

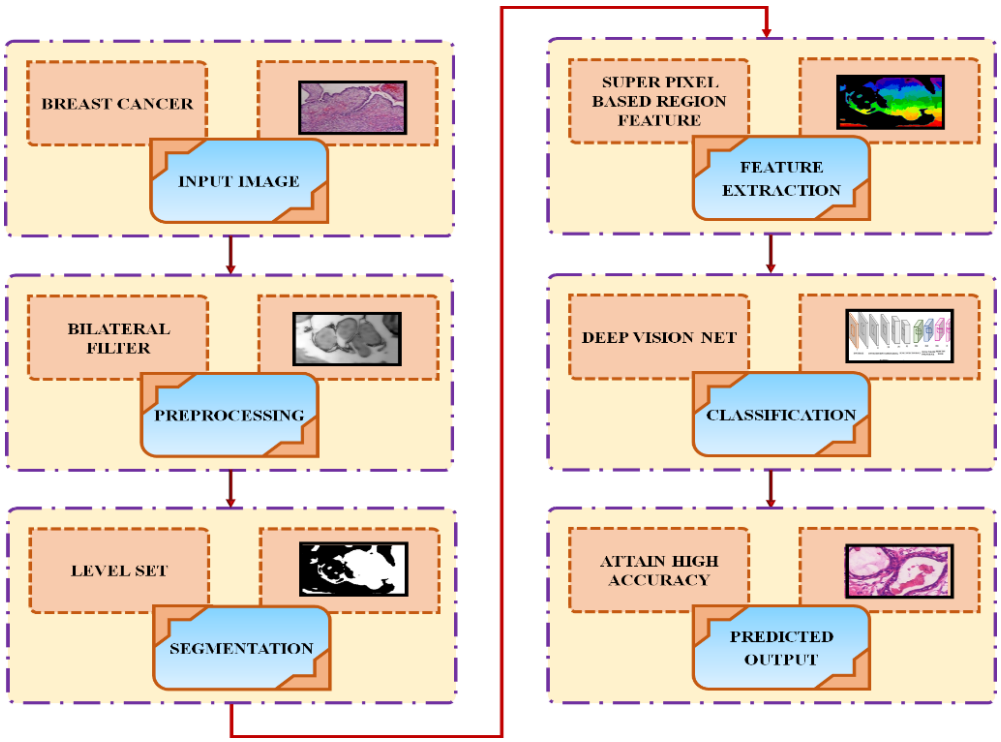

Figure 1: *Block diagram of proposed system*

The provided block diagram shows a thorough methodology for automated breast cancer diagnosis that combines DL and image processing methods. Images pertaining to breast cancer, usually acquired by mammography or histology, are entered to start the process. A bilateral filter is employed during the preprocessing step of these images. By lowering noise while maintaining critical edge information a critical component of medical image analysis this filtering technique effectively improves image quality. The preprocessed image is then segmented using a level set technique. This stage enables accurate analysis of the pertinent structures by distinguishing the region of interest, such as affected regions, from the remaining part of the image. The process moves on to the feature extraction stage after segmentation. A super pixel-based region method is used to extract features. Super pixels improve the accuracy of region-based feature recognition by combining related pixels into groups, which lowers computational complexity. A DL model called Deep Vision Net is then fed these characteristics, which stand in for different textures, forms, and patterns within the divided area. Using patterns discovered from the datasets, this neural network is particularly trained to classify images of breast cancer. In order to assist medical experts in making precise diagnoses, this classification phase is essential. Following classification, the anticipated output is shown in the last block. To provide reliable diagnostic results, the system strives for high prediction accuracy. The model is capable of handling complicated medical imaging data because to the integration of sophisticated preprocessing, segmentation, and DL components. This method drastically cuts down on human error and diagnostic time by automating the detection procedure. In order to improve patient outcomes, it offers an effective tool for early breast cancer identification.

3.1 Preprocessing-Bilateral Filter

In pre-processing step, bilateral filter is a non-linear smoothing filter that reduces noise and preserves edges. The primary advantage of this filter is used to smooth the image while maintaining the integrity of the edges, which is

crucial for maintaining important structural components. Data from the intensity and geographical domains are combined to create this filter. For a pixel located at (x,y) in an image $I(x,y)$, the output of the bilateral filter $I_B(x, y)$ is given by

$$I_B(x,y) = \frac{1}{W_P}\sum_{x'y'}(x'y') \cdot \exp\left(-\frac{(x-x')^2+(y-y')^2}{2\sigma_s^2} \cdot exp\left(-\frac{(1(x,y)-I(x'-y'))^2}{2\sigma_s^2}\right)\right) \quad (1)$$

Here, $(x'y')$ represents the coordinates of the neighboring pixels surrounding the pixel at (x, y). The parameter σ_s regulates the spatial spread, determining the extent to which neighboring pixels contribute on their spatial distance from (x, y). Similarly σ_r governs the range spread, the contribution of nearby pixels according to closely their intensity values match to that of(x, y). W_P serves as a normalization factor to ensure that the final result remains within a consistent range.

