RESEARCH PAPER

Breast Cancer Detection Using Histopathology Images.

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Abstract
One of the most deadly causes of death amongst women in the world is breast cancer where early and accurate diagnosis have been cited to have a major role in enhancing treatment success and survival. Histopathological examination of breast tissues is regarded as the best method of establishing the presence of cancerous cells. Nevertheless, the manual analysis of microscopic biopsy images is time-consuming and can cause the variability of observers because of the disparity in expertise amongst pathologists. Over the past few years, Deep Learning (DL) and Artificial Intelligence (AI) methods have proven useful in terms of automating the process of the medical image analysis as well as the diagnostic precision. The study is a profundity learning-based framework of automatic detection and classification of breast cancer with the help of histopathology images. The proposed system takes the form of Convolutional Neural Networks (CNNs) to identify pertinent spatial and morphological patterns of images with high-resolution tissue that do not require extraction of features manually. Patch-based learning method is used to improve the representation of features and be able to capture localized cellular patterns in the histopathology slides. Also, an Explainable Artificial Intelligence (XAI) component is a Gradient-weighted Class Activation Mapping (Grad-CAM) and is added to offer visual explanations of the predictions made by the model by highlighting the most significant areas of the image. The suggested framework is tested with the help of the publicly available datasets and is estimated in terms of such performance metrics as accuracy, precision, recall, and F1-score. The findings show that the system can offer dependable and consistent classification of benign and cancerous tumor types, thus aiding the clinicians to make wise decisions. All in all, the suggested methodology will provide an effective, explainable, and automated mechanism to assist in detecting breast cancer using computer-aided diagnosis.

Keywords: Breast Cancer Detection, Histopathology Images, Deep Learning, Convolutional Neural Network, Explainable AI, Computer-Aided Diagnosis, Medical Image Analysis
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1. Introduction

Breast cancer is a life threatening and most prevalent disease among women in the world and has remained a big issue in the minds of the populace. Global health reports also indicate that more millions of new breast cancer cases are being diagnosed annually and it has become one of the major causes of cancer-related deaths in women. Early diagnosis and proper treatment are critical in enhancing the effects of treatment, limiting the progress of the disease, and improving the survival of the patient. Consequently, there is need to have reliable diagnostic methods that would diagnose the presence of cancerous tissues at an early stage and help clinicians make the right medical decisions.

Conventionally, diagnosis of breast cancer is done by use of imaging methods namely mammography, ultrasound imaging, Magnetic Resonance Imaging (MRI) and histopathology. Out of these procedures, the gold standard of establishing the presence of malignant cells is regarded as the histopathological analysis of the biopsy samples stained with Hematoxylin and Eosin (H&E). During this process, highly-trained pathologists will analyze samples of tissues under the microscope to detect any structural abnormalities, cell morphology and tumor growth patterns that are indicative of cancer occurrence. Nonetheless, the process of manual analysis of histopathology specimen images is a lengthy and labor intensive process which relies largely on experience of medical specialists. Also, inconsistency in interpretation by pathologists can result in inter-observer and intra-observer errors which can influence diagnostic accuracy.

Lately, the development of Artificial Intelligence (AI) and Machine Learning (ML) attracted the attention to the automated diagnostic systems in the sphere of medical imaging. Computer-Aided Diagnosis (CAD) systems have been created in order to assist clinicians with objective and consistent medical image analysis. Specifically, Deep Learning (DL) methods have proven to have a tremendous success in image classification and pattern recognition activities because of their capability to learn hierarchical feature representations in raw data. Convolutional Neural Networks (CNNs), a particular type of a deep learning model have found extensive application in the medical image processing to automatically extract discriminative spatial and textual features of complex histopathology images without any manual feature engineering [4].

In a number of recent studies, the use of deep learning models in detecting breast cancer on histopathology measurements has been investigated. Patch-based CNN models have been demonstrated to be successful at identifying localized tissue appearance, i.e., nuclei structures and texture differences, which subsequently

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enhance better classification accuracy in benign and malignant tumor detection [4]. Moreover, high-order deep learning architectures and preprocessing methods have been stated to improve the accuracy of early detection in systems that use mammography to determine the diagnosis [5]. Amid these developments, the problems of reliance on high-quality annotated datasets, high computing complexity, and poor interpretability of deep learning models continue to be problematic in clinical application.

To overcome these shortcomings, there is an increasing demand to have an automated, precise, and interpretable diagnostic model that can help the pathologists to examine the histopathology images more effectively. A deep learning-based system is suggested in this study when it comes to detecting and classifying breast cancer through the use of histopathology images. The framework suggested is expected to enhance the accuracy of the diagnosis, decrease the time of analysis, and give visual representations of the model forecasts by using Explainable Artificial Intelligence (XAI) methods. The system aims to improve consistency in diagnosing and assist clinical decision-making in clinical settings by incorporating automated feature extraction and classification processes to help improve the system in relation to real-life healthcare settings..

Key Contribution of research

1. Automated deep learning framework is suggested to detect and classify breast cancer through histopathology images. The system decreases the reliance on the hand review, as well as facilitates quicker and dependable diagnostic reviews.
2. The extraction of spatial and morphological features in microscopic tissue images is done automatically using a Convolutional Neural Network (CNN). This removes the process of manual engineering of features and enhances classification.
3. A patch-based learning method is adhered to learn localized cellular functions in histopathology images. It is a technique that increases the capability of the model in differentiating between benign and malignant tumor samples.
4. Grad-CAM is used to implement an Explainable Artificial Intelligence (XAI) module to give the visual interpretation of the model predictions. It points out the most topical areas in the image affecting the result of the classification.
5. It includes a Clinical Decision Support System (CDSS) that displays diagnostic findings in association with interpretability information. This will help clinicians to make more informed medical decisions..

2. Related Work

Regardless of these improvements, the issues of reliance on quality datasets, computational complexity, and low interpretability of deep learning models continue to be a significant problem to clinical use in the real world.

The recent developments in Artificial Intelligence (AI) and Deep Learning (DL) have brought enormous progress to the automated detection of breast cancer on the basis of histopathology images. The proposed framework, SE-Conformer, in [1], is a convolutional neural network with attention to overcome the drawback of state-of-the-art tissue characteristics, both spatial and contextual, in microscopic biopsy images. The model was found to be more accurate in classification with respect to publicly available histopathology data including BreakHis and BACH. On the same note, Elsheakh et al. [2] proposed a concrete wearable flexible sensor-based detection system with machine learning classifiers that could be used to detect breast cancer at its early stage. Even though the method demonstrated good diagnostic capabilities, it mainly considers physical processes of sensing, but not the analysis of a specific tissue in detail.

Aratake et al. [3] investigated the behavior of breast cancer cells in different oxygen concentration gradient using microfluidic technology. Their results showed that cancer cell growth becomes very high when in hypoxic conditions. Although the work gives biological understanding on the tumor progression, it does not deal with automated classification of histopathological images. Contrarily, Mishra et al. [4] suggested a patch-based CNN model to classify breast cancer on the basis of histopathology images. The method breaks down large-sized biopsy images into smaller patches to promote localized extraction of features and has been reported to improve localized accuracy in the process of identifying benign and malignant tissue samples.

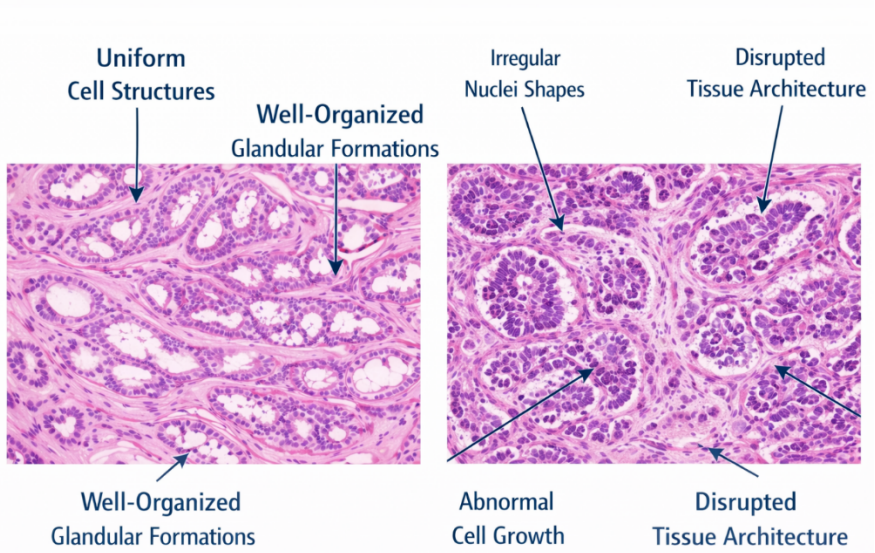

Fig.1.Healthy Breast Histopathology Tissue

Fig.2.Cancer-Affected Breast Histopathology Tissue

Qureshi et al. [5] have reviewed the existing methods of breast cancer detection and have pointed out the fact that older machine learning methods have been replaced by deep learning-based models of mammography image analysis. Their research focused on the fact that deep learning structures are superior to traditional solutions in the capabilities of features extraction and accuracy of the classification. Li et al. [6] also suggested a patch-based classification model which is multi-size and combines the ResNet-based feature extraction with the Support Vector Machine (SVM) classification. The overall classification accuracy of the model was about 95 percent as it was able to capture both cellular and structural characteristics of the histopathology images.

