Transfer Learning based Framework of VGG16 to Detect Breast Cancer using Histopathological Images

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Abstract

Breast Cancer Detection introduces a prominent confrontation for researchers and clinical experts as it is one of the major public health issues and is weighed as a leading root for cancer correlated deaths among women worldwide. Early diagnosis helps the chances of survival rate which is a crucial part, but standard breast cancer classical techniques rely on operative techniques, open procedures and time-consuming analyses. So, the standard classical techniques pave a way in demanding accurate solutions that are provided with efficient algorithms. This paper addresses these challenges by utilizing automated cancer detection that presents an ensemble deep learning approach by implementing transfer learning for breast cancer detection using histopathological images for classifying Benign and Malignant tissues. Transfer learning uses VGG16 to train the model on large dataset, by reusing the knowledge that has obtained from previous task which is considered as an input to another task thereby improving the performance. In this paper VGG16 architecture is considered as a pretrained model to train on ImageNet. Ensemble strategy is applied as a next step by taking the average of predicted probabilities, out of which the VGG16 model offers overall best accuracy of 98.83%

Keywords

CNN, Deep Learning, Transfer Learning, VGG16

1. Introduction

Artificial neural networks (ANNs) are the most advanced and progressive machine learning models in data science. The performance of models is vague and astonishing, because the models work efficiently even with one hidden layer such that the model reaches the approximate level of precision with the desired function. Deep Learning allows machines to discover with an emphasis on establishing facts precisely on patterns and knowledge in a manner to handle hidden data. The concept has been inspired by human brains using AI. Deep Learning allows machines to discover with an emphasis on establishing facts precisely on patterns and knowledge in a manner to handle hidden data. The concept has been inspired by human brains using AI (Artificial Intelligence). Machine Learning and Deep Learning can be considered, when the traditional approach fails to solve problems. To solve a specific problem, traditional approach chooses to solve a specific problem using algorithms that are programmed manually by a human or uses a set of rules that are predefined. In diverge with traditional approach, machine learning trains a model on a dataset and makes sure that the model learns how to solve the problem on its own. When a model is applied to solve a problem, by applying it to the related problems, the transfer learning which is a part of machine learning focuses on storing the knowledge gained from that model. Therefore, transfer learning can be applied on large datasets then fine tune it into a smaller dataset. Globally, every year millions of women are diagnosed with breast cancer and the death rate is increased year by year. Women from every country in the world and at any age face the issue in their breasts which leads to breast cancer. Some of the common risk factors include consumption of

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alcohol, consumption of tobacco, history of breast cancer in the family, increasing age, exposure to the radiation, hormonal issues. Breast cancer is seen mostly in the women whose age is 40 years and above. Sometimes breast cancer in women develops based on family history. However, the absence of a cancer within the family history does not imply a lower risk. The importance of early detection is necessary, as many of the people will not have any exposure to the symptoms when the cancer is in early stage. When the person is in advance state of breast cancer the symptoms will be like

- A noticeable mass or area of thickened tissue in the breast, typically painless.
- Alteration in the breast's size, contour, or overall look.
- Skin changes such as dimpling, redness, or a texture resembling an orange peel.
- Modifications in the appearance of the nipple or the surrounding areola.
- Unusual discharge from the nipple, which may include blood. If there are any symptoms of abnormal breast lump women need to have a medical checkup, even though having the lumps present inside the breast does not show any issue or problem.

Any lumps inside the breast are not malignant, in fact breast lumps when are of small size which tends to be malignant, so early preventive measures can reduce the chances of spreading to other parts of the body. Cancerous tissues may affect the other organs of the body and may lead to other issues. Usually, the cells that are present in human body are abnormal or they get old and die. When the cancer cells are being spread to other parts of the body, the healthy cells can be affected too, that's gives chance to the remaining parts of the body to not stay healthy. Some cancerous cells grow and spread fast whereas some of them grow slowly but some to spread to other parts of the body suddenly. The growth in the cancerous cell is called as a tumor which looks like a benign or malignant (cancer). The tumors that grow slowly are benign, and will not develop into tissues around them and will not affect other parts of the body. Benign lumps are not cancer. Cancerous tumors can develop rapidly and grow without regulation. The benign tumors may invade nearby tissues and structures. Cancer cells move through the bloodstream or lymphatic system, and establish new growths in remaining parts of the body. The symptoms caused by these tumors often differ based on their location in the body. The breast cancer tissue can be analyzed to its lowest magnification level which are also microscopic images and are called as Histopathological images. The quality of the histopathological images can be improved by analyzing and applying the efficient algorithms that uses preprocessing techniques which helps in color transformation, transitioning and formalization. Histopathological images play a crucial role in breast cancer datasets as they are fundamental for understanding, diagnosing, and researching breast cancer. Histopathological images in breast cancer datasets explore the diseases in terms of morphological and biological characteristics. Their inclusion fosters advancements in diagnosis, therapy, and the development of personalized treatment approaches.

2. Literature Review

The work related to breast cancer is discussed here, in this paper [1] authors used statistical methods to analyze breast cancer in pathological images. The models they have considered perform detection, segmentation, and classification on pathological images. The accuracy achieved by using deep learning algorithms had provided reliable recommendations in considering deep learning techniques for different application. In paper [2] ResNet50, Transformer which are deep learning models, and Hover-net are applied for finding breast cancer diagnosis, treatment, and prognosis prediction. The accuracy and efficiency using the deep learning models for predicting breast cancer metastasis is progressively efficient. This review [3] explains profound impact of artificial intelligence on breast cancer by identifying breast tumors and lymph node by processing large images. Artificial Intelligence based frameworks classify breast tumors where the traditional methods struggle to do. The Artificial Intelligence contributions provide enhanced accuracy, efficiency, and standardization. Authors [4] proposed model that distinguishes breast cancer samples into benign and malignant categories by applying different algorithms to predict interpretation. Algorithms like K-nearest Neighbor (KNN), convolutional neural network

