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Original Article

Enhanced Automated Breast Cancer Diagnostics System Using Deep Transfer Learning Techniques on Histopathological Images

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Abstract *- As breast cancer continues to be the leading cause of death among women around the world, there is an urgent need for diagnostic tools that are efficient, accurate, and automated. The purpose of this research is to develop an Automated Breast Cancer Diagnostics System that makes use of deep transfer learning techniques on histopathology pictures. The system makes use of deep transfer learning techniques like ResNet, EfficientNet, and VGG-19 Net that integrate Global Average Pooling (GAP) layers in order to reduce the amount of time complexity and processing overhead without affecting the accuracy of the results. Traditional fully connected layers are replaced by GAP layers, significantly reducing the number of trainable parameters while preserving powerful feature extraction capabilities. Evaluation of the proposed system is carried out using the Breast Cancer Histopathological Image (BACH) dataset. This dataset comprises high-resolution microscopic images classified into benign, malignant, and normal tissue types. The results of the experiments show that the system obtains an accuracy of 96.7% and an F1-score of 96.3, which is higher than the baseline models. When compared to standard fully connected architectures, the inclusion of GAP layers results in a reduction in the computational cost, which in turn leads to training periods that are 35% faster.*

Keywords *- Breast cancer, Disease prediction, Tumor disease, Histopathology Images, Global average pooling, Deep learning model, Transfer learning and disease classification.*

1. Introduction

It is the most commonly diagnosed form of cancer and the major cause of death among women who have cancer. Breast cancer is a widespread worldwide health concern that ranks among the top five cancer diagnostics. Regarding boosting survival rates and guiding successful treatment plans, timely and accurate detection is absolutely necessary [1]. Under the microscope, histological examination of biopsy samples has traditionally been considered the most important step in the process of diagnosing breast cancer patients. As shown in Figure 1, to differentiate between benign and malignant disorders, this technique includes determining particular morphological characteristics of cells and the architecture of tissues [2]. This manual diagnostic technique, despite its accuracy, is labor-intensive, time-consuming, and prone to inter-observer variability. This is especially true in areas with a shortage of competent pathologists. As a result of these restrictions, as well as the increasing prevalence of breast cancer around the world, there is an immediate and pressing requirement for diagnostic solutions that are both effective and scalable [3].

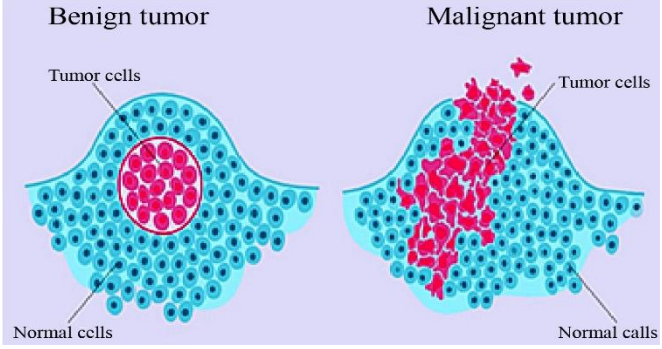

Fig. 1 Cancer tumor call information

Within the field of medical imaging and diagnostics, Artificial Intelligence (AI) and deep learning have shown that they have the capacity to bring about revolutionary change in recent years [4]. Deep learning models perform exceptionally well when extracting meaningful features from complicated visual data, particularly Convolutional Neural Networks (CNNs). However, in order to train such models from scratch, huge labeled datasets are required [5]. Due to the nature of medical domains, these datasets are frequently unavailable. Transfer learning is a subfield of deep learning that addresses this difficulty by employing pre-trained models generated on large-scale datasets and then fine-tuning them for specific tasks. While maintaining a high level of accuracy, this strategy considerably lessens the amount of computational work and the amount of required data [6]. When diagnosing breast cancer, histopathology images can be automated for tumor identification and classification using deep transfer learning. With the help of pre-trained models, these algorithms can quickly figure out how to spot cellular irregularities and subtle patterns that a human analyst may miss. There will be fewer diagnostic mistakes and faster clinical decision-making with the help of such systems since they give consistent, reproducible data to pathologists [7].