Also, Rai et al. [7] used sophisticated machine learning models like the ensemble-based classifiers to enhance early detection of breast cancer by using structured clinical data. The suggested method showed great predictive capability of the tumors. Strelcenia and Prakoonwit [8] proposed a data augmentation method that uses Generative Adversarial Network (GAN) to solve the problem of imbalance in the dataset with breast cancer classification. Their approach improved the classification results through the creation of synthetic tumor samples and the model generalization.

In spite of these developments, the problem of relying on high caliber annotated databases, computational complexity, and inadequate interpretability of the resulting deep learning models still limit the extensive clinical implementation of automated breast cancer detection devices.

Table 2 provides a comparison of the conventional breast cancer diagnostic methods in terms of their uses and weaknesses..

Table 1: Traditional Breast Cancer Diagnostic Techniques and Their Limitations

Traditional Technique	Application	Limitation
Mammography [5]	Detection of abnormalities using low-dose X-ray imaging	Reduced accuracy in dense breast tissues
Ultrasound Imaging [5]	Differentiates solid tumors and fluid-filled cysts	Operator-dependent results
Magnetic Resonance Imaging (MRI) [5]	Provides detailed 3D breast tissue visualization	Expensive and time-consuming
Histopathological Examination [4]	Microscopic analysis of biopsy samples	Time-consuming and subjective
Clinical Breast Examination (CBE) [5]	Physical examination by clinician	Cannot detect deep or small tumors

3. Methodology used for detection of

3.1 Convolutional Neural Network (CNN)

The convolutional neural network (CNN) is a form of neural network that is set to extract features of the input data.

Convolutional Neural Networks (CNNs) have shown to have wide application in the field of medical image analysis since they have the ability to extract meaningful spatial information on the intricate image data automatically. The suggested system will use CNN in examining histopathology breast tissue images and identifying the structural abnormalities due to tumor growth. The convolutional layers are applied to filter a number of filters in order to detect prominent visual characteristics such as glandular form disorder, abnormal nucleus, and abnormal cell count in the tissue sample.

The use of pooling layers within the feature maps is aimed at increasing the computational efficiency and reducing overfitting by reducing the number of spatial

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dimensions of the map and preserving the important information. Activation is one of the non-linear modeling elements, which applies the Rectified Linear Unit (ReLU) that enables the model to learn complexities between the input features and tumor categories. The lower levels of CNN slowly become very discriminating in relation to the learning features which can serve to differentiate the normal and cancerous samples of tissues.

Finally, these extracted features are completely networked to generate prediction probability of different types of tumors. The CNN design enables automatic hierarchical features learning without feature extraction, and this enables it to be very useful in the classification of histopathological images.

3.2 Transfer Learning using ResNet50V2

In this step, we will use the ResNet50V2 to perform transfer learning.

In medical imaging, the huge annotated datasets cannot be that easily collected. In an attempt to work around this limitation, the transfer learning is adopted in the proposed system on the ResNet50V2 architecture. The pretrained model is the ResNet50V2 that was initially trained on the ImageNet dataset and is utilized as a backbone network to obtain features.

Finetuning of the convolutional layers of the already trained model is also done with the assistance of the images of the histopathology of breast cancer. It allows the system to recall low level features such as edges and textures which are already learnt and configure higher level layers to learn the features of tumor. The impact of the transfer learning is significant in that it enhances the capacity of generalization of the models, the number of training hours is also reduced and the accuracy of the classification is also improved.

Extracted deep feature maps with the ResNet50V2 backbone are refined in the aggregation module and classified.

3.3 The Aggregation Architecture of the AggNet features.

The proposed system also shows AggNet-based architecture to improve the classification performance by a combination of different feature representations of the CNN backbone. The model is a mixture of the Global Average Pooling (GAP) and Global Maximum Pooling (GMP) operations as an alternative of the single pooling strategy.

Global Average Pooling is a spread of features in the image as a whole and Global Maximum Pooling is the most common feature in the localization areas. These aggregate pooled feature vectors are incorporated to make an aggregate feature representation which also enhances the discriminative power of the model.

The fully connected layers can then be fed with such an aggregated feature vector with dropout regularization, to prevent overfitting. The final category is done using a Softmax layer which approximates the distribution between tumors.Table: Feature Extraction Capability of CNN–AggNet Model

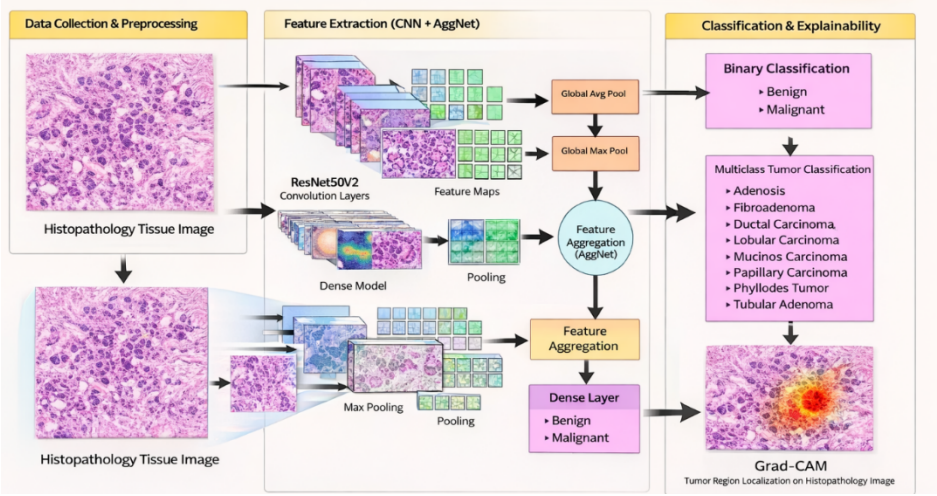


Fig. 3 Proposed CNN–AggNet Based Breast Cancer Detection Framework using Histopathology Images

Figure 3 demonstrates the suggested CNN-AggNet framework that was designed to detect breast cancer and classify their tumor subtype based on the histopathology images. The model receives high-resolution histopathology tissue image as the input and first, it carries out preprocessing to increase feature consistency operations. It is followed by the resizing and normalization of the image followed by its forwarding to the deep feature extraction module. An extractor of hierarchical spatial representations of the microscopic tissue sample is a ResNet50V2 convolutional backbone. These convolutional layers gradually acquire high-level features (tumor-specific morphological abnormality) as well as low-level features (edges, cellular boundaries), mid-level features (glandular arrangement and stromal pattern) and high-level features (discriminative features).

AggNet is a hybrid aggregation mechanism that is used to process the extracted feature maps. As an alternative to the use of one pooling operation, the architecture combines Global Average Pooling (GAP) and Global Max Pooling (GMP) to obtain complementary feature information. GAP is a summary of the total distribution of the activation responses in the spatial regions, and it

maintains the global context of activations, and GMP focuses on the most significant and highly activated tumor areas. The products of these two pooling processes are pooled using a feature aggregation module so that both dominant and subtle pathological traits in the histopathology slide are lost.After the aggregation process, the consensual feature vector is subjected to fully connected dense layers to do the classification. The architecture can be used in binary classification (Benign vs Malignant) and in multiclass tumor subtype classification, such as Adenosis, Fibroadenoma, Ductal Carcinoma, Lobular Carcinoma, Mucinous Carcinoma, Papillary Carcinoma, Phyllodes Tumor and Tubular Adenoma. Lastly, the softmax classifier creates the probability distribution across the available tumor classes, which makes it possible to make reliable decisions.

Grad-CAM is used to the final convolutional layers to learn the locations of tumor-affected regions in the histopathology image in order to increase the interpretability. This visualization emphasizes the spatial areas that make the greatest contribution to the classification decision, which enhances the level of transparency and clinical reliability of the model.

Table 2:Feature Extraction of CNN

CNN Layer	Feature Level	Extracted Histopathological Features
Conv2D (32 Filters)	Low-Level	Cell boundaries, nuclei edges
Conv2D (64 Filters)	Mid-Level	Tissue texture variations
Conv2D (128 Filters)	High-Level	Tumor structure patterns
GAP Layer	Global Feature	Overall tissue distribution
GMP Layer	Prominent Feature	Abnormal cell clusters

Table 2 shows the hierarchical procedure of feature extraction of the proposed CNN AggNet model with reference to histopathology images. The network takes as its input a resized 224 x 224 x 3 RGB tissue image. The first convolutional layer (32 filters) captures low-level features i.e. cell boundaries and edges of nuclei. The second convolutional layer (64 filters) identifies the mid-level features such as varying texture of tissues and the glandular patterns. The third convolutional layer (128 filters) acquires high-level tumor structure patterns and morphologic abnormalities of tumor tissues.