$$W_P = \sum_{x'}\sum_{y'}\exp\left(-\frac{(x-x')^2+(y-y')^2}{2\sigma_s^2} \cdot exp\left(-\frac{(1(x,y)-I(x'-y'))^2}{2\sigma_s^2}\right)\right) \quad (2)$$

The spatial weighting term $\exp\left(-\frac{(x-x')^2+(y-y')^2}{2\sigma_s^2}\right)$, assigns greater influence to pixels that are spatially closer to the target pixel (x,y). Meanwhile, the intensity weighting term, $exp\left(-\frac{(1(x,y)-I(x'-y'))^2}{2\sigma_s^2}\right)$ ensures that this filter combines information from the geographic and intensity domains. similar to I(x, y). It comes to image denoising, by eliminating lingering noise and artifacts, particularly near edges, the bilateral filter enhances the denoised image's overall visual quality while maintaining crucial structural details. Finally, by improving contrast and maintaining crucial structural regions, preprocessing moves into the segmentation stage, which helps to more precisely identify and separate significant sections.

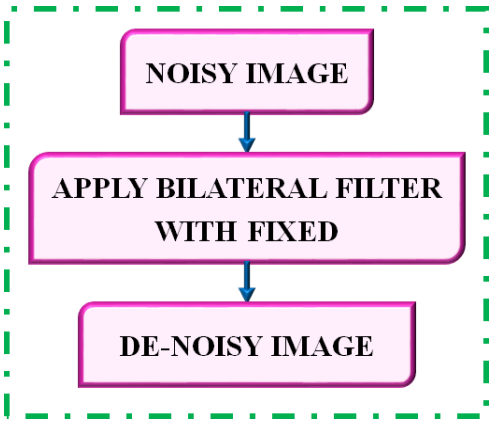

Figure 2: *Preprocessing-Bilateral Filter*

3.2 Segmentation-Level Set

Identifying breast cancer, the level set method of segmentation is utilized to precisely separate and divide the region of interest from the surrounding breast tissue in an image. It is a mathematical technique that tracks features and shapes by depicting them as changing surfaces or curves.

The idea behind level set segmentation is to indirectly represent a shape in the image domain. According to this method, the set of locations where the level set function equals zero is known as the zero-level set and is an active surface S is defined as a set of Zero-level points $p = (x, y, z)$ of the function $\phi(p, t)$. This formulation gives $S = \{p: \phi(p, t) = 0\}$, where $\phi(p, t): \Re^3 \rightarrow \Re$ and t is the evolution time step. The surface evolves along its normal direction based on the following Partial Differential Equation (PDE). Geometric and geodesic active contours, along Active Contours without Edges (ACWE), are notable level-set based models. The ACWE method uses a region-based approach. Even if an image's borders are not clearly defined, the ACWE variational technique offers a smooth division of the image into distinct sections.

$$\frac{\partial \emptyset}{\partial t} = |\nabla \emptyset| F, \ \emptyset(p, 0) = \emptyset_0(P) \quad (3)$$

Where $\emptyset_0$ is primary surface and F is a function of speed F (p, t) permits surface to enlarge to cover an area that has been segmented. Level set approaches naturally permit topological changes,

contours smoothly split or merge. By concentrating on a restricted number of contour control points, classic parametric models, on the other hand, frequently need fewer computations despite having less flexibility. In comparison, it takes a lot more memory and processing power to solve a level set PDE for a full image domain using a finite difference-based approach. Furthermore, anomalies that arise during the level set function's evolution might threaten the method's numerical stability. A popular fix for this issue is to periodically re-initialize the function, however this is time-consuming and compromise the method's accuracy. The image is divided into significant areas after segmentation. The next crucial stage is feature extraction, which quantifies important attributes like color, texture, and shape to facilitate additional analysis and interpretation.