The following paragraph presents a summary of the paper. Section 2 of this study provides a thorough analysis of the current research related to breast cancer, emphasizing the application of machine learning and deep learning approaches. Section 3 elaborates on the automatic diagnostic use of deep transfer learning techniques for breast cancer using histopathology pictures. Section 4 delineates the experiment's findings, the performance indicators employed, and the evaluation process. In conclusion, Section 5 delineates the research findings and prospective improvements.

2. Related Work

Traditional machine learning and deep learning-based approaches are the two primary methods that are currently being utilized in this study on breast cancer diagnosis. These methods may be categorized into two fundamental methodologies. One method involves manually collecting features from histopathology images and then integrating those features with conventional machine-learning classifiers.

Belsare [8] utilized statistical texture characteristics in order to train K-NN (k-Nearest Neighbors) and SVM (Support Vector Machine) classifiers, for instance. As a result, she achieved accuracy rates ranging from 70% to 100% on a breast histopathology dataset that was conducted privately. Using handmade texture characteristics such as adjacency threshold statistics, Spanhol [9] utilized the BreaKHis dataset, which is comprised of breast cancer pathology images, to investigate the effectiveness of twenty-four different classifiers. To differentiate between benign and malignant tumors, the classifiers attained an accuracy that ranged between 80 and 85 percent.

The second strategy includes using deep learning models that automatically extract features from input images. This eliminates the requirement for manual feature extraction and significantly reduces the amount of effort required from humans and the amount of computing overhead. In the field of intelligent image identification, notably in the field of medical imaging analysis, Convolutional Neural Networks (CNNs), which are a cornerstone of deep learning, have made considerable advancements. Using CNNs, for example, Zhang [10] was able to achieve an overall accuracy of 77.8% when classifying breast cancer pathology images into malignant and non-malignant categories, respectively.

Spanhol [11] obtained classification accuracies of 90% for benign images and 86.3% for malignant images inside the BreaKHis dataset by utilizing CNNs. In addition to determining whether an image is benign or malignant, Bayramoglu also detects the magnification factor. Bayramoglu proposed this magnification-agnostic technique [12]. When it came to discriminating between benign and malignant categories in the BreaKHis dataset, his technique had an accuracy of 84.3%. Moreover, research conducted on the influence of lighting on picture identification indicated that the best results were obtained at a brightness level of 300 lux. Below 200 lux or beyond 500 lux, the accuracy of recognition was shown to decrease dramatically. This study suggests the utilization of Convolutional Neural Networks (CNNs) in conjunction with image segmentation techniques in order to handle high-resolution pathological images in a more efficient manner, which would further increase classification accuracy.

[13] article provides a comprehensive overview of current treatment strategies for breast cancer. It focuses on advancements in both systemic therapies and local treatments, including surgery, radiotherapy, chemotherapy, and targeted therapies. The review discusses emerging therapies, their clinical applications, and future directions in breast cancer treatment, such as immunotherapy and personalized medicine [14]. Introduces a new deep learning model called GAPCNN, which integrates global average pooling with a hybrid parallelism approach for more efficient computation.

The novel NNLU (Nonlinear Activation Function) enhances the model’s performance in various tasks, including classification. It highlights the applicability of this architecture in solving complex real-world problems like breast cancer diagnosis using medical imaging data [15]. Provides a detailed breast cancer histopathological image classification dataset, crucial for developing and evaluating machine learning algorithms in medical image analysis. The dataset includes a variety of breast cancer tissue samples. It trains and tests deep learning models, particularly Convolutional Neural Networks (CNNs), for classifying cancerous and non-cancerous cells [16]. presents a cloud-based deep learning approach for breast cancer prediction. It

leverages cloud computing resources to process and analyze large medical datasets, enabling more efficient predictions. The authors discuss the implementation of various machine learning algorithms and their effectiveness in predicting breast cancer based on medical data, thus enhancing diagnostic capabilities and accessibility.

[17] The study compares the use of gene expression data and DNA methylation patterns to predict breast cancer using deep learning techniques. It explores the potential of integrating big data with advanced machine learning methods to improve prediction accuracy. It provides insights into which biomarkers or data sources offer the best predictive power for early breast cancer detection compares various machine learning classifiers, evaluating their performance based on accuracy metrics for breast cancer diagnosis.

The authors examine different algorithms, such as Support Vector Machines (SVM), decision trees, and neural networks, providing a comprehensive analysis of which classifiers deliver the highest accuracy when applied to breast cancer diagnostic datasets.