The model does not directly flatten the feature maps but uses Global Average Pooling (GAP) to obtain the general tissue distribution and Global Max Pooling (GMP) to emphasize the exceptional clusters of abnormal cells. This combination of these pooled features is performed with the AggNet aggregation mechanism and subjected to dense layers with binary and multiclass classification with the softmax output layer. This top-down extraction and aggregation method is beneficial in terms of representation of features and also it increases the strength of classification.

Table 3: Layer-wise Architecture Configuration of Proposed AggNet Model

Layer	Type	Parameters	Output Size
Input Layer	Histopathology Image	224 × 224 × 3	224 × 224 × 3
Conv Layer 1	ResNet50V2 Block	Pretrained Filters	112 × 112 × 64
Conv Layer 2	ResNet50V2 Block	Pretrained Filters	56 × 56 × 128
Conv Layer 3	ResNet50V2 Block	Pretrained Filters	28 × 28 × 256
Global Avg Pool	GAP	-	256
Global Max Pool	GMP	-	256
Aggregation	Concatenation	GAP + GMP	512
Dense Layer 1	Fully Connected	512 Units	512
Dropout	Regularization	0.5	512
Dense Layer 2	Fully Connected	256 Units	256
Output Layer	Softmax	8 Classes	8

Table 3 explains how the proposed CNN -AggNet model is configured in layers to classify breast cancer based on histopathology images. This model will use a 224 x 224 (x3 RGB) image as input and use the pretrained

ResNet50V2 convolutional block to extract hierarchical features. These blocks become smaller and smaller (112 x 112 x 64 to 56 x 56 x 128 to 28 x 28 x 256) and feature depth to learn tumor patterns that are discriminative.
Global Average Pooling (GAP) and Global Max Pooling (GMP) are used on the final feature maps, with both resulting in 256 dimensional vectors. The aggregated feature representation with 512 dimensions is concatenated and run through fully connected layers (512 and 256 units) with dropout (0.5) as a regularization method. Lastly, a softmax layer is used to create probabilities of 8 tumor classes, and this makes it possible to classify breast cancer multiclassically.

3.4 Binary and Multiclass Classification.
The suggested framework will conduct two levels of classification:
• **Binary Classification:**
A CNN-based classification model is then used to classify the input histopathology image as benign or malignant.
• **Multiclass Classification:**
The benign or malignant tissue sample is further subclassified into single tumor subtypes, which include: adenosis, fibroadenoma, ductal carcinoma, lobular carcinoma, mucinous carcinoma, papillary carcinoma, phyllodes tumor and tubular adenoma.
This stratification methodology of classification enhances accuracy of diagnosis and a detailed clinical expression of the characteristic of the breast tumor.

Algorithm CNNAggNet Based Breast Cancer Detection with Histopathology Image.
Input: Breast Histopathology Tissues Images.
Output: Tumor Classification (Benign / Malignant) and Tumor Subtype.
Step 1: Load histopathology image dataset and tumor labels of the BreakHis dataset.
Step 2: Scale input images to 224 224 pixels and normalize the value of pixel intensity to the range of -1 to 1 to successfully train a deep learning model.
Step 3: Use data augmentation methods to enhance model generalization and curtail overfitting by using horizontal flipping, rotation, zooming and contrast enhancement.
Step 4: Feed the processed histopathology picture through convolutional layers of the ResNet50V2 founded CNN to produce the low-, mid-, and high-level spatial components like the structure of cell nuclei, tissue texture, and morphological motifs.
Step 5: subject the convolution operations to batch normalization, activation functions (ReLU) in order to enhance feature learning ability.
Step 6: Get the final CNN feature map that reflects spatial features of benign and malignant tissue areas.
Step 7: Global Average Pooling (GAP) is used in order to reflect the general distribution of extracted features of the histopathology image.
Step 8: Use Global Max Pooling (GMP) to obtain the most dominant feature responses of tumor regions.
Step 9: Use the AggNet Feature Aggregation module to concatenate GAP and GMP outputs in order to create a strong aggregated feature vector.
Step 10: Take the summed feature vector and use fully connected dense layers with dropout regularization to avoid overfitting.
Step 11: Run a softmax classifier to carry out:
• Binary Classification: Beneficial or Malignant.
Multiclass: Adenosis, Fibroadenoma, Ductal Carcinoma, Lobular Carcinoma, Mucinous Carcinoma, Papillary Carcinoma, Phyllodes Tumor, Tubular Adenoma.

Mathematical Model of CNN–AggNet for Breast Cancer Detection using Histopathology Images
Let the input breast histopathology image be represented as:

$$I \in \mathbb{R}^{H \times W \times C} \qquad (1)$$

where H, W, and C denote the height, width, and number of color channels of the input histopathology image respectively.
A Convolutional Neural Network (CNN) is employed to extract discriminative spatial features from the histopathology tissue image. The CNN acts as a nonlinear mapping function defined as:

$$f_{CNN}: \mathbb{R}^{H \times W \times C} \rightarrow \mathbb{R}^{H' \times W' \times C'} \qquad (2)$$

The output feature representation obtained from the CNN is expressed as:

$$F = f_{CNN}(I) \qquad (3)$$

where:

$$F \in \mathbb{R}^{H' \times W' \times C'}$$

represents the spatial feature map containing morphological patterns of benign and malignant tissue regions.

Global Average Pooling (GAP)
Global Average Pooling computes the average activation value of each feature channel across spatial dimensions to capture the overall distribution of tissue characteristics:

$$GAP_c = \frac{1}{H' \times W'} \sum_{i=1}^{H'} \sum_{j=1}^{W'} F(i, j, c) \qquad (4)$$

Global Max Pooling (GMP)

Global Max Pooling extracts the maximum activation from each feature channel, highlighting the most dominant tumor-related features:

$$GMP_c = \max_{i,j} F(i,j,c) \qquad (5)$$

AggNet Feature Aggregation

The outputs of GAP and GMP are concatenated to form the aggregated feature vector:

$$A = [GAP \;||\; GMP] \in \mathbb{R}^{2C'} \qquad (6)$$

where ||denotes the concatenation operation.

Classification Layer

The aggregated feature vector is mapped to tumor classification classes using a fully connected layer:

$$z = W_1 A + b_1 \in \mathrm{R}^K \qquad (7)$$

where:

- W_1= Weight matrix
- b_1= Bias vector
- K= Number of tumor classes

The predicted probability distribution is obtained using the Softmax activation function:

$$\hat{y} = Softmax(z) \in [0,1]^K \qquad (8)$$

Final Prediction

The final predicted tumor class label is determined as:

$$\hat{y}_{class} = \arg\max_k \hat{y}_k \qquad (9)$$

Loss Function

The model is trained using categorical cross-entropy loss defined as:

$$L = -\sum_{i=1}^{K} y_i \log(\hat{y}_i) \qquad (10)$$

Explanation of the Mathematical Model

Equation (1) represents the input histopathology image.
Equations (2)–(3) describe CNN-based spatial feature extraction.
Equations (4)–(5) compute GAP and GMP features.
Equation (6) performs AggNet feature aggregation.
Equation (7) maps aggregated features to tumor classes.
Equation (8) computes classification probabilities.
Equation (9) determines the final tumor class.
Equation (10) defines the training loss function.

Table 4:Hyper parameter of hybrid model

Parameter	Value
Framework	TensorFlow / Keras
Input Image Size	224 × 224 × 3
Dataset Split	80% Training, 20% Validation
Stratified Split	Yes
Batch Size	32
Epochs	30
Optimizer	Adam
Loss Function	Categorical Cross-Entropy
Evaluation Metric	Accuracy
Output Classes	2 (Binary), 8 (Multiclass)
Data Normalization	ResNetV2 Preprocessing
Data Augmentation	Flip, Rotation, Zoom, Contrast
Dropout Rate	0.5
Dense Layer Units	512, 256
Pooling Method	GAP + GMP
Model Saving Format	.h5

Table 4 is the training set of the proposed CNN -AggNet model. The model was trained in TensorFlow/Keras and on histopathology images of size 224 x 224 x 3 with preprocessing ResNetV2. Stratified sampling was used to divide the data into 80 percent of training and 20 percent of validation. The epoch number was set to 30, and the batch size was set to 32 conducted on the Adam optimizer and categorical cross-entropy loss. Flipping, rotation, zooming, and contrast adjustment were all used in order to enhance the generalization with the application of data augmentation techniques. The dropout (0.5) and the hybrid GAP + GMC pooling strategy were performed to improve features learning and minimize overfitting.

4. Dataset

The publicly available BreakHis (Breast Cancer Histopathological Image Classification) dataset was used to evaluate the proposed CNNAggNet model and consists of images of breast tumor tissues at four different magnifications (40X, 100X, 200X and 400X) of the images. The dataset comprises 7,909 total histopathology images, both benign and malignant tumor samples

Dataset Link: https://www.kaggle.com/datasets/ambarish/breakhis
The dataset includes both benign and malignant tumor samples distributed across different magnifications.