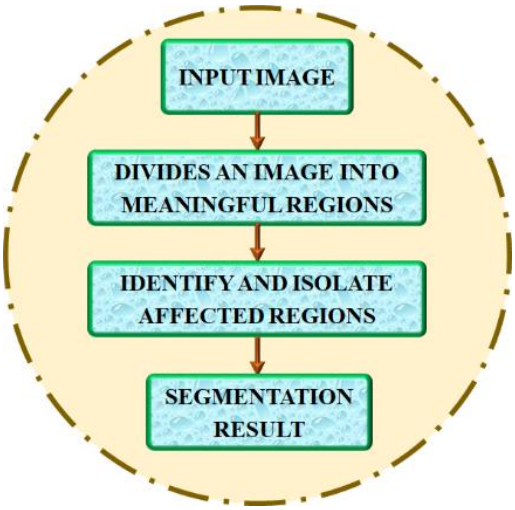

Figure 3: *Feature Extraction Using Superpixel-Based Regional Characteristics*

3.3 Feature Extraction- Super Pixel Based Region Feature

A crucial component of breast cancer detection, feature extraction improves analysis efficiency and accuracy by distilling complex image into a more manageable and useful set of qualities. Superpixel-based feature extraction greatly reduces the amount of elements required in a future processing step by grouping visually comparable pixels into coherent zones. The intersections of several superpixels are excellent choices for locating important focal areas because the borders created by superpixel segmentation reflect organic changes in image content. A superpixel is a small, asymmetrical group of neighboring pixels with comparable brightness, texture, and color. It efficiently divides an image into relevant sections by grouping pixels according to their similarity. The overall complexity of ensuing image processing tasks is greatly decreased by using superpixels to represent image attributes. The average of the feature representations of each pixel that the encoder extracted makes up a superpixel's features. The following are the feature-averaged pooling steps:

$$H_n = \frac{1}{|\Omega_{s_i}|}\sum_{\kappa\epsilon\Omega_{s_i}} h_k \qquad (4)$$

Where Ω_{s_i} represent the superpixel's set of pixels, and h stands for the pixel feature vector. In particular, combine the superpixel's geometric properties such as area, perimeter, aspect ratio, and center point with the pooled feature map. These characteristics are standardized according to the categories in which they fall. Since samples with reduced feature distances are thought to be more comparable, the super pixel based region feature technique is used in this study to choose the k samples as positive examples. Each sample is therefore linked to both N-K-1negative and k positive samples. The appropriate loss is defined in accordance with the superpixel contrastive loss's goal of maximizing separation from the N-K-1 negative samples is.

$$L_s = \frac{1}{N}\sum_{i=1}^{N}\sum_{i=1\ j\epsilon N_k(i)} -log\frac{\exp(sim(H_i,H_j)/\tau}{\sum_{t=1}^{N}[1t\neq i\exp(\mathrm{sim}(H_i,H_t)/\tau]} \qquad (5)$$

Where $(sim(H_i, H_j)$ is a similarity function that calculates the similarity between H_i,

$1_{j\neq 1} = \{0,1\}$ is an indicator function and τ is the temperature coefficient. In this way, contrastive

learning and the intrinsic characteristics of superpixels are used to make the learnt representation more discriminative. This strategy reduces the requirement for intricate data augmentation, in contrast to conventional multi-view contrastive techniques that necessitate the intensive building of positive and negative sample pairings. The next stage is to use the significant features that have been extracted from the input image to categorize the image into predetermined groups. This change from feature extraction to classification is essential because the classifier produce precise and effective predictions because to the extracted features, which operate as a condensed representation of the raw image.

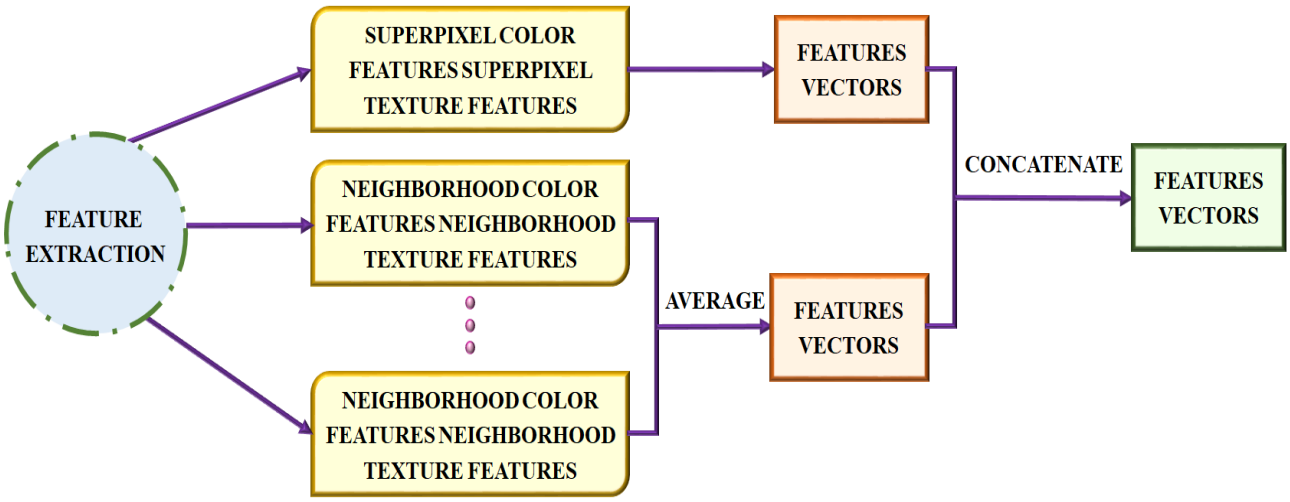

Figure 4: *Superpixel-based feature extraction process.*

3.4 Classification- Deep Vision-Net

Deep Vision Networks are used for classification in order to reliably differentiate between various categories. By efficiently comprehending minute variations in medical images, Deep Vision Networks improve the classification process in the context of breast cancer prediction, improving diagnostic performance. To precisely locate and define affected areas in images of breast tissue, a novel deep vision-based instance classification technique is developed. This method incorporates two state-of-the-art models, Architecture, SPPNet, and DCNet, which are renowned for their superior performance in image classification applications. A strong deep vision-net architecture designed for medical image analysis is created by combining these models. As seen in Figure 5, the cutting-edge models is better at learning intricate structures and accurately classifying them, which is essential for identifying and dividing up affected areas.