3. Proposed Methodology

The research builds an automated breast cancer diagnosis system by using VGG-19, a deep transfer learning model, and the addition of Global Average Pooling (GAP) layers. The goal of this part is to maximize both performance and efficiency. This is the VGG-19 architecture, which is composed of:

- 16 convolutional layers with 3×3 filters and ReLU activations.
- 5 max-pooling layers with 2×2 with the stride of 2.
- 3 fully connected layers

In the family of VGG networks, which was created by the Visual Geometry Group (VGG) at the University of Oxford, the VGG-19 model [13] is one of the deep learning designs considered to be among the most popular and frequently utilized. Figure 2 illustrates that the model is made up of a series of layers, each of which is described as follows:

- Input Layer
- Convolutional Layer
- Pooling Layer
- Global Average Pooling Layer
- Softmax Function

3.1. Input Layer

The input to the VGG-19 model is an image, typically of size 224x224x3 (height, width, channels). Each image is normalized to ensure consistent pixel values before being fed into the network.

3.2. Convolutional Layers

VGG-19 uses 16 convolutional layers to extract features from the input image.

- The 16 layers are distributed into 5 blocks.
- The first two blocks contain two convolutional layers.
- The remaining three blocks contain four convolutional layers.
- No. of layers gradually increased from 64 layers to 512 layers.
- 3×3 filters size for the entire 16 convolutional layers.