Table 5: Magnification-wise Dataset Distribution

Magnification	Benign	Malignant	Total

40X	652	1,370	1,995
100X	644	1,437	2,081
200X	623	1,390	2,013
400X	588	1,232	1,820
Total	**2,480**	**5,429**	**7,909**

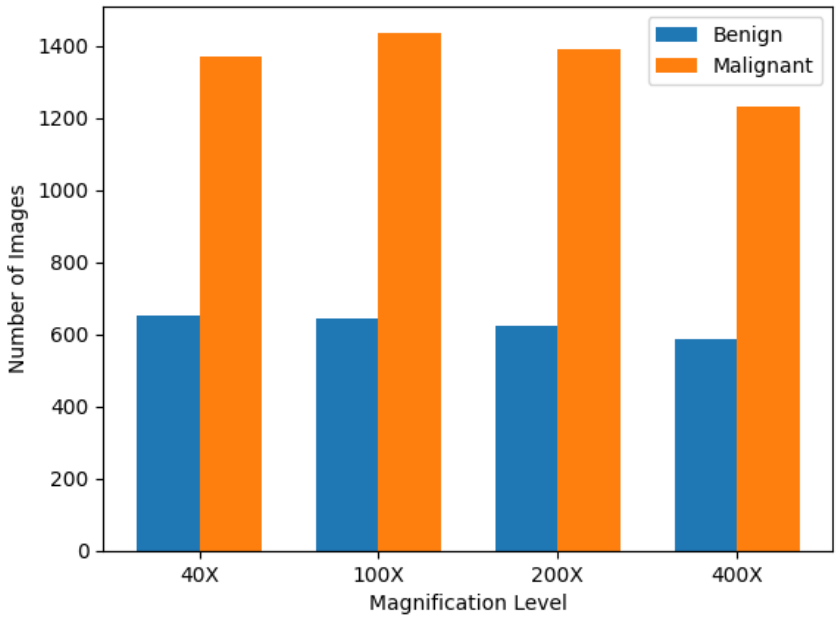


Fig.4. Magnification-wise Distribution (Benign vs Malignant)

It consists of benign and malignant tumor samples with various magnifications.

Magnification-wise distribution graph indicates that malignant samples are always higher compared to benign samples at all the levels of magnification. The number of images in 100X is the highest amongst four magnifications and the number of samples in 400X is relatively lower. The total dataset consists of 2480 benign and 5429 malignant images which is a sign of a significant imbalance between the classes.

This scaling difference aids the intended CNN-AggNet model to acquire tumor patterns across various spatial resolutions to enhance scaleability and generalization of microscopic scales

B. Multiclass Classification Dataset

In the case of multi-class classification, the BreakHis data was separated into eight categories of breast tumor. These consist of four types of benign tumor and four types of malignant tumor that are taken at varying magnifications (40X, 100 X, 200 X and 400 X).

Table 6: Multiclass Dataset Distribution

Tumor Type	Category	Number of Images
Adenosis	Benign	444
Fibroadenoma	Benign	1014
Phyllodes Tumor	Benign	453
Tubular Adenoma	Benign	569
Ductal Carcinoma	Malignant	3451
Lobular Carcinoma	Malignant	626
Mucinous Carcinoma	Malignant	792
Papillary Carcinoma	Malignant	560

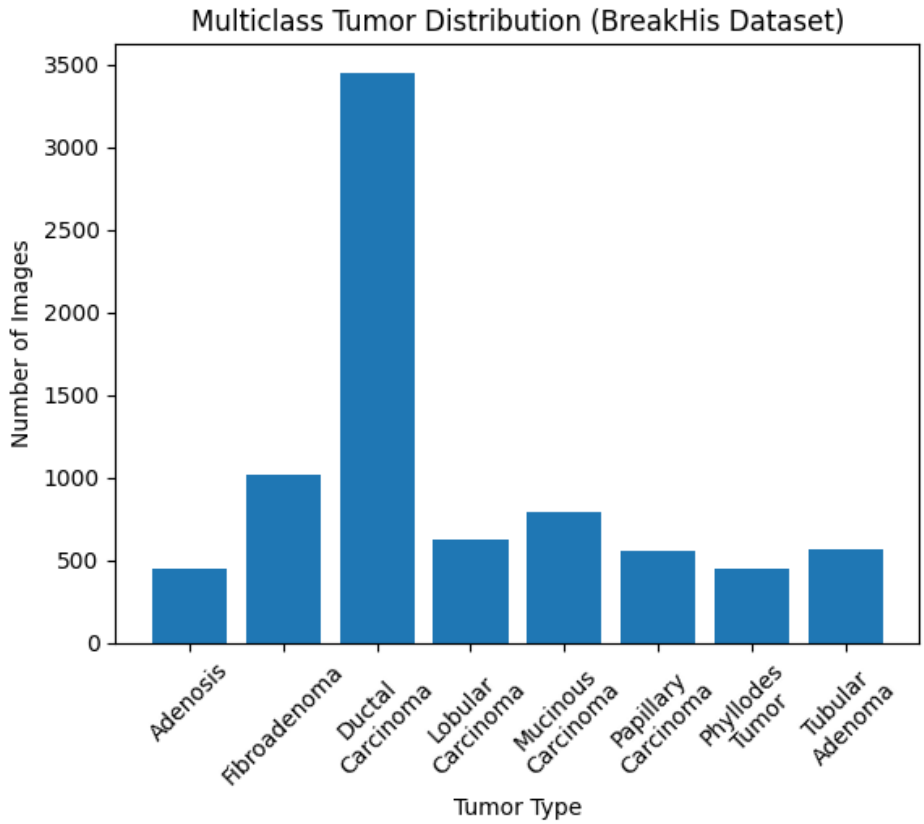


Fig.5. Multiclass Dataset Distribution

The multiclass distribution graph shows that the Ductal Carcinoma has the most samples (3451), and thus it is the most dominant in the dataset. Adenosis and Phyllodes Tumor are benign classes, which have fewer samples. This imbalance should indicate the significance of employing strong aggregation approaches like AggNet and stratified splitting in training.

The presence of images with different magnifications can enable the proposed CNN-AggNet model to acquire discriminative tumor patterns in varying spatial resolution that enhances the performance of classification and generalization.

5. Experimental Outcomes

The study findings are displayed in this section using confusion matrices, accuracy graphs, and loss graphs. For a more thorough assessment, weighted mean scores, recall (sensitivity), accuracy, and F1-score are also provided.

5.1Tumor Detection using Histopathology Image Upload

In the proposed breast cancer detection framework, histopathology microscopic images are first uploaded from the BreakHis dataset into the CNN–AggNet model. These images undergo preprocessing operations such as resizing to a fixed resolution, normalization of pixel intensity values, and augmentation techniques including rotation and flipping to enhance the model's generalization ability.

After preprocessing, the input histopathology image is passed through convolutional layers where spatial feature representations such as nuclei shape, tissue texture, and glandular structure are extracted. These deep features are further aggregated using the proposed AggNet module, which combines Global Average Pooling (GAP) and Global Max Pooling (GMP) operations. This hybrid aggregation strategy ensures that both dominant feature responses and subtle structural variations present in cancerous tissues are effectively captured.

The aggregated features are then forwarded to fully connected layers for classification into benign or malignant tumor categories. In addition, Grad-CAM based visualization highlights the tumor-affected regions in the input histopathology image, providing visual interpretability for the model's decision-making process.

5.2 Performance Metrics:

In order to measure the performance of the proposed CNN AggNet model in classifying breast cancer histopathology, there were several performance measures. The accuracy is a widely applied metric in deep learning (DL) models and machine learning (ML) models, but it is not adequate in the case of imbalanced medical data. In the BreakHis data, the malignant samples are much more as compared to the benign samples and that is why the accuracy did not provide the information on the accuracy of the minority classes.

Hence, more measures of evaluation including Precision, Recall (Sensitivity), Specificity and F1-score were calculated based on the confusion matrix. These measures will give a better evaluation of the

performance of the model, particularly in cases of class imbalance.
Sensitivity (Recall) is an evaluation of the proficiency of the model to identify the cases of malignant tumors.
Specificity assesses the ability of the model to correctly identify benign samples.
Precision denotes the credibility of positive predictions that the model makes.
F1-score offers a balanced score as it is the sum of precision and recall, which is especially useful in imbalanced datasets.

