

OPTIMIZING BREAST CANCER CLASSIFICATION THROUGH INNOVATIVE 2-STEP TRANSFER LEARNING APPROACH

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ABSTRACT

According to the American Cancer Society's statistics of breast cancer for 2023, an estimated 297,790 new cases of invasive breast cancer were expected to be diagnosed in U.S. women. As the seriousness can be seen from the stats, the early detection of breast cancer is crucial for effective treatment, exploring the computer aided detection system as alternatives to labor-intensive manual histopathological analysis. This research aims to develop a deep learning model for breast cancer classification. An Innovative 2-step training technique was employed to optimize the transfer learning process, enhancing the effectiveness of the models. Leveraging a modified PatchCamelyon dataset, consisting of 220,025 image samples, the study rigorously evaluated four prominent models: DenseNet121, VGG19, InceptionResNetV2, and Xception. Notably, VGG19 showcases the exceptional performance by achieving the highest accuracy of 96.53% on the test set and 96.58% on the validation set, aiming to refine the model's performance for accurate breast cancer classification.

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1. INTRODUCTION

Breast cancer is one of the most prevalent cancers in women, ranking second after lung cancer and bronchial cancer (Baskaran & Ramanujam, 2018). It is significant in its severity, aggressiveness, and prognosis. It can start in either one or both breasts. It is most likely to occur in women, but men can get breast cancer too (American Cancer Society, 2024a). It's important to understand how it evolves and leads to life threatening situations. Cancer commences when healthy cells change and grow out of control, forming a mass or sheet of cells called a tumour. A tumor can be classified as benign or malignant. A malignant tumour is cancerous, which means it can grow and spread to other parts of the body whereas, a benign tumour is the tumour which can grow but it will not spread (American Cancer Society, 2024b). Breast cancers spread through the lymphatic system or the bloodstream. The moment it enters the lymphatic

system, it first arrives at nearby lymph nodes. This can be called the early stage. The flourishing cancer may shed a cell or a group of cells which can use the lymphatic system as a roadway for travelling throughout the body (The Breast Centre, 2024).

The danger of this can depend upon its type, stage of diagnosis, individual's overall health and effectiveness of treatment. Hence detecting it early is very crucial and can greatly be beneficial for the patients. Various techniques like medical image processing and digital pathology have been developed for this purpose. A biopsy is the absolute way to make a diagnosis of breast cancer (Mayo Clinic, 2024). Detecting cancer through breast tissue biopsies involves differentiating between benign and malignant lesions. However, assessing extensive histopathological images manually poses challenges due to variations in its appearance, structure, and texture (Li et al., 2019). This is a manual analysis which is labour-intensive, time-

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consuming, and frequently reliant on subjective human interpretation.

To resolve these issues, integrating AI into screening methods, like analysing biopsy slides, boosts the efficacy of treatments. Machine learning and deep learning stand out as essential components of AI needed for breast cancer imaging. Computer aided detection systems using machine learning algorithms have emerged, aiming to classify tumours as benign or malignant, with malignant tumors requiring prompt treatment to mitigate complications. Deep learning, the complex form of machine learning, has outperformed traditional methods in analysing medical images, excelling in tasks such as classification, detection, segmentation, and computer-aided diagnosis. Computer Aided Diagnosis (CAD) systems and Quantitative Image Analysis (QIA) techniques have been developed to assist radiologists in interpreting medical images (Ha et al., 2018; Satsangi et al., 2024; Jain et al., 2023). These systems aim to improve the accuracy of clinicians and patient outcomes by identifying subtle abnormalities such as suspicious masses, calcifications, micro-calcifications, and other anomalies in medical images.

The various methods and modes have been employed for the classification of cancerous cells using histopathological images. Most of the approaches include transfer learning techniques, CNN architectures, Linear Regression and Deep Neural Networks. Our research work proposes the advanced and most efficient transfer learning networks which proved to be effective for the detection of breast cancer. With the utilization of unique way of training our model, we were able to achieve outstanding evaluation metric parameters.

The main contributions of the research paper are:

- 1) The use of cutting-edge deep learning models for the automated classification of breast cancer. The research employs sophisticated transfer learning techniques capable of diagnosing the Breast Cancer from biopsy images.
- 2) A unique training approach, 2-step transfer learning, has been utilised to increase the efficacy of the transfer learning models.
- 3) The exhaustive evaluation and comparison of the four prominent transfer learning models namely VGG19, DenseNet121, InceptionResNetV2 and Xception.