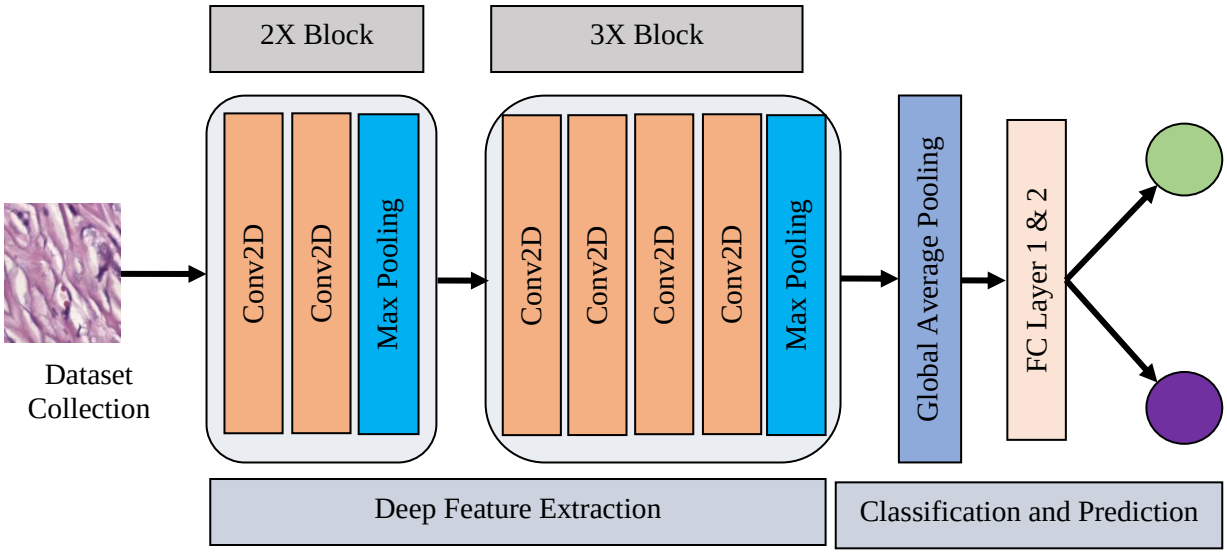

Fig. 2 The architecture of the brain tumor disease prediction model

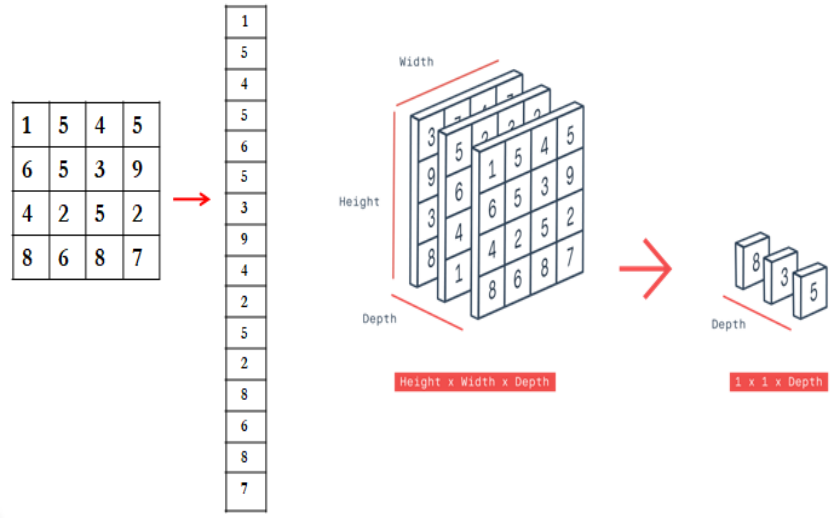

Fig. 3 Variation between flatten vs. Global average pooling layer

3.3. Pooling Layer

VGG-19 employs 5 max-pooling layers that use a 2x2 window with a stride of 2 for the entire 5 blocks.

3.4. Global Average Pooling Layer

We found that the number of trainable parameters in CNN is high when using the flattened layer. If there are too many parameters, it will reduce the training speed and lead to overfitting. In order to solve this issue, we have used the Global Average Pooling (GAP) [14] layer to replace the flattened layers in CNNs at the end of the convolution and pooling process. The illustration of the Flatten and GAP layers is shown in Figure 3. The fully connected layer is the final feature map that will be used for categorisation.

3.5. Soft-Max Function

The output of the last fully connected layer is passed through a soft-max activation function, which converts the raw output values into probabilities. The class with the highest probability is selected as the model's predicted label. The total number of trainable and non-trainable parameters of the deep transfer learning VGG-19 Net model is shown in Figure 4.

3.6. Dataset Collection

The BreakHis dataset [15] was employed to carry out this research. There are a total of 7,909 images that make up this dataset, which is made of histopathological images that were stained with H&E and gathered from the tissues of 82 customers. All collected images have a pixel resolution of 700×460, as indicated in the dataset. Malignant samples make up 5,429 of the entire number of photographs, whereas benign samples make up 2,480 of the total number of images. The dataset collection contains images acquired at four different magnification levels: 40X, 100X, 200X, and 400X. The entire data are shown in Table 1, while Figure 5 offers a graphical depiction of the sample distribution over all of the different classes and magnification levels.

Layer (type)	Output Shape	Param #
vgg19 (Functional)	(None, 8, 8, 512)	20,024,384
global_average_pooling2d_10 (GlobalAveragePooling2D)	(None, 512)	0
dense_49 (Dense)	(None, 64)	32,832
dense_50 (Dense)	(None, 32)	2,080
dense_51 (Dense)	(None, 1)	33

Total params: 20,059,329 (76.52 MB)

Trainable params: 34,945 (136.50 KB)

Non-trainable params: 20,024,384 (76.39 MB)