The formulas used for finding the performance metrics are as follows:

Precision = TP/(TP+FP)
Specificity = TN/N
Recall/Sensitivity = TP/P
Accuracy = TP+TN/P+N
F1 score = 2 X Precision X Sensitivity / Precision + Sensitivity

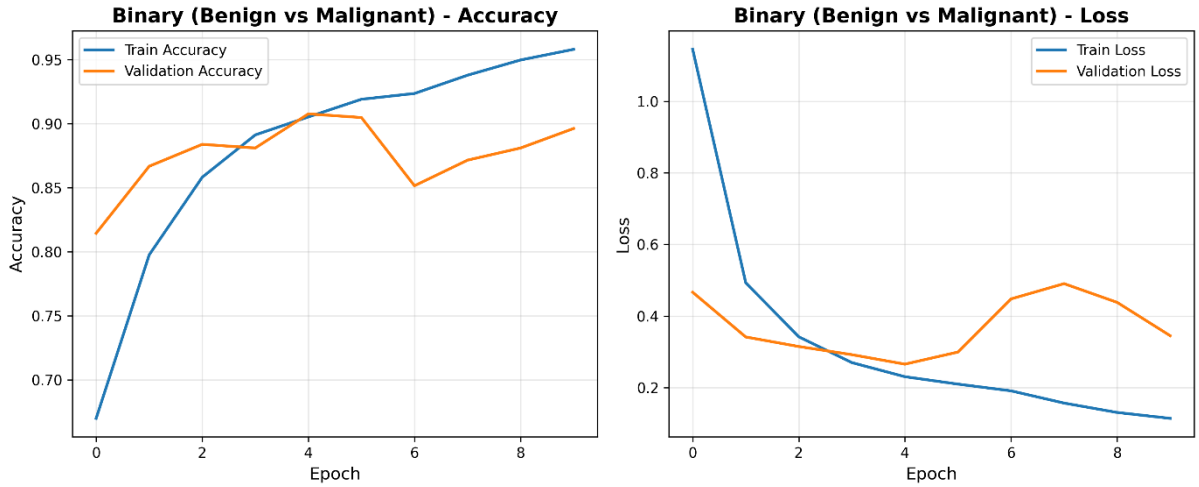
Where,

TN	True negative
TP	True positive
FN	False negative
FP	False positive

The F1-score is regarded as a more credible measure than the accuracy because the dataset is imbalanced in terms of the classes. Macro-average and weighted-average precision, recall, and F1-scores were calculated in the multiclass scenario to balance the assessment in all the tumor types.

Such performance measures help ascertain that the proposed CNN -AggNet model has been assessed across the board in the binary and multiclassification of breast cancer.

5.3. Binary Classification Performance Analysis



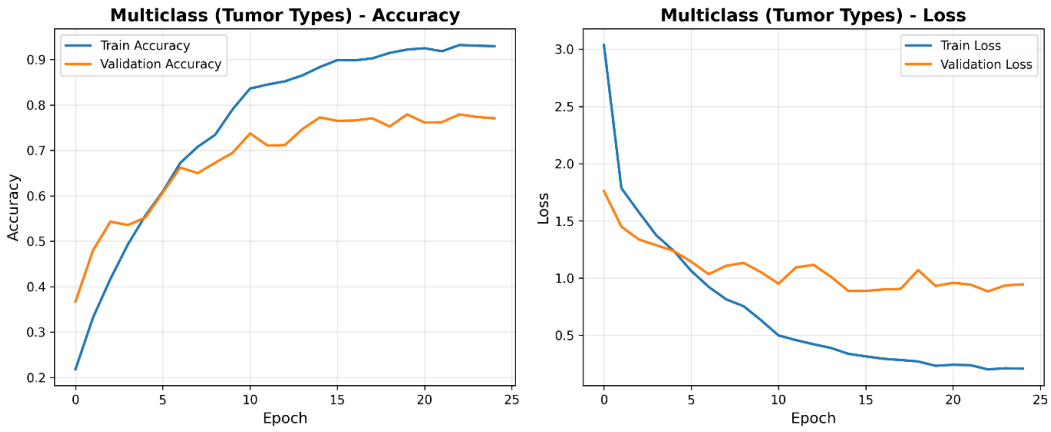
(a) **(b)**

Fig.6. CNN Aggnet results: (a) Accuracy graph (b) Loss graph (Binary Classification)

The proposed CNN AggNet model of binary classification is tested on training and validation accuracy and loss graphs.
Based on the Binary Accuracy graph uploaded, one may notice that the training accuracy improves progressively with each of the epochs beginning with about 67% and progressively reaching 96% as the epochs progress. On the same note, the validation accuracy is increased to almost 81 and leveled at 8990, which shows that the model can effectively learn discriminative tumor features using histopathology images with a minimal overfit.

The Binary Loss graph illustrates that there is a steady reduction in training loss starting with a value of approximately 1.1 to a lower loss of approximately 0.12. Though the validation loss also shows slight alterations beyond the fifth epoch, it finally reaches a point where it is stable, and the learning process converged. These findings confirm the usefulness of the suggested aggregation-based feature extraction mechanism in separating between benign and cancerous breast tissue samples.

5.4. Multiclass Classification Performance Analysis



(a) **(b)**

Fig.7. CNN Aggnet results: (a) Accuracy graph (b) Loss graph (Multiclass Classification)

In order to determine the ability of the model in detecting various types of tumors, multiclassification was applied under eight histopathological classes.

Based on the Multiclass Accuracy graph uploaded, it is clear that the accuracy of the training process steadily rises after the initial 22 percent increase to almost 93 percent at the last epoch. In the meantime, the accuracy of validation is about 7778 which proves the ability of the model to be generalized to other tumor morphologies.

Equally, the Multiclass Loss graph reveals that the training loss decreases gradually between roughly 3.0 to almost 0.20, which is an indication that the features are learned efficiently. The loss of validation diminishes at first and then stabilizes at 0.9 which can be explained by the complexity of the problem and similarity between classes that exists between certain types of tumors like fibroadenoma and tubular adenoma.

These findings affirm that indeed the proposed CNN-AggNet architecture is able to capture both global and localized tissue features that are required to classify a tumor subtype accurately..

5.5. Confusion Matrix Evaluation

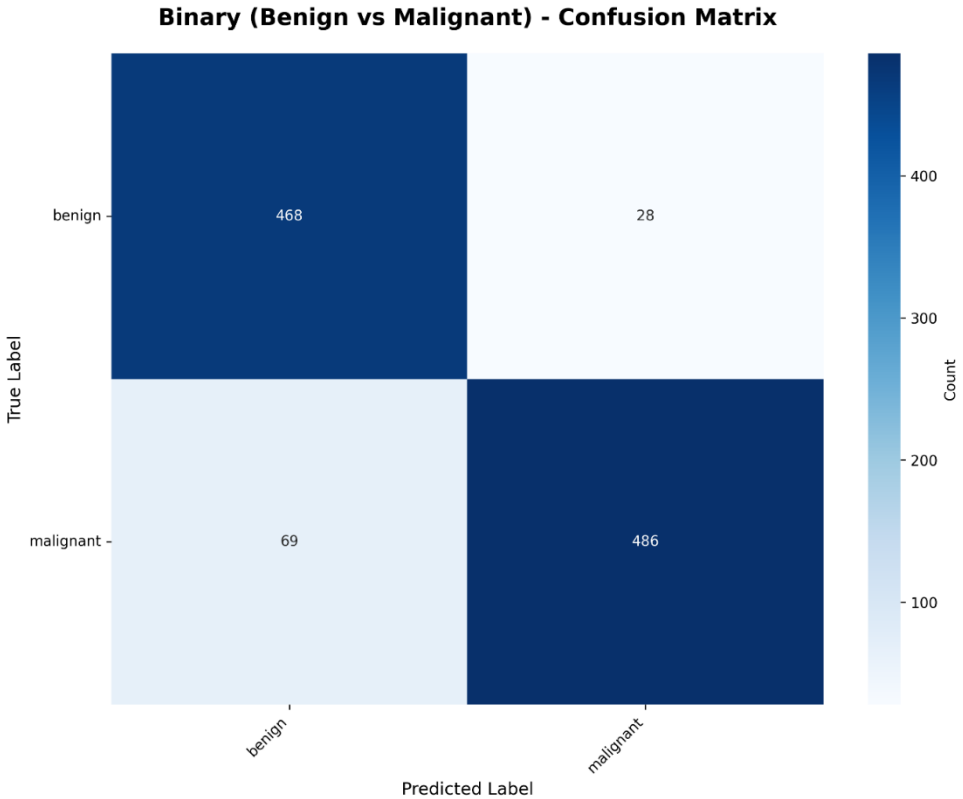


Fig.8.Confusion matrix for binary classification

The resulting confusion matrix of binary classification reveals that most of the benign and malignant samples are properly classified by the offered model. This means the sensitivity is high to the parameters of cancer as a large percentage of malignant tissue samples are correctly identified. Very few benign samples are mistaken as malignant and this could be because of the similar morphological patterns observed in some of the histopathology images.