The remaining paper is structured as follows: Section 2 focusses on the prior research works and Section 3 addresses research strategy and methodology, which further includes dataset description, pre-processing, and description of transfer learning models. Section 4 presents the results and findings, while Section 5 offers a discussion of the work presented. Lastly, Section 6 suggests directions for future research.

2. LITERATURE REVIEW

This section provides an overview of prior research in breast cancer detection using image classification and machine-learning aided technologies for early detection.

In recent years, the rapid advancement of artificial intelligence has led to widespread utilization of machine vision technology across diverse domains. Traditionally cancer detection is known for its time-consuming nature, labour intensiveness, and heavy reliance on pathologists' experience, thereby falling short of meeting the demand of modern medical treatment. Computer vision presents a promising solution by mitigating the limitations associated with conventional detection methods in identifying cancerous cells. The research study (He et al., 2022) examines the computer vision's applications in detecting cancer cells in histopathological images. It assesses existing methods in image pre-processing, segmentation, feature extraction and recognition, providing insight into current research and future trends to guide further studies in cancer cell detection.

Recent advancements in biomedical image analysis leveraging deep-learning neural networks offer significant potential to enhance Computer Aided Diagnosis (CAD) system and Quantitative Image Analysis (QIA) techniques (Ha et al., 2018; Satsangi et al., 2024; Jain et al., 2023). This study delves into elucidating the connection between mammography and histopathology phenotypes, aiming to integrate biological aspects. To bridge this gap the study proposed a novel computer-based approach termed the mammography-Histology-Phenotype-Linking-Model.

This model aims to establish a mapping of features and phenotypes mammographic abnormalities and their corresponding histopathological representation.

Transfer learning based histopathologic image classification introduces detection using deep feature extraction (Deniz et al., 2018). This study employed two models, AlexNet (Krizhevsky et al., 2017) and VGG16 (Simonyan & Zisserman, 2014), for feature extraction and utilized AlexNet for subsequent fine-tuning. Additionally, a Support Vector Machine (SVM) was employed to classify images.

Another study (Udendhran et al., 2022) proposed an ensemble transfer learning (ETL) framework to classify images into well-differentiated, moderately differentiated and poorly differentiated categories. Initially, the authors constructed a transfer learning structure based on InceptionV3 (Szegedy et al., 2015), Xception (Chollet, 2016), VGG16 (Simonyan & Zisserman, 2014), and ResNet50 (He et al., 2015) models. Then they introduced an ensemble learning strategy utilizing weighted voting to enhance classification performance. Continuing with ensemble techniques, the study (Kassani et al., 2019) proposed an ensemble model employing three pre-trained CNNs-VGG19 (Simonyan & Zisserman, 2014), MobileNet (Howard et al., 2017), and DenseNet (Huang et al., 2016). This model focused on feature extraction, leveraging a multi-layer perceptron classifier for the classification task. Additionally, various pre-processing methods and CNN tuning techniques such as stain normalization, data augmentation, hyperparameter tuning, and fine tuning were utilized for model training. The author validates the performance of this model

across four publicly available benchmark datasets, namely ICIAR, BreakHis, PatchCamelyon and Bioimaging.

Prior research works marks the beginning of the advancement in early detection of the life-threatening disease, breast cancer. It can be concluded from the above discussion that various methods and modes have been employed for the classification of cancerous cells using histopathological images. Most of the approaches include transfer learning techniques, CNN architectures, Linear Regression and Deep Neural Networks. Our research work proposes the advanced and most efficient transfer learning networks which proved to be effective for the detection of breast cancer. With the utilization of unique way of training our model, we were able to achieve outstanding evaluation metric parameters.

3. METHODOLOGY

The research employs four novel transfer learning models, namely VGG19, DenseNet121, InceptionResNetV2, and Xception.