(CNN), ResNet50V2 architecture are proven to results on a variety of image classifications. The models were applied on breast cancer histopathology image dataset and performed well with an accuracy of 95%. In this paper [5] VGG16 has been demonstrated by applying it on skin cancer detection by making the image quality having a better accuracy, on skin cancer detection and provides future improvements in the field. This paper [6] presents classification of breast cancer on histopathology images using deep learning. The pre-trained models VGG16 and VGG19 are applied and are effective in classifying histopathology images of breast cancer. Accurate classification and unbiased prediction of breast lesions is done in [7] where deep learning approach using CNN architectures like MobileNetV2, VGG16, and EfficientNetB7 along with transfer learning being applied. Applied these models on erroneous outputs of noisy images, variations in input data. In this paper [8] DenTnet algorithm classifies the breast cancer using histopathological images where transfer learning solves the problem of extracting features and the proposed DenTnet method shows the comparison of deep learning methods in terms of detection accuracy. The work in [9] performs the classification of breast cancer samples by applying transfer learning technique based on lightweight Squeeze Net architecture, a variant of CNN. Both Gradient Color Activation Mapping (Grad CAM) and the mechanism for image coloring are used for fine-tuning and satisfactory results are achieved.

3. Methodology

When the knowledge abstracted by a machine from previous task in the process of improving the other task which is achieved by transfer learning in machine learning. The knowledge acquired from the already trained model is given as an input to other model when the problem is related. For example, if a model is trained to classify whether an image contains a cat, in the process of training, the model grasps the properties or features of cat like fur patterns, whiskers, breed, ear shapes, and eyes. Now, if the pre-trained model's knowledge which is referred as transfer learning tries in classifying an image which contains a dog, it might perform well because dogs and cats share some similar features or properties like fur, ear shapes, breed and general body structure. Transfer learning model reuses the knowledge which it has gained while being trained for another task, instead of starting from scratch. Transfer learning exploits its way of working in a way that what has been achieved during the training of one task will improve or will be advantageous when working with another task by using the knowledge it has gained from previous tasks.

Transfer learning applies the methods for breast cancer diagnosis using two ways; one is via ultrasound imaging, and the other is pre-training data that depends on source data. One method is cross-domain, where the model is already trained by considering natural images and cross-modal is second method, here the model that is pre-trained on medical images is used. Feature Extraction and Fine-Tuning are two main techniques in transfer learning shown in Figure 1. Feature Extractor technique extracts meaningful features from the pre-trained model based on the input data like image data and text data without affecting the existing models' parameters. The pre-trained model that is used in feature extractor considers only the last layers which are later replaced and trained on new dataset. Feature Extractor works by considering the following steps;

- A pre-trained model like ResNet, VGG, or BERT which have already acquired general features from a large dataset (e.g., ImageNet for images, or a large text corpus for language models).
- The model's final classification layers can be removed as these are based on a particular task.
- Replace the final classification layers with new layers tailored to the target task.
- Train only the new layers on the smaller target dataset, while the rest of the model remains frozen.

Fine-tuning involves unfreezing the pre-trained model either partially or fully and updating its weights along with the newly added layers during training on the new dataset. Therefore, the model adapts its features based on target task necessary requirements. Fine-Tuning works by considering the following steps;

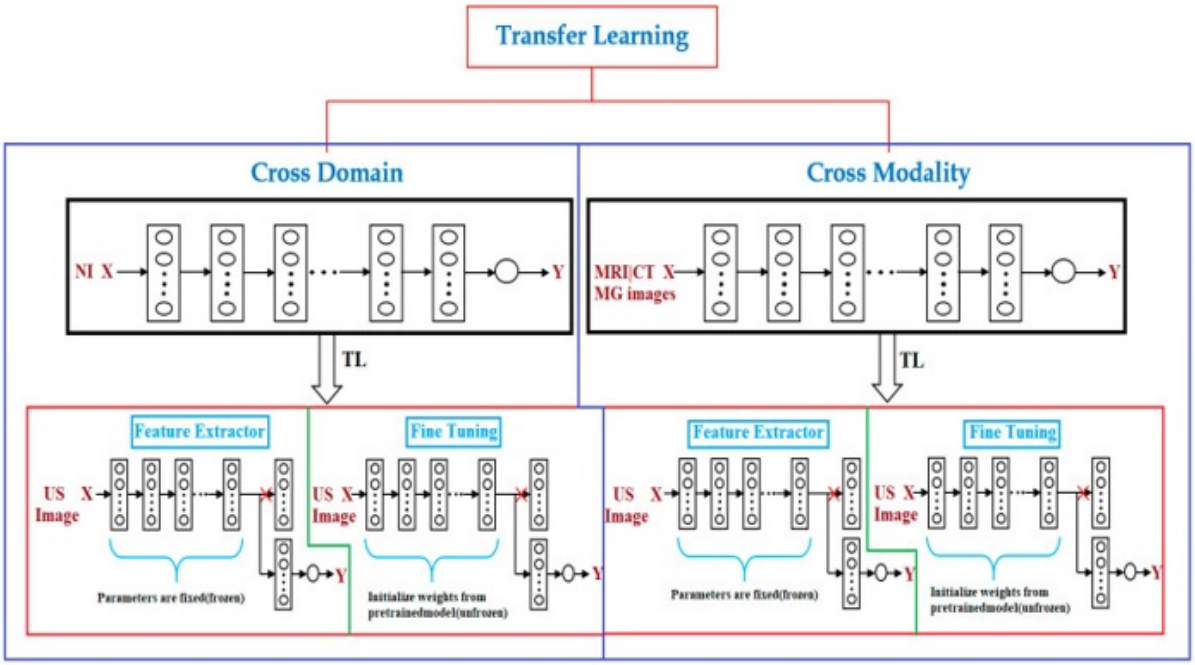

Figure 1: Feature Extraction and Fine-Tuning. (https://www.mdpi.com/cancers/cancers-13-00738/article_deploy/html/images/cancers-13-00738-g001-550.jpg).