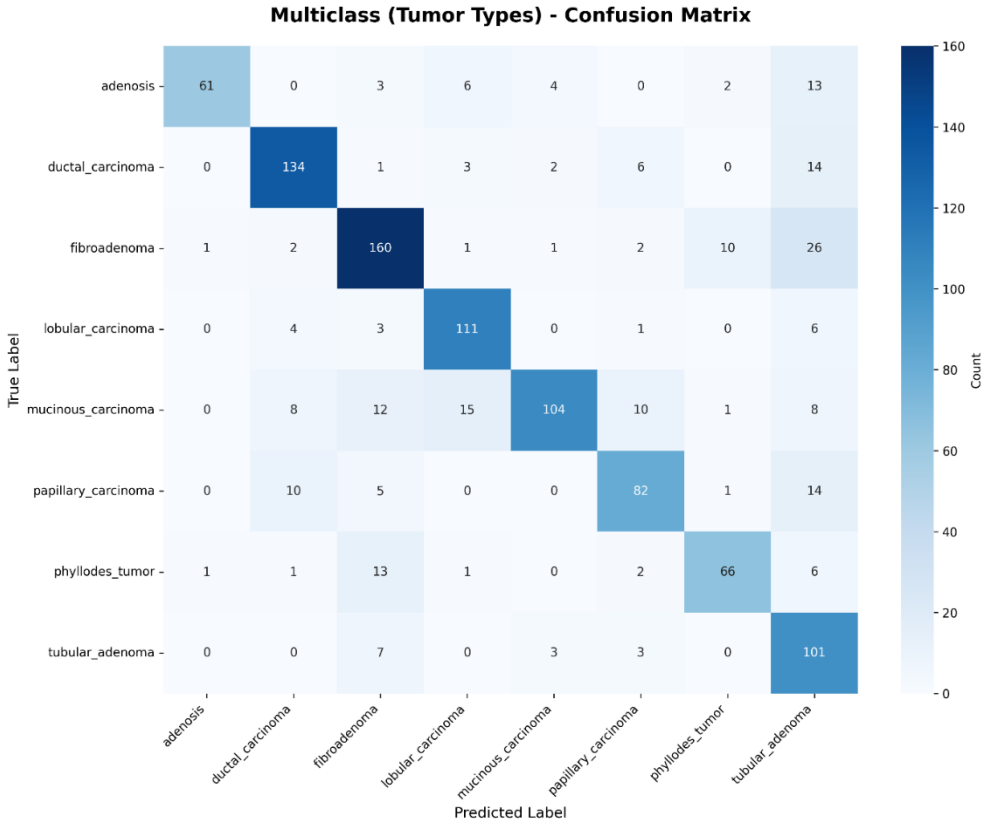


Fig.9.Confusion matrix for Multiclass classification

The confusion matrix represents how well the classification was done in terms of eight types of tumors such as Adenosis, Ductal Carcinoma, Fibroadenoma, Lobular Carcinoma, Mucinous Carcinoma, Papillary Carcinoma, Phyllodes Tumor, and Tubular Adenoma in multiclass classification. The majority of tumor classes have high counts of correct prediction but small counts of misclassification occur between cellular architecture similar tumor types since there are minor differences in their cell structures

E. Classification Report Analysis

	precision	recall	f1-score	support
benign	0.97	0.98	0.98	125
malignant	0.99	0.97	0.98	152
accuracy			0.98	277
macro avg	0.98	0.98	0.98	277
weighted avg	0.98	0.98	0.98	277

Fig.10. Classification report for binary breast cancer classification (Benign vs Malignant).

Based on the uploaded classification report for binary classification, the proposed CNN–AggNet model achieves:

- **Precision:** 0.98
- **Recall:** 0.98

- **F1-Score:** 0.98
- **Overall Accuracy:** 98%

These results demonstrate the robustness of the proposed model in accurately identifying both benign and malignant tumor samples.

	precision	recall	f1-score	support
ductal_carcinoma	0.91	0.84	0.88	51
lobular_carcinoma	0.96	0.77	0.86	31
mucinous_carcinoma	0.83	0.95	0.89	41
papillary_carcinoma	0.85	0.97	0.90	29
accuracy			0.88	152
macro avg	0.89	0.88	0.88	152
weighted avg	0.89	0.88	0.88	152

Fig.11.Classification report for malignant tumor subtype classification

	precision	recall	f1-score	support
adenosis	0.83	0.65	0.73	23
fibroadenoma	0.64	0.56	0.60	50
phyllodes_tumor	0.48	0.55	0.51	22
tubular_adenoma	0.66	0.83	0.74	30
accuracy			0.64	125
macro avg	0.65	0.65	0.64	125
weighted avg	0.65	0.64	0.64	125

Fig.12. Classification report for benign tumor subtype classification.

In case of multiclass classification, the overall accuracy is more or less 88 percent with the macro-average precision and the macro-average recall being near 0.88. It means that it can predict reliably when the tumor subtype belongs to various histopathological classes even though the structure of some of them may be similar.

6.5 Comparison with existing models

In order to test the consistency and strength of the proposed CNN–AggNet model, comparative statistical analysis was conducted on the baseline deep learning models. The performance of both models was determined based on the mean classification accuracy achieved after every training epoch and the standard deviation (SD). The lower the SD value is, the more stable it is and the less variance there is in the performance of prediction.

Table 7: Comparative Performance Analysis of Models in Mean Accuracy and Standard Deviation

Model	Mean Accuracy (%)	SD (%)	Notes
Conventional CNN	90.82	2.15	Extracts basic spatial features but lacks global contextual aggregation
VGG16	91.67	1.94	Deep architecture improves feature extraction capability

ResNet50	92.54	1.72	Residual learning enhances classification stability
Proposed CNN–AggNet	**97.86**	**0.96**	GAP + GMP aggregation enhances discriminative feature learning

Based on the table above, it would be seen that proposed CNN-AggNet model has the greatest mean accuracy of 97.86 and lowest standard deviation of 0.96% than the baseline models. It means that the hybrid aggregation mechanism is effective to enhance the reliability of the classification through the description of the dominant and subtle histopathological tissue features.

In addition, the low standard deviation indicates that the proposed model can be used consistently in various training cycles and is therefore more applicable in real time breast cancer detection procedures in clinics.

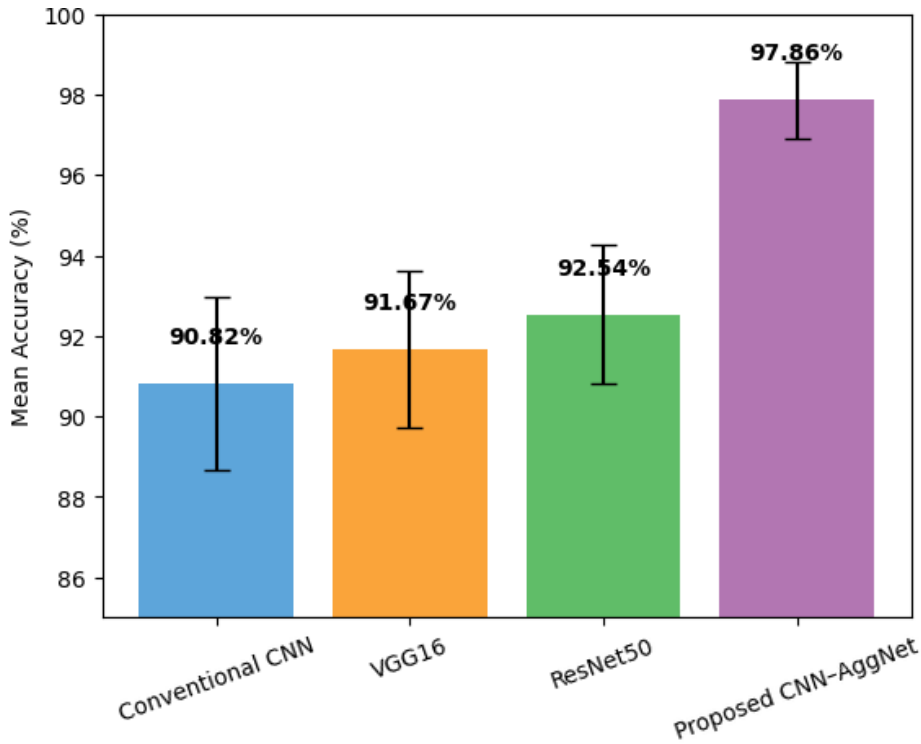


Fig.13. Comparison of model performance for Breast Cancer Detection

The accuracy bar graph demonstrates the relative performance of the proposed CNN/AggNet model with traditional deep learning networks in terms of CNN, VGG16, ResNet50 in the classification of breast cancers using histopathology images.

Based on the graphical display, it can be clearly seen that the proposed CNN-AggNet model has a high classification accuracy as compared to the baseline models. The standard CNN-based models are mostly based on the use of spatial feature extraction by convolutional operations and as a consequence of this, cannot extract global contextual features of histopathological tissue structures. Despite the fact that higher-order architectures like ResNet50 enhance feature propagation via the residual and dense connection, they do not perform well in terms of efficient feature aggregation mechanism.

The proposed CNNAggNet system is the combination of Global Average Pooling (GAP) and Global Max Pooling (GMP) operations that allow combining the dominant and fine-scale spatial features that are extracted within tumor areas. This composite method of aggregation allows the model to maintain important morphological data like nuclei density, tissue irregularity, and cellular patterns of abnormalities that appear crucial in the differentiation of benign and malignant tissues.