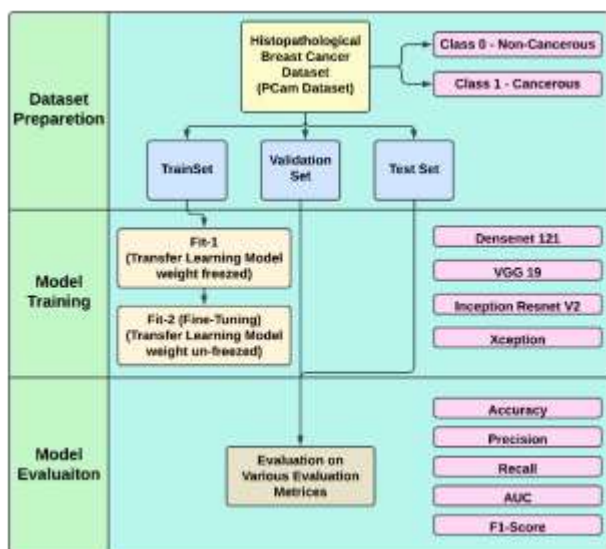


Figure 1. In-depth methodology

The novelty lies in the unique way of training the transfer learning models. In this section, we will dwell upon the materials, i.e., the dataset used and the overall workflow of the study. Figure 1 describes the overall workflow of the study.

3.1. Dataset Description

This research utilizes a refined version of the PatchCamelyon (PCam) benchmark dataset (Cukierski, 2018), which was adjusted to eliminate duplicate images found in the original PCam dataset. Some samples of the dataset are shown in figure 2. The dataset has 2 classes and can be used for binary image classification task. A positive label indicates the existence of tumour tissue in the central 32x32px region, while tumour tissue in the outer region is disregarded.

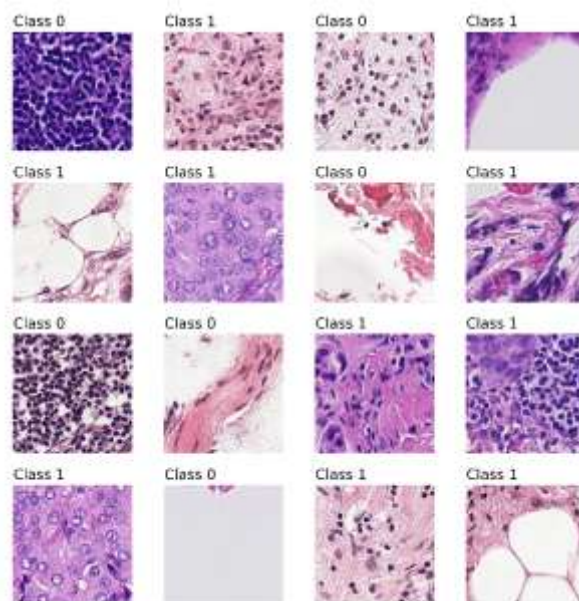


Figure 2. Sample Images from the PatchCamelyon (PCam) Dataset

This feature allows for the implementation of fully convolutional models that exhibit consistent behaviour across entire pathology scans.

3.2. Dataset Split

The dataset comprises a total of 220,025 pathology images, with a distribution among training, testing, and validation sets as follows: Training data accounts for 70% of the dataset, with 154,017 images, while testing and validation datasets each represent 15% of the dataset, with 33,004 images each.

Table 1. Distribution of Data among Train, Test and Validation Sets

Dataset	Class 0	Class 1	Total
Train	91635	62382	154017
Validation	19636	13368	33004
Test	19637	13367	33004
Total	130908	89117	220025

This structured division ensures a comprehensive evaluation of model performance while maintaining balance and reliability across all datasets. The train test validation split has been tabulated in Table 1.

3.3 Transfer Learning Models

Transfer learning using convolutional neural networks (CNNs) strives to boost performance on a new task by leveraging previously acquired knowledge from similar tasks (Marques et al., 2022). This section contains the architecture of all the four transfer learning models used. The description in the table 2 provides with the insights of the models.

3.3.1. DenseNet121

The neural network design for detecting histopathologic cancer leverages transfer learning by using DenseNet121 (Huang et al., 2016) as its base model. After the base model Batch normalization layers are strategically

positioned to stabilize and enhance the model's training efficiency by normalizing input activations. The flattened layer serves to reshape the output from the DenseNet121 base model before passing it through dense layers. The final dense layer, acting as the output layer, comprises one node, indicative of a binary classification task, with sigmoid activation function. This architecture, encompassing 7,189,249 total parameters.

3.3.2. InceptionResNetV2

The second neural network design architecture for detecting histopathologic cancer relies on InceptionResNetV2 (Szegedy et al., 2017) as its pre-trained model foundation. With a substantial base containing 54,336,649 parameters, this architecture aims to utilize the knowledge embedded within Inception ResNetV2 specially for the intended tasks. After the base model, batch normalization is employed to augment the model's training stability and efficiency. The flattened layer then reshapes and transforms the extensive output from the base model into a one-dimensional array, facilitating subsequent dense layers to perform feature extraction. The final dense layer which consists of 1 node and sigmoid activation function, signifying the binary classification nature of the task. This model, totaling 54,367,649 parameters. The detailed breakdown for two distinct fitting phases illustrates the parameter distribution throughout the training process, highlighting the model's adaptability and robustness.