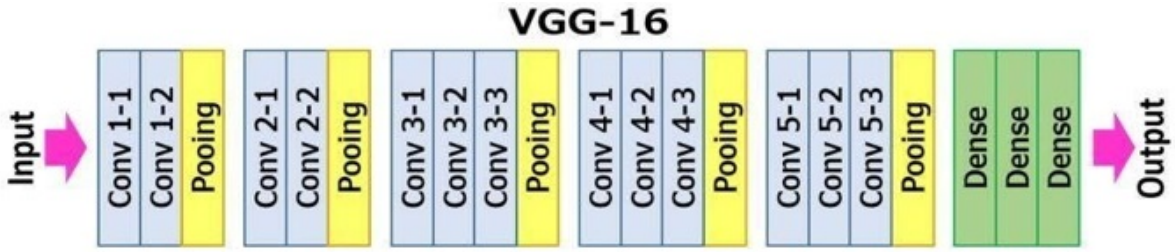

Figure 2: VGG16 Architecture. (https://medium.com/@mygreatlearning/everything-you-need-to-know-about-vgg16-7315defb5918).

- A pre-trained model from the feature extraction step is considered.
- Unfreeze some or all of the layers of the model.
- Training is performed on the new dataset, by considering a smaller learning rate for the pre-trained layers so as to avoid overwriting the learned features drastically.
- Both the pre-trained layers and the new layers are updated to improve the performance when working with target task.

The pre-trained model [10] [11] that is considered for Feature Extractor is VGG16 the histopathological image data are passed as the input data and text data from sources that are accessible before moving on to the pre-processing stage. VGG16 is a pre-trained transfer learning model that is trained, tested, and validated on the histopathology images dataset. Based on analyzing and processing the results using the transfer learning detection of breast cancer can be identified. A convolutional neural network (CNN) is a one of the kinds of artificial neural network which contains input layer, along with output layer, and can have many hidden layers. VGG16 is one of the types of CNN and is a proficient algorithm for image classification with transfer learning.

The VGG16 architecture shown in Figure 2, explains that the 16 in VGG16 are the 16 layers that have weights and the convolutional layers that are present are 13, the count of Max Pooling layers is 5, the 3 Dense layers are considered which add up to 21 layers. The 16 layers that are considered have weights which are recognized as learnable parameters layer. VGG16 performs the processing using a simple

design that uses a fixed filter size of 3×3 with a step size (stride) of 1. Uses padding where the output size matches the input size after convolution is performed. The Max Pooling Layers uses 2×2 filters with a stride of 2 in order to reduce the size of the image while keeping important features. Throughout the network processing the convolution and max pooling layers are repeated with the same pattern by allowing the structure to be predictable and systematic. Each block of convolution layers has a standard number of filters which are specified in detecting patterns like edges or textures.

- Conv Block 1: has 64 filters used to find simpler patterns like edges.
- Conv Block 2: has 128 filters used to detect more detailed patterns.
- Conv Block 3: has 256 filters used in finding complex patterns.
- Conv Block 4 and 5: has 512 filters each used in finding highly complex patterns.

After the convolution and pooling layers, the network processing has three fully connected (FC) layers. The first two layers are large, with 4096 neurons each that are used in extracting features. The last FC layer returns 1000 neurons as outputs, each representing as one of the classes in the ImageNet classification task. A SoftMax layer at the end converts these 1000 outputs into probabilities for classification. Transfer learning [12] is applied on histopathological image datasets to predict breast cancer, VGG16 is a pretrained model that is applied for feature extraction capabilities and pretraining on large image datasets like ImageNet. VGG16 works effectively for performing image classification. The system architecture shown in Figure 3, which uses transfer learning with VGG16 to predict breast cancer from histopathological image datasets is performed using the below steps;

Step-1: Histopathological Image Breast Cancer Dataset:

The histopathological image breast cancer dataset is a collection of images regarding the breast tissue samples that are captured under a microscope to enhance their cellular structures. These datasets are typically used for diagnosing, classifying, and understanding breast cancer through machine learning and deep learning techniques. These Images are collected from biopsy samples or surgical specimens of breast tissue. The necessity of these images is to identify and classify breast cancer in a person if the tumor is benign, malignant, or specific grades of cancer. The resolution of image ranges from low-resolution to high-resolution.

Step-2: Data Preparation:

Dataset Collection, the histopathological image dataset is collected with classes like benign and malignant and Data Preprocessing is performed, where the images which are passed as input are resized by VGG16 into 224x224 pixels and when normalization is performed the pixel values lie between [0,1] or [-1,1]. In Data Augmentation, techniques like flipping, rotation, zooming, and brightness adjustments are performed on the images based on the requirement and necessity required by the model.

Step-3: Transfer Learning:

A model is trained by considering one task and is reused or adapted to a different task. However, making a model to be trained from scratch based on the knowledge acquired from a pretrained model helps in solving a new problem. Feature extraction, uses a pretrained model to extract general features (edgeseatures. The new layers are added on top of the pretrained mode, corners, textures), while later layers extract task-specific fl to match the target task's output. Only the newly added layers are trained, while the pretrained layers remain frozen. Fine-tuning unfreezes some layers of the pretrained model in order to adapt the new features from new dataset and retraining it along with the new layers for the target task.

Step-4: Loading Pretrained Model VGG16:

Pretraining of a model is done on the ImageNet dataset by ensuring the necessary weights are assigned. ImageNet contains millions of labelled images to perform image classification tasks e.g., animals, vehicles, household items. VGG16 as the Pretrained mode is trained on ImageNet to provide an input or starting point for other image-related tasks through transfer learning. The generic image features like edges, textures, and shapes are extracted from images which can be fine-tuned and often require high-resolution processing on Histopathological images. Fine-Tuning, is performed by the pretrained model to train breast cancer dataset while freezing some layers or retraining fully. Fine-tuning is performed to prevent the weights being updated by the convolutional layers during training.