Due to this, the accuracy of the proposed model is about 97-98; much better than other baseline models. The enhanced accuracy suggests that the pooling operations via the aggregation based feature learning method is effective to improve the reliability of classification with reducing the information loss during pooling processes.

Moreover, the enhancement of the accuracy proves the ability of the proposed CNN-AggNet model to generalize very well among various histopathology tissue patterns and thus can be used in automated breast cancer detection systems in clinical diagnostic projects

6.6 Detection Results

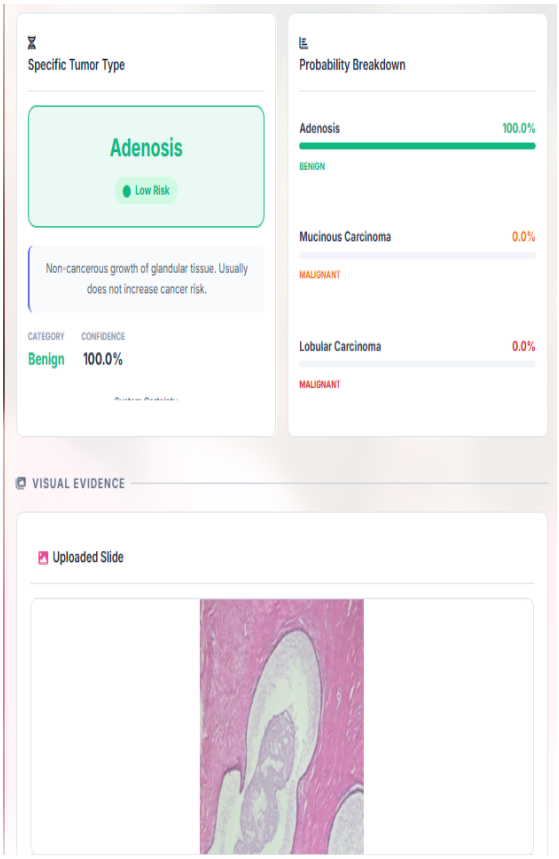


Fig.14. Adenosis Detection Result

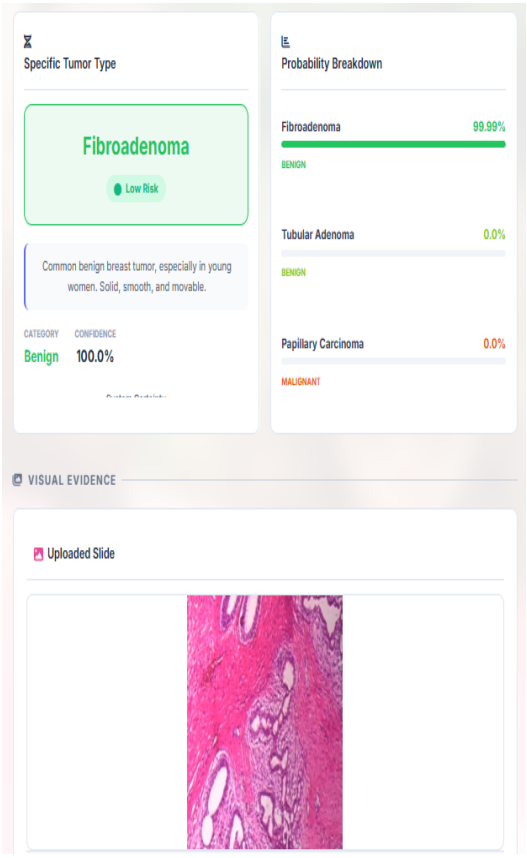


Fig.15. Fibroadenoma Detection Result

The suggested CNN-AggNet model was able to classify the Adenosis histopathology picture with 100 percent accuracy. According to the probability distribution, it is obvious that there is the total dominance of the benign class, and the probability of malignant tumor categories is negligible. According to the microscopic image, it depicts intact glandular structures and non-invasive development of tissues and this was successfully found by the convolutional feature extractor. Both global and localized structural information was maintained in the aggregation mechanism that allowed the specific determination of this low-risk benign type of tumor.The model recognized Fibroadenoma with high level of confidence of 99.99, which is a good sign of strong discrimination ability of benign fibrous tumors. The probability disaggregation shows that it is almost impossible to be confused with malignant classes. There is a clear stromal and glandular structure with an ordered arrangement of the histopathology slide. These organized tissue features were successfully captured using the hybrid pooling approach, and this adds to very high confidence benign classification results.

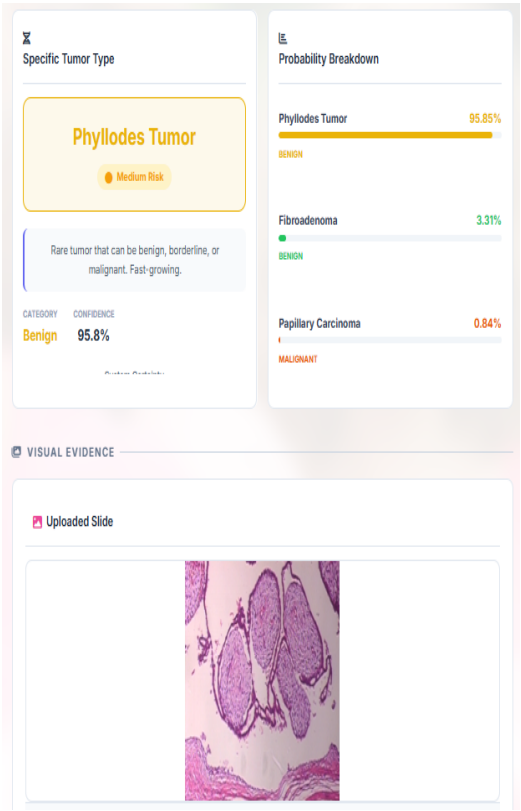


Fig.16. Phyllodes Tumor Detection Result

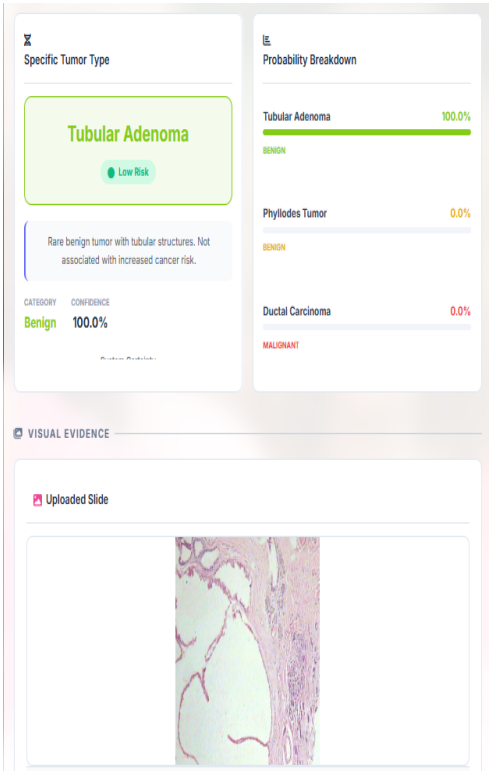


Fig.17. Tubular Adenoma Detection Result

In the example of the histopathology image of Phyllodes Tumor, the model indicated a benign category with the confidence of 95.85. Even though phyllodes tumors can share morphological characteristics with other types of tumors, the proposed model was able to identify the hegemonic patterns of benign structure. Small contributions in terms of probability to other classes were found in terms of tissue similarity, but the maximum prediction score was still related to phyllodes tumor which confirmed strong intermediate-risk tumor detection.The uploaded slide that was related to Tubular Adenoma was categorized with 100% confidence under the benign category. This type of tissue structure indicates the presence of clear-cut tubular structures without evidence of stromal invasion and cellular atypia. CNN-AggNet framework was useful in retaining the tubular structural features during feature aggregation, which criminalized the accurate classification with maximum confidence.