3.3.3. VGG19

The third neural network architecture designed for detection of histopathologic cancer utilizes VGG19

(Simonyan & Zisserman, 2014) as its base pre-trained model. With a composition of 20,100,353 parameters, the architecture incorporates customized layers to optimize performance for the specific classification objective. Post the VGG19 base model, a batch normalization layer is employed to enhance stability of training process. The subsequent flattened layer transforms the output into a one-dimensional array, preparing the data for feature extraction through dense layers. The final dense layer, which consists of 1 node with one sigmoid activation classify into 2 classes. The detailed breakdown for two fitting phases provides insight into the dynamic nature of parameter distribution during training, offering insight into the model's adaptability and emphasizing the model's adaptability.

3.3.4. Xception

The fourth neural network architecture developed for histopathologic cancer detection utilizes the Xception (Chollet et al., 2016) model as the pre-trained base. The architecture, totalling 21,164,777 parameters, aims to utilize the high-level features learned by Xception for the specific classification task. The model incorporates batch normalization after the Xception base to enhance training stability, followed by a flattened layer that transforms the multidimensional output into a one-dimensional array. The final dense layer with 1 node and utilizing a sigmoid activation function, indicating the binary nature of the classification task. The detailed breakdown for two fitting phases provides insight into the model's adaptability and dynamic parameter distribution during training.

Table 2. Model Summaries

Layer No.	Layer Type/Name	Model Architecture 1 (Densenet121)		Model Architecture 2 (Inception Resnet V2)		Model Architecture 3 (VGG 19)		Model Architecture 4 (Xception)	
		Para-meters	Activation Function/ Dropout Rate	Para-meters	Activation Function / Dropout Rate	Para-meters	Activation Function / Dropout Rate	Para-meters	Activation Function / Dropout Rate
1	Base Model (Transfer Lear.)	7037504	-	54336736	-	20024384	-	20861480	-
2	Batch Normalization	4096	-	6144	-	2048	-	8192	-
3	Flatten	0	-	0	-	0	-	0	-
4	Dense	147472	Relu	24592	Relu	73744	Relu	294928	Relu
5	Dropout	0	0.5	0	0.5	0	0.5	0	0.5
6	Dense	136	Relu	136	Relu	136	Relu	136	Relu
7	Dropout	0	0.5	0	0.5	0	0.5	0	0.5
8	Batch Normalization	32		32		32		32	
9	Dense (Output Layer)	9	Relu	9	Relu	9	Relu	9	Relu
Total Parameters		7189249		54364649		20100353		21164777	
For Fit 1	Trainable Parameters	149690		27825		74929		299194	
	Non-Trainable Parameters	7039586		54399824		20025424		20865592	
For Fit 2	Trainable Parameters	7103537		54304017		20099322		21106137	
	Non-Trainable Parameters	85712		63632		1040		58640	

3.4. 2-Step Transfer Learning

The training procedure adopts a two-phased approach. It begins with the pre-trained base model being frozen to leverage its knowledge without modification. This phase enables the model to learn from the dataset and adapt its parameters to the specific task of breast cancer detection. After this initial training phase, the pre-trained model is unfrozen, allowing its weights to become trainable. This 2-step training strategy facilitates the model to benefit from both the general features learned by the pre-trained base and the task-specific adaptations achieved through training the entire architecture.

This rigorous 2-step training strategy affords the model the dual advantage of leveraging both the broad, generalized features acquired from the pre-trained base and the nuanced, task-specific adaptations honed through training the entire architecture. By seamlessly integrating prior knowledge with targeted refinements, this approach cultivates a more nuanced understanding of the dataset, leading to heightened performance and robustness in breast cancer detection. Moreover, it mitigates the risk of overfitting by progressively fine-tuning the model's parameters, fostering a more adaptive and generalizable framework for addressing the complexities inherent in medical imaging tasks.

4. RESULTS

The performance of the proposed breast cancer classification models employs transfer learning, namely DenseNet121, VGG19, InceptionResNetV2, and Xception. They were extensively examined across training, validation, and testing datasets and the results are tabulated in table 3.