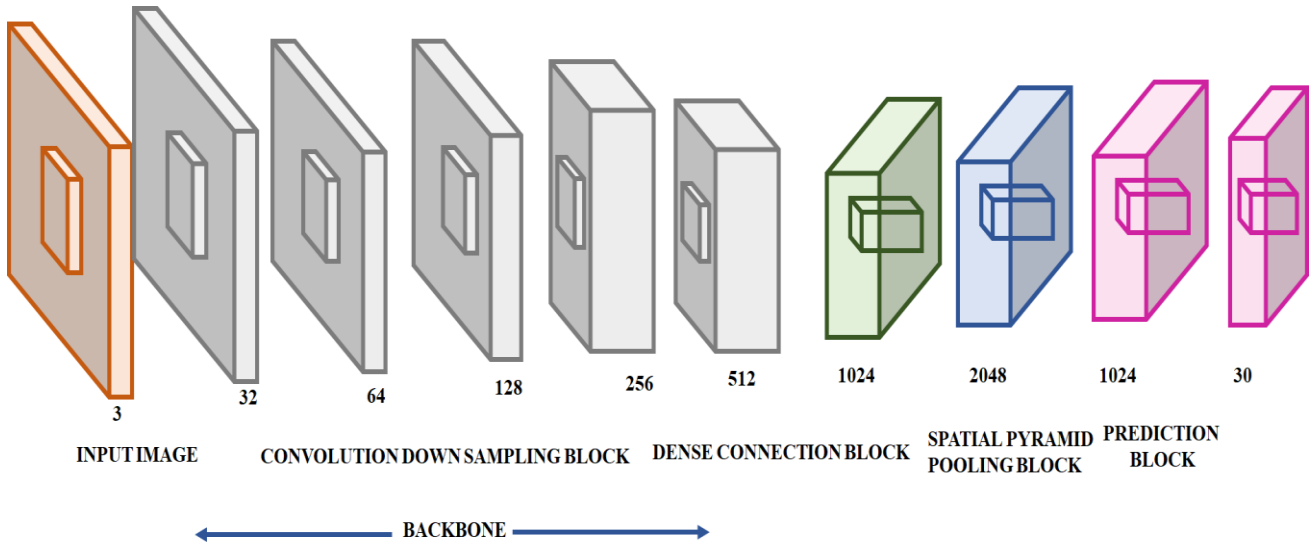

Figure 5: Deep Vision Net Architecture

In order to accomplish the underlying objectives, this model divides the input-constructed graph into a series of ordered patches and performs calculations both within and between tokens. Examine a vision transformer network that performs a prediction task by processing an input-constructed graph G, which is defined by width α, height β, and channel dimension δ. The associated output is shown as follows:

$$P_{Head} = \delta o H^{p} o H^{p-1} o \dots o H^{1} o X(G) \quad (6)$$

The encoding network is represented as, $X(.)$,which helps tokenize the patches of images from the input-constructed graph G into the positioned tokens T, and the intermediate P^{th} transformer blocks that utilize $\delta(.)$Self-attention to transform the inputs are denoted as $\delta(.)$. Assume that, all tokens are transformed from $P-1^{th}$ layer using the transformer block at P^{th} layer using,

$$T_{1:I}^{P} = H^{P}(T_{1:I}^{P-1}) \quad (7)$$

In this case, I stands for the total number of tokens, and the updated token is indicated as $T_{1:I}^{P-1}$. A recurring characteristic by using dimension C across all layers for all tokens, the vision transformer facilitates the capture and learning of global halting mechanisms through joint layer monitoring. Deep vision networks have been used more and more prediction of breast cancer, it is used to accurately identify abnormal patterns in diagnostic imaging. These networks outperform conventional techniques in early and automated breast cancer diagnosis by learning intricate spatial hierarchies and extracting complex visual data, which improves accuracy, sensitivity, and robustness in recognizing affected tissues.

4. Results and Discussion

The Deep Vision Net model is used to predict breast cancer in this section on results and discussion. Kaggle provides the dataset required for testing and training. Python programming language used for the model's implementation. The deep learning model is trained using 7,000 images in total. 1,500 test images are used for evaluation in order to confirm the correctness of the predictions.