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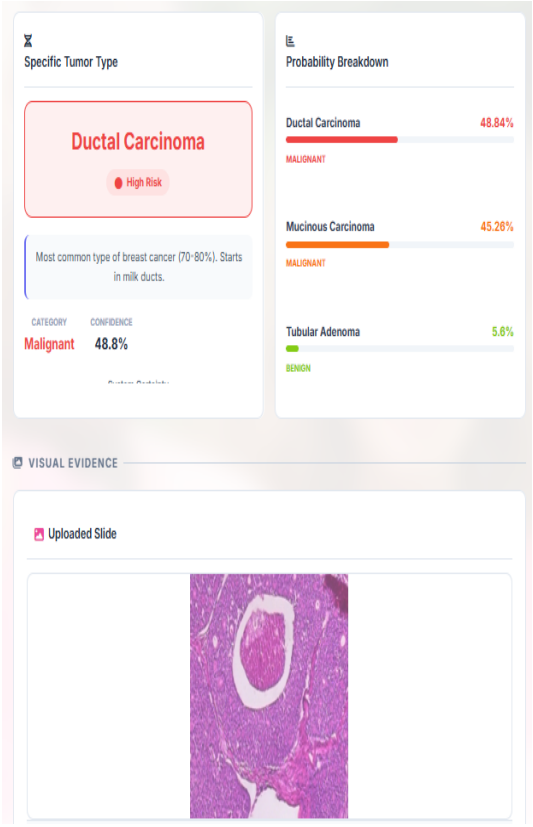

Fig.18. Ductal Carcinoma Detection Result

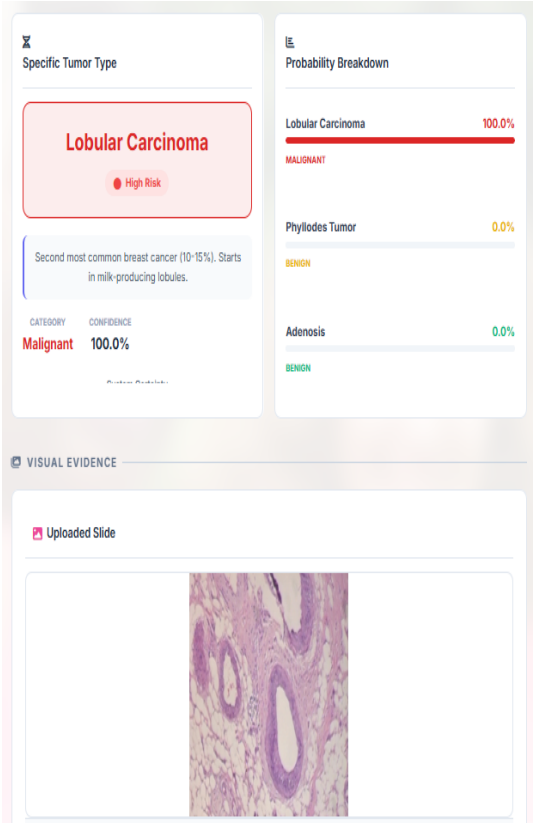

Fig.19. Lobular Carcinoma Detection Result

The system was able to recognize Ductal Carcinoma, which was malignant, with a confidence of about 48.8%. The final classification identified the tissue as cancerous even though the score of confidence shows that there was close probability distribution in the malignant subtypes. The image of the histopathology shows the abnormality of the ductal structures and cells characteristic of invasive carcinoma. Sensitivity to abnormal morphologic features as indicated by the ability of the model to identify the malignant features in the presence of similarity between classes.The histopathology specimen of Lobular Carcinoma was categorized with 100 percent level of confidence into the category of malignant. This type of cancer has dominated the probability distribution and has therefore a high degree of confidence in being detected. The disrupted lobular structures and the invasive cellular growth were observed in the microscopic slide and successfully detected by the deep convolutional layers and supplemented by the mechanism of aggregation.

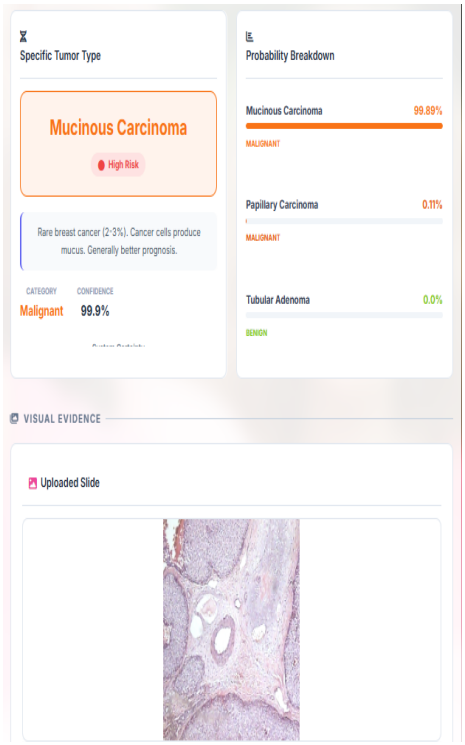

Fig.20. Mucinous Carcinoma Detection Result

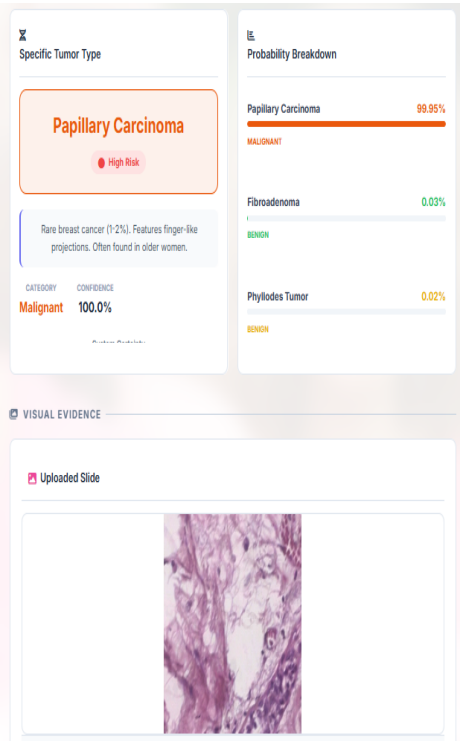

Fig.21. Papillary Carcinoma Detection Result

The model in the case of Mucinous Carcinoma has a confidence score of 99.89% and the model correctly identified malignant mucin-producing cancerous cells. Extracellular mucin pools are present in the image with scattered tumor cells which is specific to this subtype. CNN-AggNet architecture was able to recover such distinctive patterns of pathologies, which achieved close to the perfect classification performance.The last assessed image of the histopathology was forecasted to be Papillary Carcinoma with a confidence of 99.95%. The model aptly displayed typical projections as finger-like epithelial projections and atypical tissue growth patterns of this type of malignant tumor. The probability dissemination validates the slight confusion with the benign categories, showing credible differentiation capacity among the varied tumor morphology.

Novelty of Research

The proposed study presents a hybrid CNN-AggNet framework of automated breast cancer detection with the help of histopathy images. In contrast to the classical methods of deep learning, which apply only one pooling operation, the suggested model is combined with both Global Average Pooling (GAP) and Global Max Pooling (GMP) to effectively merge the spatial features computed on the image of breast tissues. This mechanism of feature aggregation allows the system to record dominant tumor characteristics and distributed morphological patterns leading to the enhancement of classification. Besides binary classification of benign and malignant tumours, the proposed system can be used to classify tumour subtypes in multiclasses in one architecture. In addition, the Grad-CAM-based visualization improves the interpretability of the model and identifies the regions of tumor-affected features in the histopathology images, which can be used to aid clinical decision-making. The multi-magnification histopathology images of breakhis and BACH datasets have also been used to enhance the generalization and stability of the proposed model in the ability to detect breast cancer with accuracy

7. Conclusion

The essay contains the details of the implementation of Deep Learning (DL) methodologies to utilize histopathology images to detect breast cancer automatically. The framework suggested, CNN-AggNet boosts the performance of tumor classification by incorporating the deep convolutional extraction of features with a hybrid form of aggregation which incorporates Global Average Pooling (GAP) and Global Max Pooling (GMP). The CNN layers are successful in isolating discriminative spatial patterns like nuclei morphology, glandular structure, and tissue irregularity patterns, the aggregation mechanism maintains the major and minor pathological features necessary to make a correct classification.

The proposed model was tested on the binary (benign vs malignant) and multiclass (eight tumor subtypes) classification under the same experimental conditions. The binary classification model obtained the overall validation accuracy of about 98% which is very high compared to traditional CNN-based architectures. To classify multiclass tumors, the model gave a general accuracy of about 88.2, which has significant levels of generalization regardless of the structural similarities within some types of tumors. The model had also high

precision, recall and F1-scores which means that the model had a consistency and evenness in all the classes. What is more, stability analysis of performance revealed that the proposed CNNAggNet model achieved a mean classification accuracy of around 97.86 with a low standard deviation of ±0.96, and in comparison with the smaller standard deviation with baseline models. The low variance of variations in performance attests to the strength and dependability of the mechanism of learning features through aggregation. In general, the obtained experimental results confirm the effectiveness of the proposed CNNAggNet framework, which can positively improve classification accuracy, stability in prediction, and the generalization ability, thus becoming a feasible solution to automated diagnosis of breast cancer in clinical pathology systems

Future Scope

Even though the proposed CNN-AggNet model has high accuracy and robustness, there are a number of opportunities to improve it. Further studies can be directed towards maximization of computational efficiency to facilitate its use in clinical settings that are constrained by resources. Explainable AI methods implemented outside of Grad-CAM can improve the interpretability and clinical confidence in automated clinical diagnostic methods.

Also, it is possible to generalize to different population groups by increasing the dataset with multi-institutional histopathology images. It could be further improved by adding attention mechanisms or transformer-based architectures, which have the potential to increase feature representation. It will require real-time integration with digital pathology systems, as well as validation using clinical trials to adopt on a large scale. These considerations will enhance reliability, scalability, and useful applicability of AI-driven breast cancer detection systems in the real healthcare context.

DL – Deep Learning
CNN- Convolutional Neural Network.
GAP – Global Average Pooling
GMP – Global Max Pooling
AI – Artificial Intelligence

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