Step-5: Adding Custom Classification Layers:

To adapt the output of the pretrained VGG16 model applied on breast cancer histopathological images, the model is trained on classifying images from ImageNet dataset where the output layers are not directly usable for labelled custom dataset like benign and malignant classification. So, removing of original classification layers and replacing with the custom layers tailored to your dataset is done. Global Average Pooling (GAP), Converts the feature maps which are having high-dimensions and outputs from VGG16 convolutional layers into smaller representation. The risk of overfitting is reduced by considering a smaller number of parameters. Adding ReLu activation with Dense Layers, dense layers make the decisions on the features that are extracted by the VGG16 model by bringing out a meaningful output. To do this, ReLU (Rectified Linear Unit) activation is added to the dense layers to make the model learn complex relationships that are specific to histopathological images where the tumors are benign and malignant. Applying SoftMax and sigmoid activation for final output layer, the final output is predicted by performing classification using the activation functions. The Sigmoid Activation is considered for binary classification benign or malignant with a single value between 0 and 1. SoftMax Activation is considered for multi-class classification which outputs probability for multiple classes.

Step-6: Train the Model:

Training is performed on the dataset, based on categories like training, validation, and test sets. The model gets trained on the augmented dataset using custom classification layers. While performing training, the model adjusts its weights based on the patterns it finds from the 70-80% data of the total dataset is considered. The validation set checks the model's performance during training to overcome overfitting issue, by considering about 10-15% of the total dataset. Test set is considered to know the entire processing of model's performance after training is done where 10-15% from entire dataset is considered.

Step-7: Initial Evaluation of the model:

Before evaluating the model, it needs be applied on the validation or test dataset which are not considered during training. This initial evaluation paves a way and determines whether fine-tuning is necessary for a model.

Step-8: Fine-Tune the Model:

After performing the training on the model, the upper layers of the pretrained VGG16 model are unfrozen. As the layers are fine-tuned on the histopathological dataset by considering a smaller learning rate in order to adapt to the learned features based on the specific patterns in the dataset whether the tumor is benign and malignant. Therefore, learning rate is reduced to avoid pretrained weights for fine tuning.Transfer learning makes the model to define based on the existing knowledge which is gathered from the features of ImageNet to learn specific features relevant to histopathological images. The layers' weights are not updated during training done by the VGG16, and only the newly added layers that are fully connected are allowed to be trained. So, the top layers are unfrozen to update weights while training is performed. The lower layers of the VGG16 model extracts basic features like edges and textures, when unfreezing is done on top layers, the model can bring out some specific features related to breast cancer images.

Step-9: Evaluate the Model:

A model is evaluated after performing training, where the performance is measured on new data. The performance is evaluated on the test set. The evaluation is measured by considering various metrics like accuracy, precision, recall. Different insights based on different aspects are considered to check the model's performance with imbalanced datasets that are available in medical image classification tasks (e.g., predicting breast cancer). Accuracy metrics reviews the overall correctness of the model based on both true positives and true negatives along with the available number of predictions. Precision measures the correctness of positive predictions by explaining how accurate your model is dealing with predicting positive cases. In breast cancer detection, you want to minimize false positives to avoid unnecessary treatments for patients decide are the predicted positive instances (e.g., malignant) are true positives. It is especially important when false positives are high, so when wrongly classifying a benign case as malignant. Recall measures the ability to detect all actual positive cases and is treated as Sensitivity or True Positive Rate that the actual positive instances (e.g., malignant cases) were correctly