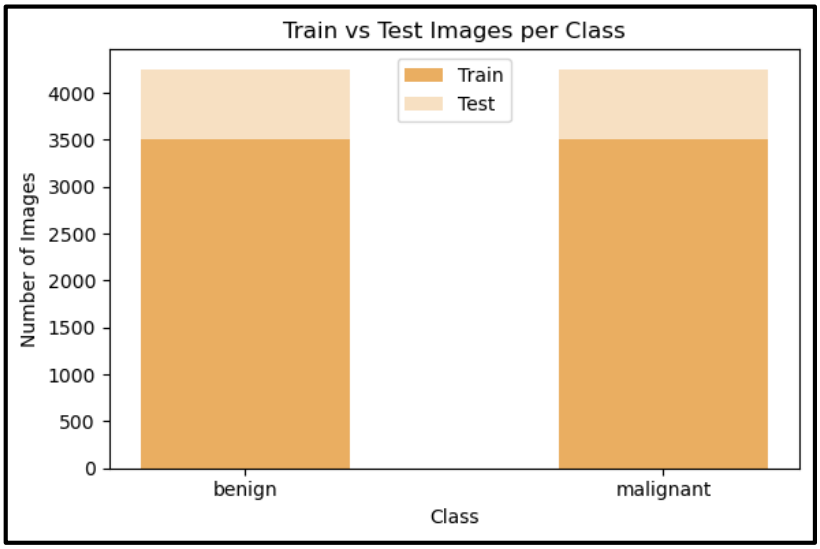

Figure 6: *Train vs Test Images per Class*

A bar chart showing the distribution of training and testing images among benign and malignant classes is shown in Figure 6. There are around 3,500 training images in each class, for a total of 7,000 training examples. The distribution of test sets used to evaluate the model is also depicted in the chart. Each class is assigned roughly 750 test images. 1,500 test samples are included in the dataset overall to evaluate model performance.

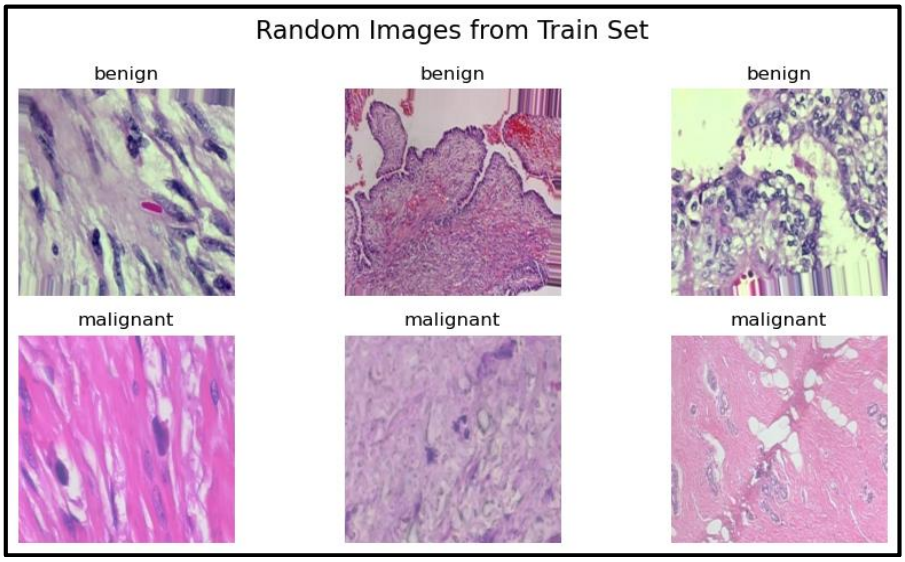

Figure 7: *Random Images from train Set*

Random samples from the training dataset are shown in Figure 7, displaying both benign and malignant tissue types. These images are histopathology scans that are used to train the breast cancer detection algorithm. The model uses the tissue's visual characteristics to learn to identify cancerous patterns. The two classes differ significantly in terms of cellular structure and texture. These changes are essential to the algorithm's ability to classify data accurately.