4.1. Model Performance in Fit 1

In the initial fitting phase, the models displayed impressive performance across the training, validation, and testing datasets. The DenseNet121 model achieved an accuracy of 89.14% on the training set, 88.44% on the validation set, and 88.31% on the testing set. Xception and InceptionResNetV2 demonstrated competitive outcomes, with accuracies ranging from 85.37% to 85.41% in the training set, 83.99% to 84.47% in the validation set, and 84.02% to 84.90% in the testing set. The VGG19 model achieved the highest training accuracy of 90.08% but slightly lower accuracy in validation (86.52%) and testing (86.58%) sets.

4.2. Model Performance in Fit 2

During the second fitting phase, which involves fine-tuning, models exhibited a significant improvement in their performance. All the transferring learning models achieved exceptional accuracy, surpassing 99% on train set. However, the model's evaluation on validation and test sets, shows their actual performance. InceptionResNetV2 achieved 92.71% and 93.01% on validation and test sets respectively. Xception surpassed

the accuracy of InceptionResNetV2 with 93.62% and 93.76% on validation and test sets respectively.

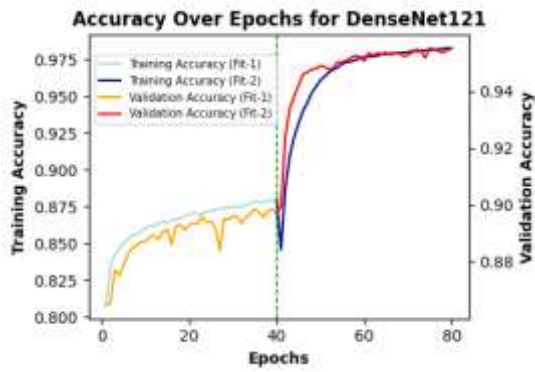
Table 3. Evaluation metrics of model architecture

Evaluation Metrics	Training Set		Validation Set		Testing Set	
	Fit1	Fit2	Fit1	Fit2	Fit1	Fit2
DenseNet121						
Accuracy	89.14	99.89	88.44	95.51	88.31	95.70
Precision	87.47	99.71	86.58	95.76	86.15	95.80
Recall	85.42	99.94	84.58	93.02	84.79	93.48
F1-Score	86.43	99.82	85.57	94.38	85.46	94.63
AUC	95.49	99.90	95.01	97.61	94.91	97.88
VGG19						
Accuracy	90.08	99.92	86.52	96.58	86.58	96.53
Precision	91.67	99.98	86.94	96.94	87.08	97.12
Recall	83.05	99.82	78.52	94.54	78.52	94.22
F1-Score	87.14	99.89	82.52	95.72	82.58	95.65
AUC	96.26	99.99	93.63	98.93	93.58	98.84
Xception						
Accuracy	85.41	99.92	84.47	93.62	84.90	93.76
Precision	89.57	99.99	88.07	92.80	88.30	93.11
Recall	72.42	99.83	71.32	91.36	72.29	91.37
F1-Score	79.27	99.91	78.81	92.07	79.77	92.23
AUC	93.00	99.99	92.03	96.34	92.55	96.67
InceptionResNetV2						
Accuracy	85.37	99.94	83.99	92.71	84.02	93.01
Precision	87.64	99.98	85.59	92.26	85.51	92.56
Recall	74.36	99.89	72.72	89.49	72.89	89.97
F1-Score	80.51	99.94	78.68	90.83	78.82	91.24
AUC	92.65	99.99	91.32	96.11	91.55	96.30

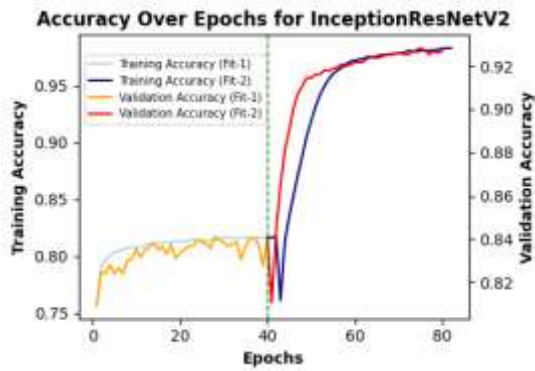
DenseNet121 gave neck-to-neck competition to VGG19 with its remarkable accuracies of 95.51% and 95.70% on validation and test sets respectively. VGG19 achieved the highest accuracies of 96.58% on validation set and 96.53% on test set.