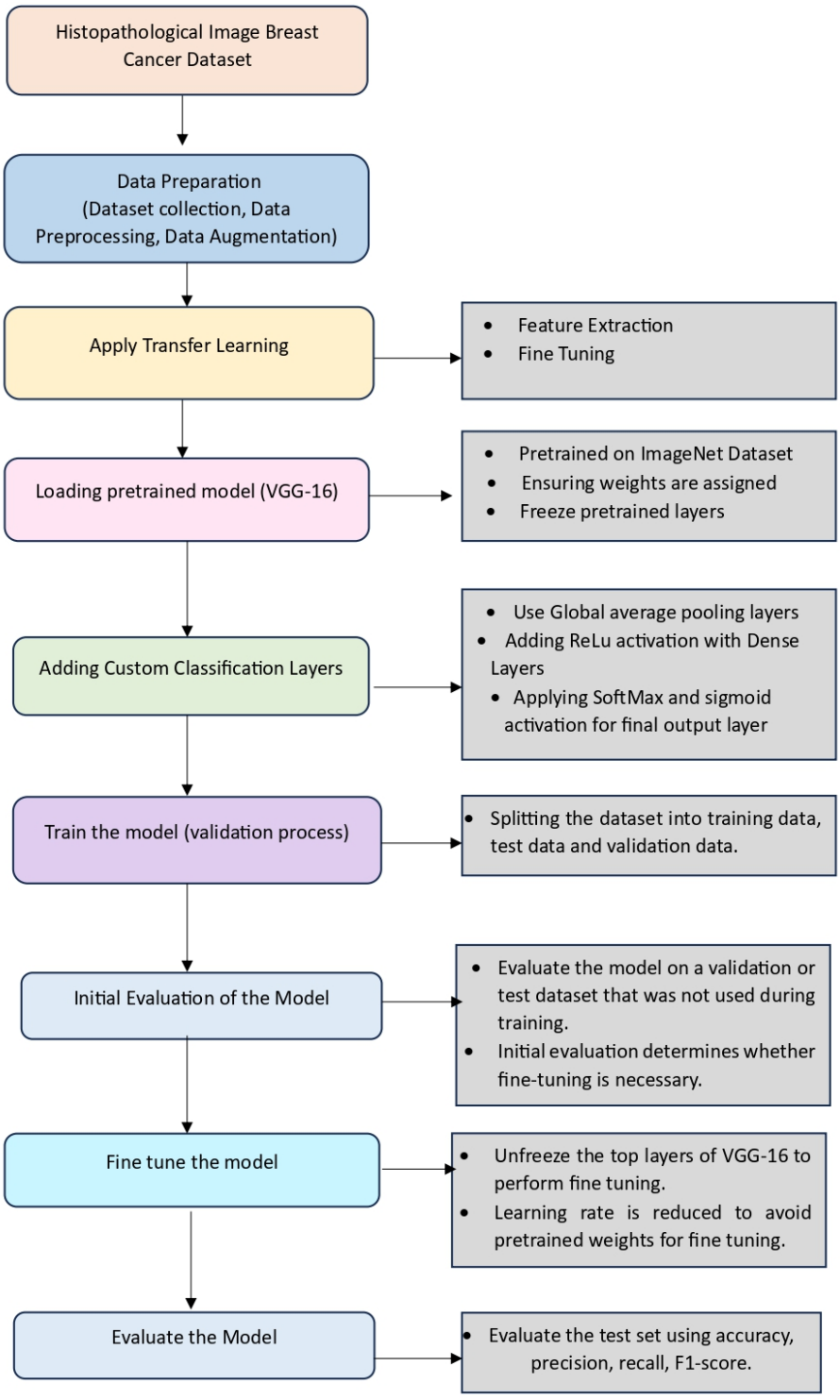

Figure 3: System Architecture.

identified by the model. The model is evaluated by considering these metrics, to understand how accurate the model is but also handles false positives and false negatives errors that can be critical in breast cancer detection. F1-Score calculates the average mean weight to smaller values of precision and recall. It is a balanced metric that combines the model's ability to avoid false positives which is precision and false negatives which is recall. The F1-score is useful when working with imbalanced datasets.

4. Comparative Analysis

A comparative analysis of present work with two earlier works of ours [13] [14] [15] [16] in predicting breast cancer, focusing on key aspects such as dataset type, methodologies, computational cost, performance, interpretability, and scalability are discussed in Table-1;

Table 1
Comparative Analysis of different Algorithms on Predicting Breast Cancer

Aspect	CSV Dataset (LightGBM & LSTM) [13]	Histopathological Images (GAN & ResNet) [14]	Histopathological Images (VGG16)
Dataset	Structured/tabular data with clinical and numerical features.	Histopathological images, raw medical data requiring preprocessing.	Histopathological images, directly utilized for classification.
Approach	LightGBM for feature selection and LSTM for sequential data processing.	GAN for data augmentation and ResNet for deep feature extraction & classification	VGG-16 for feature extraction and direct classification
Data Size Dependency	Performs well with relatively small datasets	Requires large datasets for training GAN effectively	Can work with medium datasets using transfer learning
Model Complexity	Moderate (tabular data methods are well-established)	High (dual models: GAN for augmentation, ResNet for classification)	Moderate (simpler CNN structure with transfer learning)
Accuracy	High for structured data	High for images when GAN performs effective augmentation	Competitive, leveraging pre-trained weights for better generalization
Feature Extraction	Relies on engineered features and LSTM for sequential patterns	Deep features learned through ResNet	Deep hierarchical features learned through VGG-16
Overfitting Risk	Low to moderate, depending on feature engineering	High without careful tuning of GAN and ResNet	Moderate, mitigated by transfer learning and regularization
Training Time	Short (efficient with LightGBM & LSTM)	Long (GAN + ResNet require significant training time)	Moderate (transfer learning reduces training requirements)
Preprocessing	Requires feature engineering and cleaning	Requires image preprocessing (normalization, resizing)	Minimal image preprocessing required
Scalability	Highly scalable for larger structured datasets	Limited scalability due to high computational demands	Scalable with modern GPUs and efficient frameworks
Application Suitability	Suitable for clinical settings with numerical data	Research-oriented, addressing challenges in medical imaging	Clinical application-ready with focus on image-based diagnosis

5. Results

The analysis is performed by considering Breast Cancer Histopathology Image dataset which consists of 277,524 image patches of size 50x50 (198,738 IDC negative and 78,786 IDC positive). The images are in png format.The VGG16 model ensures that the prediction is evaluated by considering the metrics precision, recall and F1-Score and avoids overfitting. When evaluating the model's prediction performance on a test dataset, which provides unbiased assessment of the model's prediction performance using the metrics precision, recall and F1-Score.

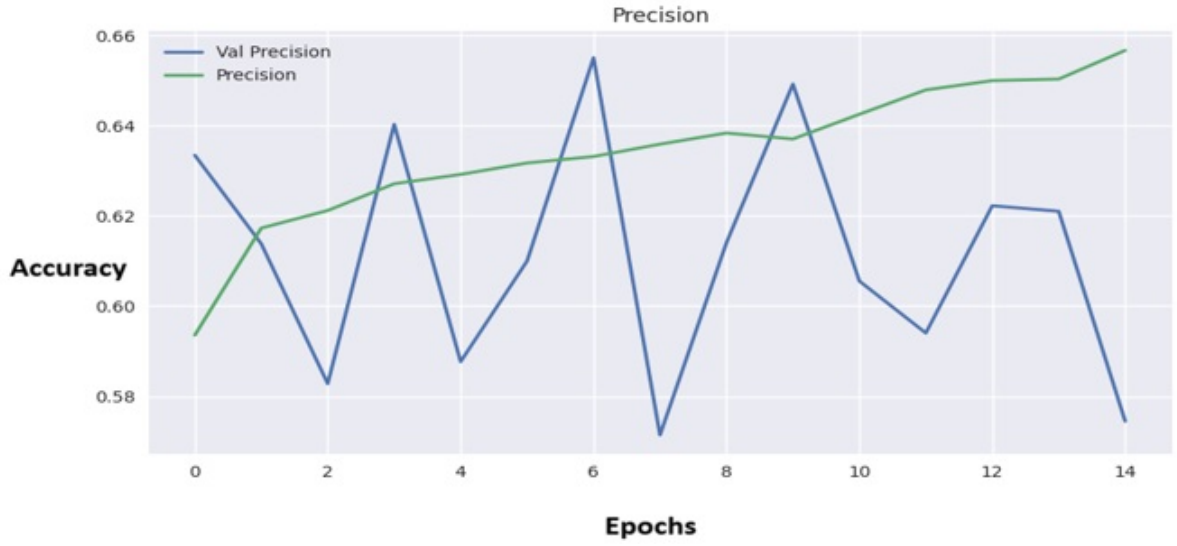

Figure 4: Precision performance metric vs Epochs.