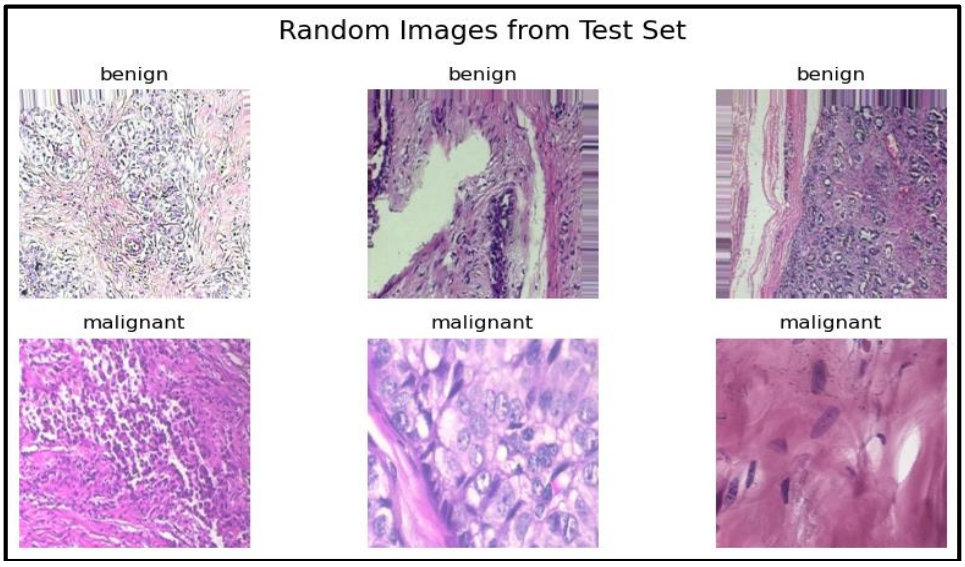

Figure 8: *Random Images from test Set*

Random samples from the test dataset are shown in Figure 8, which includes images of both normal and cancerous tissue. Following training, the system ability to apply on previously encountered data is evaluated using these samples. Every image is an evaluation of a histopathology scan. There are clear variations in the cellular organization and tissue structure. These differences help the model correctly differentiate between cases that are benign and those that are malignant.

Figure 9: *Original Images*

The original, raw input image used in the diagnostic pathway is shown in Figure 9. Complex tissue architecture and intricate cellular patterns are captured in this raw image. Accurate medical analysis requires such complex qualities. This image serves as the system's initial point for additional processing.

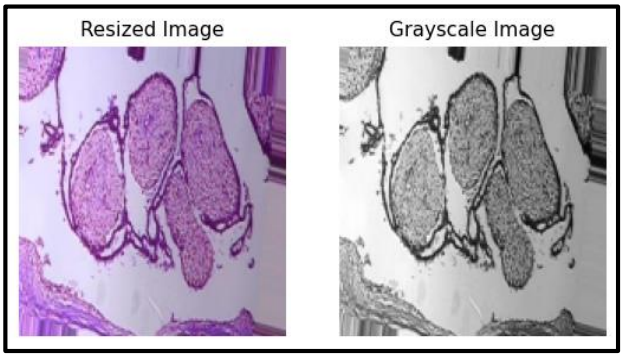

Figure 10: *Resized Image into Grayscale Image*

The preprocessed versions of the original input image are shown in Figure 10. The image on the left has been adjusted to fit the model's needed input dimensions. The grayscale conversion, which lowers color complexity while maintaining significant structures, is seen in the right image. These preprocessing techniques aid in highlighting important aspects of the picture. Consequently, they help to increase the precision of feature extraction and categorization.

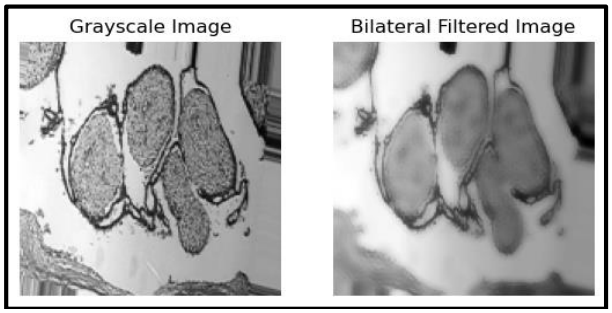

Figure 11: *Grayscale Image into Bilateral Filter Image*

Figure 11 represented the resized image is displayed on the left side of the image, standardizing the dimensions to ensure clarity throughout the dataset. When feeding images into deep learning models with fixed input sizes, resizing is crucial. The grayscale version, which only shows intensity values after color information is eliminated, is shown on the right. This preserves important structural patterns while simplifying the image and lowering computing complexity. In order to improve model performance and lower noise in medical image analysis, both preprocessing steps resizing and grayscaling are essential.

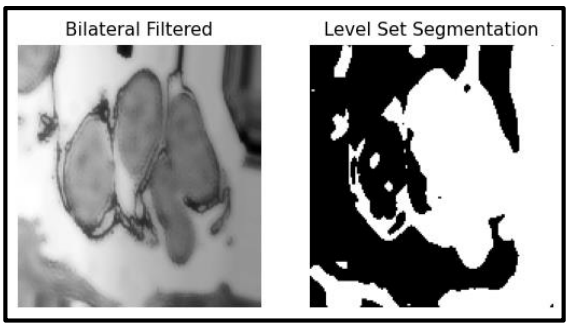

Figure 12: *Bilateral Filtered into Level set segmentation*

Figure 12 demonstrates the transition from bilateral filtering to level set segmentation. The bilateral filter efficiently reduces noise while maintaining the image's key edges. Level set segmentation then accurately delineates complex tissue boundaries based on intensity differences. Together, these steps enhance the precision of region detection for improved classification outcomes.