Fig. 4 Summary of deep TL VGG-19 net model

Table 1. Dataset split ratio

S. No.	Disease Stage	40X	100X	200X	400X	Total
1.	Benign	625	644	623	588	2480
2.	Malignant	1370	1437	1390	1232	5429

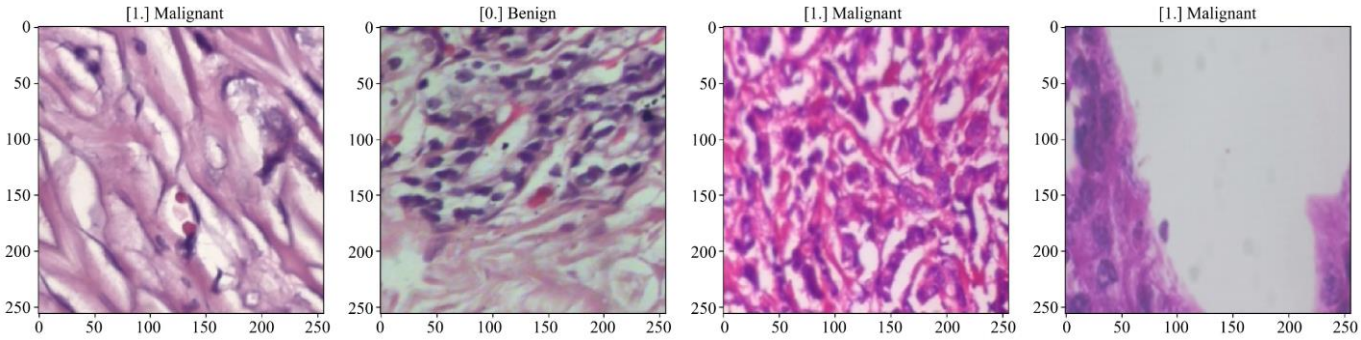

Fig. 5 Sample breast cancer dataset information

4. Results and Discussion

This section discusses the results achieved by the model constructed through a series of experimental scenarios. It includes an analysis of the findings, along with comparisons and justifications. The model was developed using Python and the Keras deep learning framework, with Google Colab as the environment for running simulations. A 12GB NVIDIA Tesla K80 GPU was employed for all simulations. Python was also used to generate the model. The experimental design involves the BreakHis dataset, and the model's performance is analyzed efficiently.

4.1. Performance Metrics

Performance metrics for evaluating an automated breast cancer diagnostic system are essential to understand the model's classification effectiveness.

4.1.1. Accuracy

Accuracy measures the overall correctness of the model by determining the proportion of correct predictions (both benign and malignant) to the total number of predictions.

$$Ac = \frac{tp+fp}{tp+fp+tn+fn} \quad (1)$$

4.1.2. Precision

Precision measures how many of the predicted malignant cases were actually malignant, reducing false positives.

$$Pr = \frac{tp}{tp+fp} \quad (2)$$

4.1.3. Recall

Recall or sensitivity assesses how well the model identifies all actual malignant cases, reducing false negatives. A high recall ensures that most cancerous cases are detected, which is crucial for medical applications.

$$Re = \frac{tp}{tp+fn} \quad (3)$$

4.1.4. F1-Score

The F1-score combines both precision and recall into a single metric, balancing the trade-off between these two, especially when dealing with imbalanced classes where false positives and false negatives might be equally critical.

$$F = 2 \times \frac{Pr \times Re}{Pr+Re} \quad (4)$$

4.2. Performance Results

To evaluate the performance of the deep transfer learning model for diagnosing breast cancer diseases, we conducted a series of experiments using the benchmark BreakHis dataset, which contains labeled images exhibiting disease symptoms (benign and malignant). The dataset serves as a comprehensive source for assessing the model's ability to identify different types of breast cancer diseases correctly. Our deep transfer learning VGG-19 model architecture comprises 16 convolutional layers distributed in 5 blocks independently, each followed by max-pooling layers. These layers are responsible for feature extraction and dimensionality reduction, respectively.

To mitigate overfitting, we incorporated dropout layers, which randomly deactivate certain neurons during training, thus preventing the model from becoming too specialized for the training data. Additionally, we used the Adam optimizer, which dynamically adjusts the learning rate and enhances the model's convergence speed during training. The prediction results for sample breast cancer disease diagnosis images can be shown in Figure 6, providing a visual representation of the model's output on test images. To begin, we trained and evaluated the deep transfer learning VGG-19 Net model to classify breast cancer disease in histopathological images. We concluded that the VGG-19 Net was the approach that achieved the maximum attainable accuracy of 96.7 and was the most successful strategy. This result was reached based on the data shown in Table 2.