Precision metric which shows the correctly identified positive cases out of all predicted positives which is stable from 0.633 to 0.574 as shown in Figure 4.

Figure 5: Recall performance metric vs Epochs.

Recall metric shows the correctly identified positive cases out of all actual positives which is Somewhat stable from 0.747 to 0.811 as shown in Figure 5.

F1-Score metric shows the average mean weight of smaller values of precision and recall which is

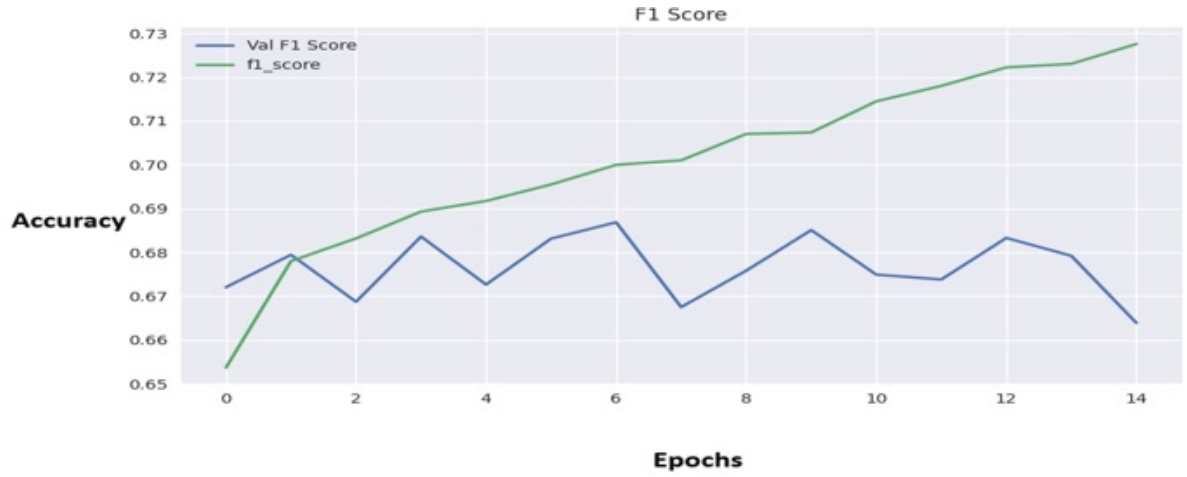

Figure 6: F1-Score performance metric vs Epochs.

somewhat stable from 0.672 to 0.664 shown in Figure 6. The graph in Figure 7 indicates the model's performance, the training accuracy is excellent, as the epochs increase the test accuracy has made the model reliable for real-world histopathological image classification tasks. The graph in figure 8, highlights model is fitting the training data very well, and makes sure there is less consistent test loss.

Figure 9, explains the performance metrics versus epochs as to visualize the training and validation

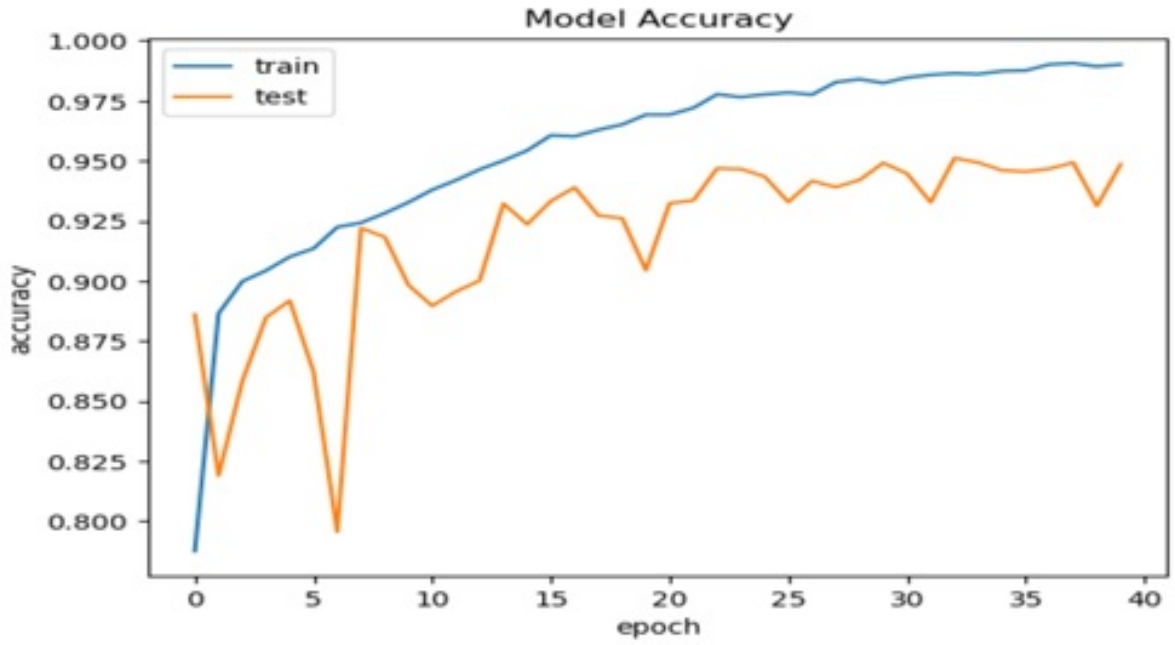

Figure 7: VGG16 Model accuracy analysis for Histopathological Image Dataset.

performance of the model based on epochs that are considered or consumed when training along with performance metrics precision, recall and F1-Score on the training dataset across epochs.