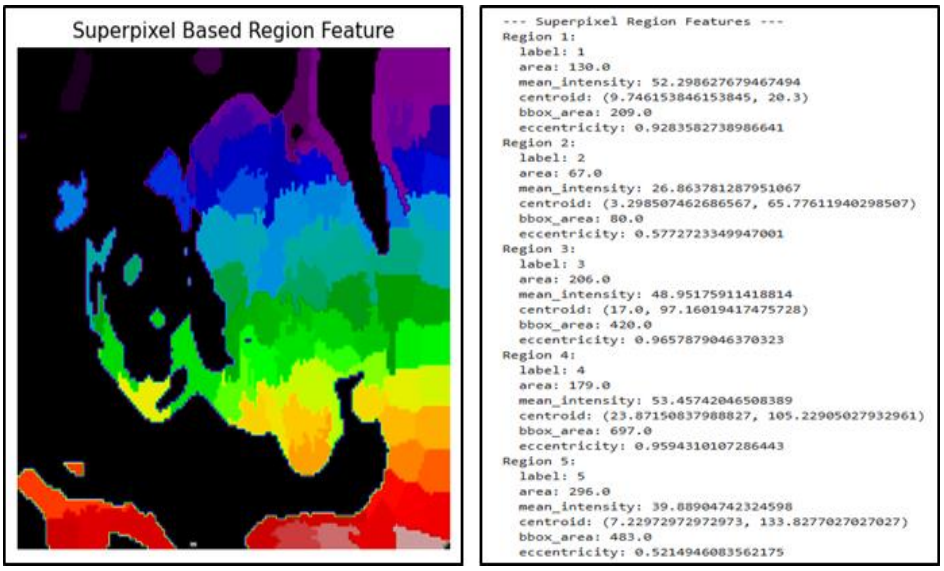

Figure 13: *Superpixel Based Region Feature*

Superpixel based region feature is shown in figure 13. Superpixel-based region segmentation, which divides the image into uniform color-texture regions for effective analysis, as demonstrated in the image on the left. This approach maintains crucial boundaries while simplifying intricate structures. Each superpixel region's retrieved features, such as intensity, centroid, bounding box, and eccentricity, are listed in the right panel. For machine learning models, these numerical descriptors aid in quantifying region attributes. In medical imaging tasks, superpixel segmentation improves feature representation.

4.1 Performance metrics for Breast Cancer Prediction

This results show the model identify and categorize cases of breast cancer. Reliable and balanced prediction capability is indicated by the constant values across all metrics. The high precision of the model validates its capacity to obtain relevant features from the dataset. Table 1 provides an overview of the performance evaluation.

Table 1: *Performance Metrics*

Performance metrics	Values
Accuracy	96%
Precision	96%
Recall	96%
F1-score	96%

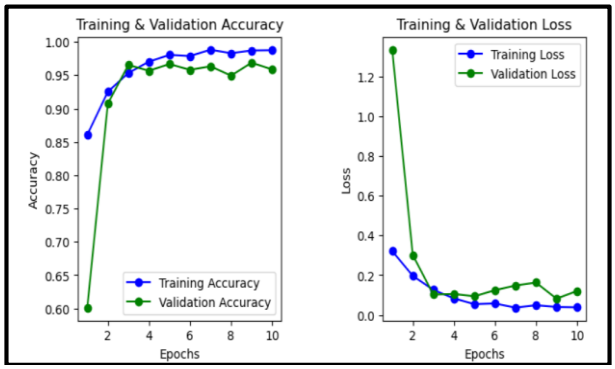

Figure 14: *Training, Validation Accuracy and loss*

Figure 14 displayed a Training, Validation Accuracy and loss. After a few epochs, the training and validation accuracy graphs stabilize over 95%, demonstrating a quick improvement. Early in training, loss graphs show that both training and validation loss have sharply decreased to low values. Strong generalization is suggested by the training and validation metrics' tight alignment. Overall, there is no noticeable overfitting or underfitting, and the model operates effectively.

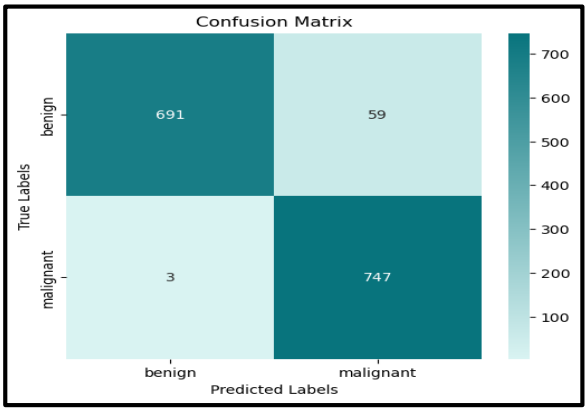

Figure 15: *Confusion Matrix*

Confusion Matrix is shown in figure 15. The model properly identified 691 benign and 747 malignant cases, according to the confusion matrix. Only three malignant cases were mistakenly categorized as benign, while 59 benign cases were misclassified as malignant. This suggests that malignant tumors can be detected with great sensitivity. All things considered, the model performs well in classification with few false negatives.