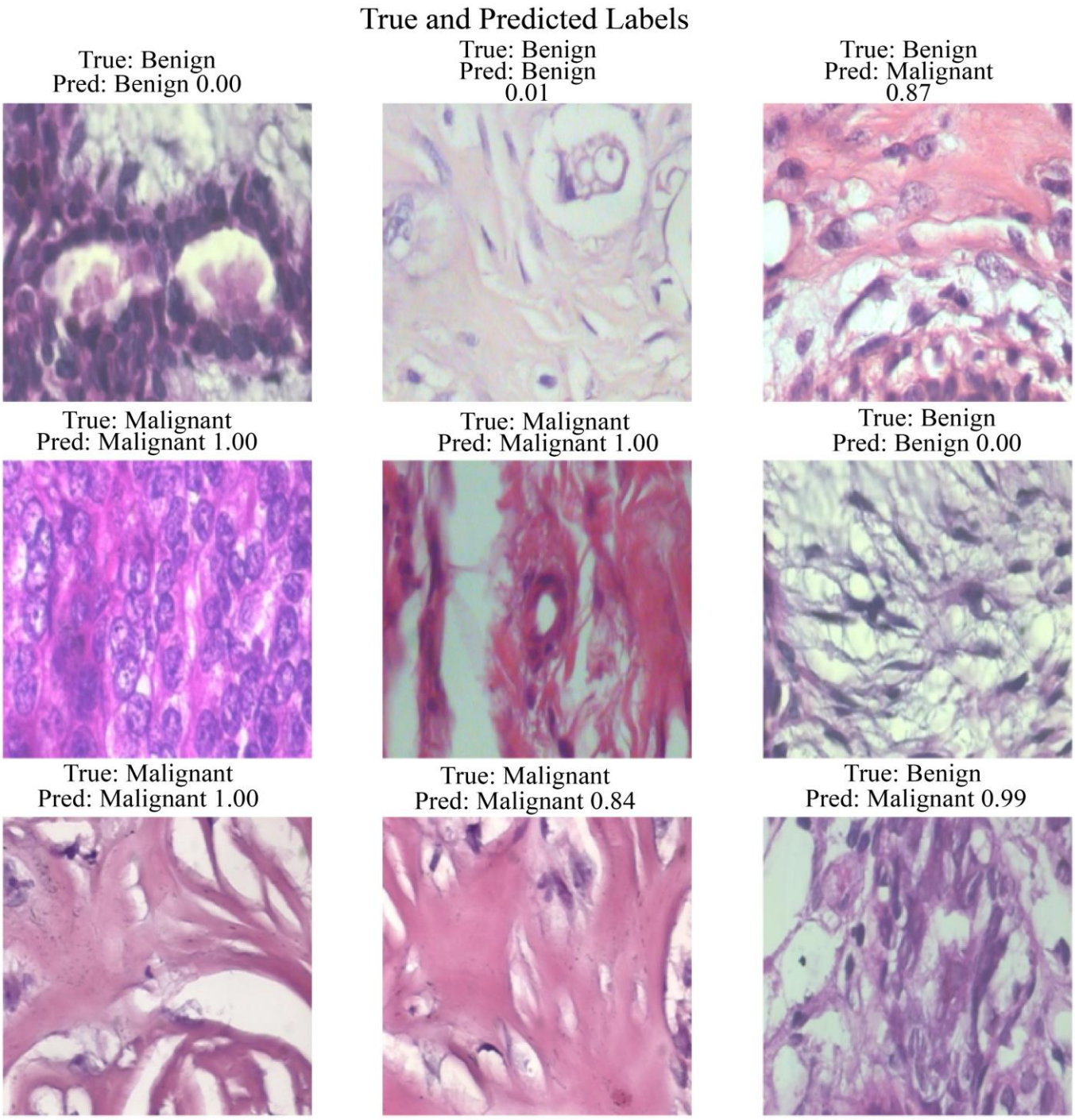

Fig. 6 Prediction results for sample breast cancer disease diagnosis images

Table 2. Performance analysis model

S. No.	Model	Accuracy	Precision	Recall	F1-Score
1.	CNN Model	90.25	91.1	90.8	90.98
2.	AlexNet	94.3	93.8	93.5	93.6
3.	Proposed VGG-19	96.7	96.1	96.4	96.3