The line graphs compare training and validation metrics and verifying if there is any large gap between training and validation metrics. Loss vs. Epochs describes how training and validation loss change over time. Accuracy vs. Epochs shows the model's accuracy using precision/recall/F1-score during training and validation. However, the model's accuracy is shown good. Training the Model using VGG16 on the training data and the performance is justified based on the validation data and test dataset after each epoch shown in Figure 10.

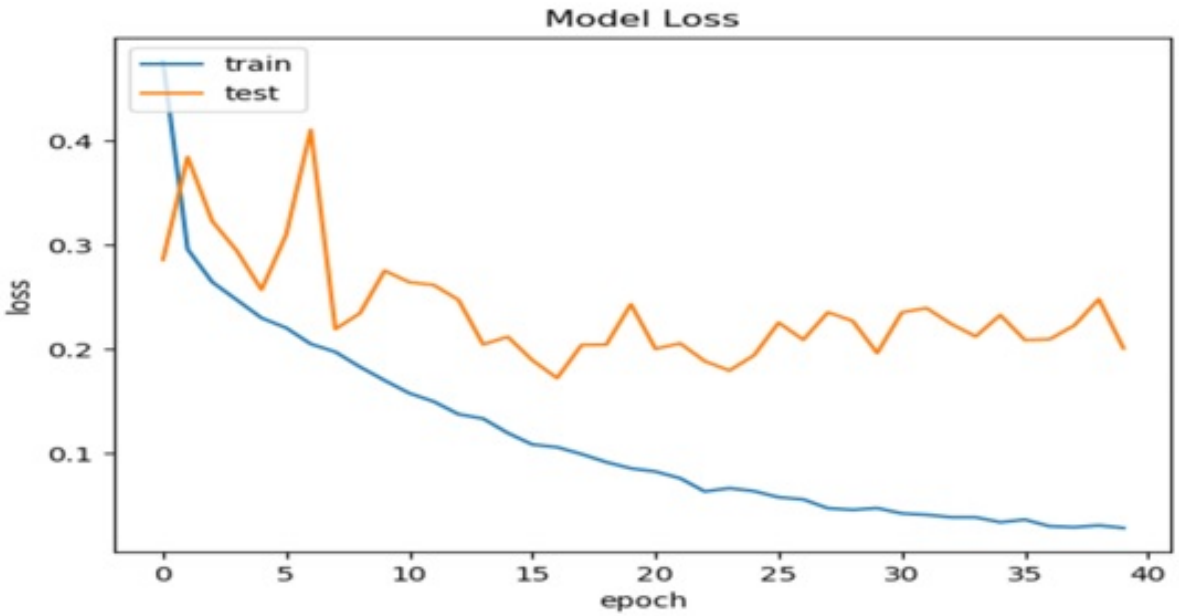

Figure 8: Validation and Training loss Progression for Histopathological Image Dataset.

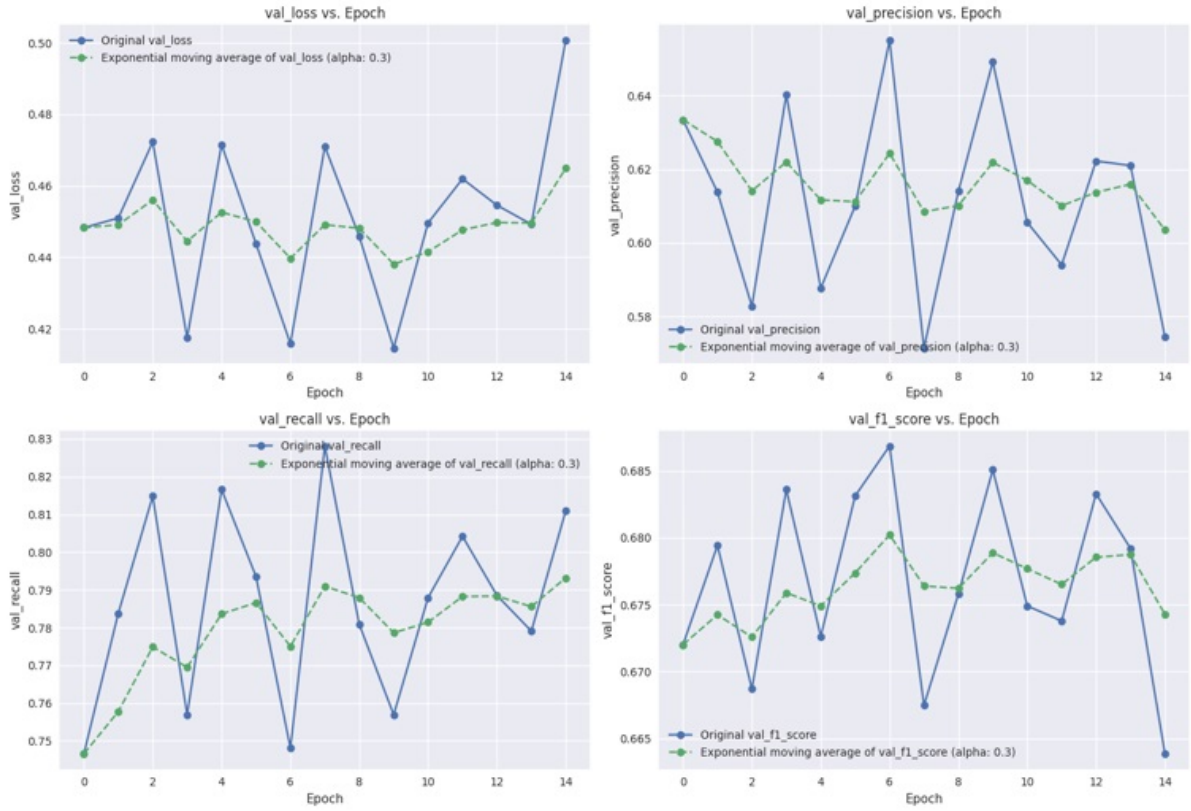

Figure 9: Performance Metrics versus Epochs.