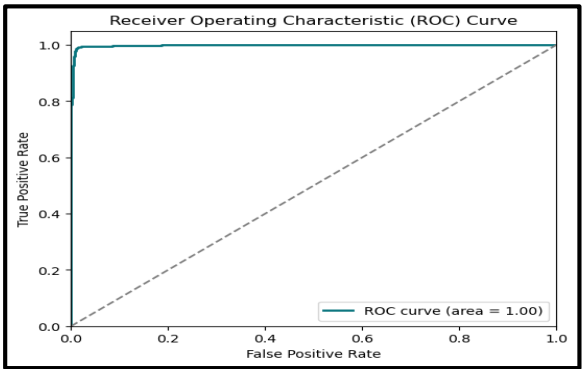

Figure 16: *Receiver Operating Characteristic (ROC) Curve*

Figure 16 represented the ROC Curve. The model's capacity to differentiate across classes is demonstrated by the ROC curve. A flawless classification result is showed by an AUC (Area under Curve) score of 1.00. This illustrates the model's superior diagnostic capacity for binary classification.

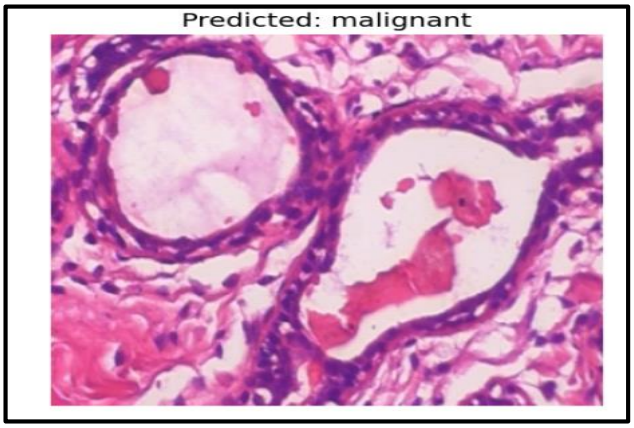

Figure 17: *Predicted Output*

A histological tissue sample examined by the trained model is shown in the figure 17. The tissue is malignant according to the model's prediction based on morphological patterns and texture. The classification of malignancy is supported by the presence of dense nuclei and abnormal cell structures. This result demonstrates how well the model detects malignant tissue.

4.2 Performance Comparison of the Proposed Method

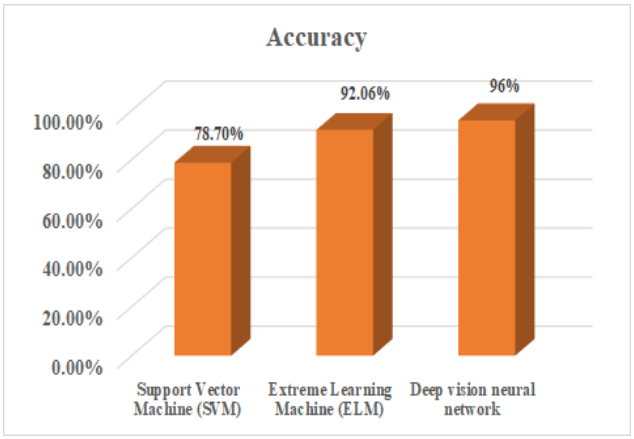

Figure 18: *Comparison of Accuracy*

Figure 18 shows that the accuracy of three categorization techniques used to predict breast cancer is contrasted in the bar chart. SVM performed moderately well, with an accuracy of 78.7% [9]. ELM's accuracy of 92.06% was superior [19]. With the maximum accuracy of 96%, the proposed Deep Vision Neural Network fared better than both.

Table 2: *Comparison for the proposed method*

Method	Precision
ELM [19]	80.25%
Catboost [20]	76.5%
Deep vision neural network	96%

The precision values of three distinct classification techniques are contrasted in table 2. ELM demonstrated a greater precision of 80.25% [19] than CatBoost, which only managed 76.5% [20]. With a 96% precision rate, the Deep Vision Neural Network outperformed the others. This suggests that compared to the other approaches, the suggested deep learning strategy yields findings that are noticeably more accurate.

5. Conclusion

This paper presents a DL vision framework for automated breast cancer diagnosis and prediction. This method is extremely effective and non-invasive makes use of diagnostic imaging modalities. Bilateral filtering, initial phase of image preprocessing, efficiently eliminates noise while maintaining key characteristics. Within complicated medical images, level set segmentation makes it possible to precisely identify affected areas. Region features based on superpixels improve the quality and depth of information that is extracted. To accurately and consistently classify affected spots, a Deep Vision Network was utilized. Even faced with complicated and diverse image data, the suggested model shows excellent learning capabilities. The framework's efficacy in actual medical situations is validated by evaluation outcomes. With an accuracy, precision, recall, and F1-score of 96% this system produces reliable, consistent diagnostic predictions. This high accuracy improves the results of early intervention by guaranteeing that even minute signs of cancer are quickly identified. The robust architecture of the system reduces diagnostic variability by enabling consistent performance across a variety of datasets. All things considered, the suggested paradigm has a lot of potential for being incorporated into clinical

workflows and helping radiologists make quicker and more precise decisions.

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