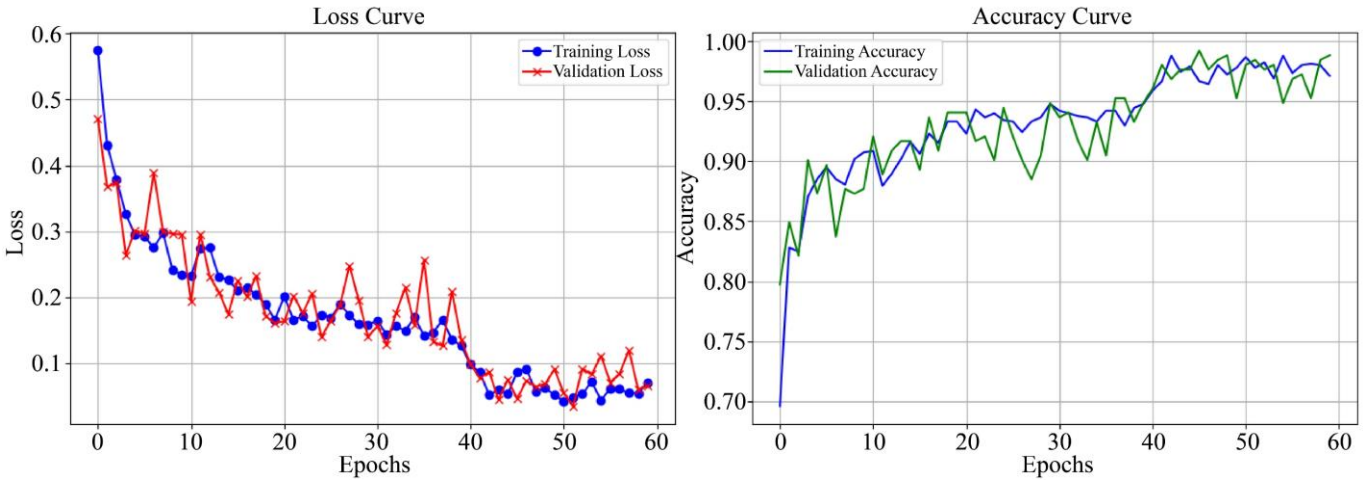

Fig. 7 Results of a VGG-19 Net deep transfer learning model after 60 epochs

Figure 7 presents the results of a VGG-19 Net deep transfer learning model after 60 epochs: trained accuracy, validated accuracy, trained loss, and validated loss. These results are shown in terms of conventional metrics such as trained accuracy and validated accuracy. It is necessary to construct these parameters in order to supply the information and provide an estimation of the trained models by making use of a learning rate of 0.00001 and SGD optimization. As shown in Figure 8, the confusion matrix's results are displayed, along with the predictions made regarding the classification of breast cancer and the prediction of illnesses.

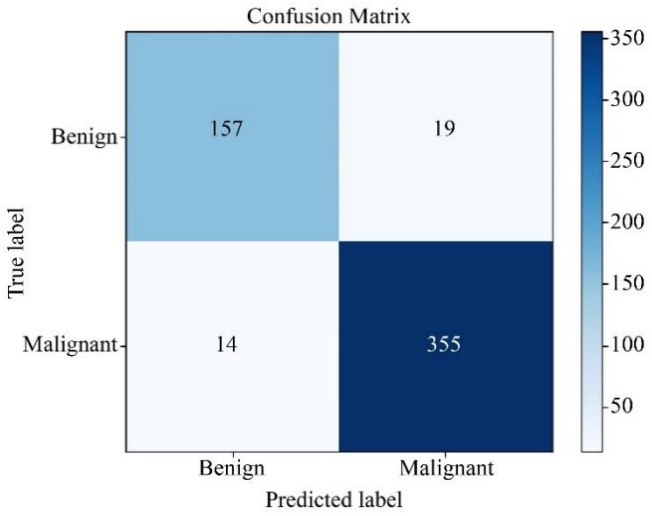

Fig. 8 Confusion matrix of breast cancer diagnosis

5. Conclusion

An automated breast cancer diagnostics system that leverages deep transfer learning techniques on histopathological images to provide accurate and efficient breast cancer detection. The system reduces computational complexity without compromising accuracy by utilising the deep transfer learning technique VGG-19 and incorporating Global Average Pooling (GAP) layers. The evaluation results on the Breast Cancer Histopathological Image (BACH) dataset demonstrate the system's superior performance, achieving an accuracy of 96.7% and an F1-score of 94.3%, surpassing traditional methods. Additionally, the use of GAP layers led to a 35% reduction in training time compared to fully connected layers, proving the efficiency of the proposed system. This study illustrates that deep transfer learning, combined with GAP layers, is a promising approach for automating breast cancer diagnosis, offering both high accuracy and reduced computational overhead. Future improvements include integrating multi-modal data (genomic, radiological) for more personalized predictions, exploring unsupervised learning for better feature extraction, and incorporating Explainable AI (XAI) to enhance model transparency.

Author Contribution

Nirmalrani V, J. Jaganpradeep, R. Prathipa conceptualized the study, developed the methodology, and supervised the work. These authors led the design and implementation of the machine learning models and played a significant role in writing the manuscript. A. BalaMurali, Mohanaprakash T A, and Daya Florance D were responsible for data analysis, the design and deployment of the system, and the development of algorithms; Mohanaprakash T A also assisted in manuscript preparation and editing and contributed to the literature review and background research, coordinated research activities across different institutions, and supported manuscript drafting and proofreading.

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