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Epoch 1/300
1750/1750 [==============================] - 323s 179ms/step - loss: 0.1992 - recall: 0.7521 -
precision: 0.5935 - f1_score: 0.6537 - val_loss: 0.4483 - val_recall: 0.7466 - val_precision:
0.6334 - val_f1_score: 0.6720
Epoch 2/300
1750/1750 [==============================] - 73s 42ms/step - loss: 0.1871 - recall: 0.7763 - p
recision: 0.6173 - f1_score: 0.6780 - val_loss: 0.4509 - val_recall: 0.7838 - val_precision:
0.6138 - val_f1_score: 0.6794
Epoch 3/300
1750/1750 [==============================] - 72s 41ms/step - loss: 0.1831 - recall: 0.7830 - p
recision: 0.6212 - f1_score: 0.6832 - val_loss: 0.4722 - val_recall: 0.8148 - val_precision:
0.5828 - val_f1_score: 0.6687
Epoch 4/300
1750/1750 [==============================] - 73s 42ms/step - loss: 0.1799 - recall: 0.7902 - p
recision: 0.6271 - f1_score: 0.6893 - val_loss: 0.4175 - val_recall: 0.7569 - val_precision:
0.6403 - val_f1_score: 0.6836
Epoch 5/300
1750/1750 [==============================] - 73s 42ms/step - loss: 0.1769 - recall: 0.7957 - p
recision: 0.6292 - f1_score: 0.6917 - val_loss: 0.4715 - val_recall: 0.8166 - val_precision:
0.5877 - val_f1_score: 0.6726
Epoch 6/300
1750/1750 [==============================] - 72s 41ms/step - loss: 0.1752 - recall: 0.8006 - p
recision: 0.6317 - f1_score: 0.6955 - val_loss: 0.4438 - val_recall: 0.7936 - val_precision:
0.6100 - val_f1_score: 0.6831
Epoch 7/300
1750/1750 [==============================] - 75s 43ms/step - loss: 0.1718 - recall: 0.8092 - p
recision: 0.6331 - f1_score: 0.7000 - val_loss: 0.4158 - val_recall: 0.7481 - val_precision:
0.6550 - val_f1_score: 0.6868
Epoch 9/300
1750/1750 [==============================] - 72s 41ms/step - loss: 0.1673 - recall: 0.8189 - p
recision: 0.6383 - f1_score: 0.7070 - val_loss: 0.4458 - val_recall: 0.7809 - val_precision:
0.6140 - val_f1_score: 0.6758
Epoch 10/300
1750/1750 [==============================] - 73s 41ms/step - loss: 0.1652 - recall: 0.8234 - p
recision: 0.6370 - f1_score: 0.7074 - val_loss: 0.4146 - val_recall: 0.7569 - val_precision:
0.6492 - val_f1_score: 0.6851
Epoch 11/300
1750/1750 [==============================] - 74s 42ms/step - loss: 0.1629 - recall: 0.8278 - p
recision: 0.6425 - f1_score: 0.7145 - val_loss: 0.4496 - val_recall: 0.7880 - val_precision:
0.6055 - val_f1_score: 0.6749
Epoch 12/300
1750/1750 [==============================] - 77s 44ms/step - loss: 0.1604 - recall: 0.8308 - p
recision: 0.6479 - f1_score: 0.7180 - val_loss: 0.4619 - val_recall: 0.8042 - val_precision:
0.5940 - val_f1_score: 0.6738
Epoch 13/300
1750/1750 [==============================] - 75s 43ms/step - loss: 0.1578 - recall: 0.8374 - p
recision: 0.6500 - f1_score: 0.7222 - val_loss: 0.4545 - val_recall: 0.7885 - val_precision:
0.6222 - val_f1_score: 0.6833
Epoch 14/300
1750/1750 [==============================] - 72s 41ms/step - loss: 0.1553 - recall: 0.8383 - p
recision: 0.6503 - f1_score: 0.7230 - val_loss: 0.4492 - val_recall: 0.7791 - val_precision:
0.6210 - val_f1_score: 0.6792
Epoch 15/300
1750/1750 [==============================] - 74s 42ms/step - loss: 0.1532 - recall: 0.8439 - p
recision: 0.6567 - f1_score: 0.7275 - val_loss: 0.5007 - val_recall: 0.8110 - val_precision:
0.5745 - val_f1_score: 0.6639
375/375 [==============================] - 69s 184ms/step - loss: 0.5096 - recall: 0.8218 - pr
ecision: 0.5700 - f1_score: 0.6611
```

Figure 10: Training a model by considering 375 epochs.

6. Conclusion

This study presents a robust framework leveraging transfer learning with the VGG16 architecture for breast cancer detection using histopathological images, addressing critical challenges in early diagnosis. The pretrained model VGG-16 uses the ensemble strategy to enhance classification accuracy and the model successfully differentiates between benign and malignant tissues. The proposed approach achieves an impressive accuracy of 98.83%, demonstrating its potential as an effective tool for

automated breast cancer detection. By reusing knowledge from pre-trained models, the framework not only reduces computational overhead but also ensures high performance in a critical application area.

7. Future work

Future work could explore integrating additional architectures, fine-tuning hyperparameters, and extending the approach to multiclass classification tasks or other histopathological datasets to validate its generalizability and scalability from pre-trained models.

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Declaration on Generative AI

The author(s) have not employed any Generative AI tools.

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