4.3. Graphical Interpretation of accuracy and loss curves

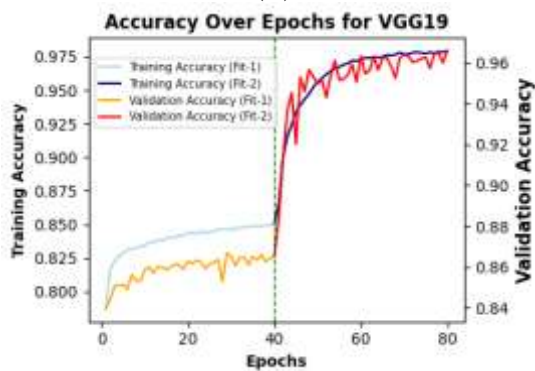
The graphical representation offers a comprehensive insight into the training progression of accuracy and loss metrics over epochs. The accuracy and loss graphs are shown in figures 3 and 4 respectively. Initially, during the fit-1 training phase covering the first 40 epochs, the models grapple with achieving significant accuracy improvements or substantial reductions in loss. However, with the subsequent introduction of fit-2 training, a remarkable transformation becomes apparent. Accuracy experiences a discernible surge, ultimately converging with precision, while loss metrics witness a notable decline, dipping below the critical threshold of 0.3. This robust improvement underscores the efficacy and potency of the meticulously orchestrated 2-step training paradigm, showcasing the models' enhanced performance without imposing undue computational demands.



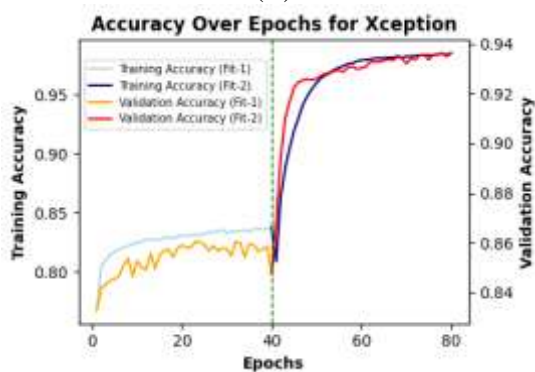
(A)



(B)

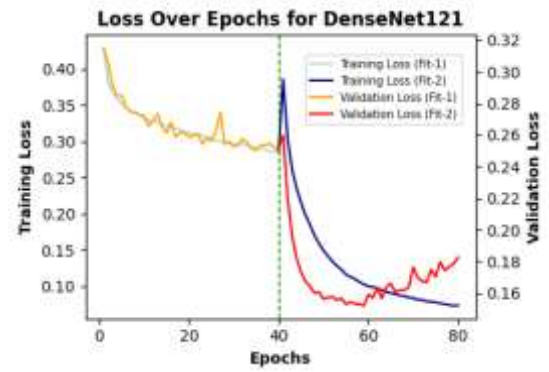


(C)

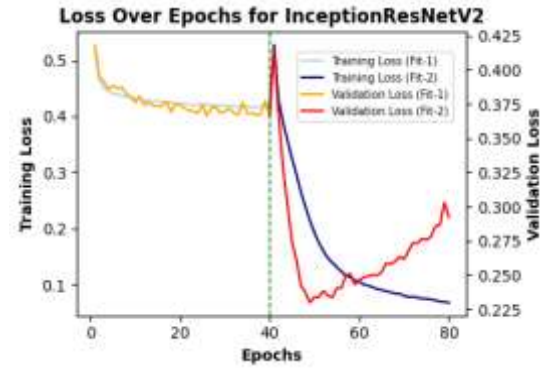


(D)

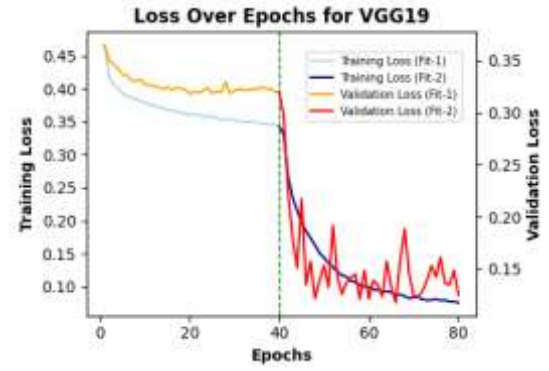
Figure 3. Accuracy over Epochs Curves for (A) DenseNet121 (B) InceptionResNetV2 (C) VGG19 (D) Xception



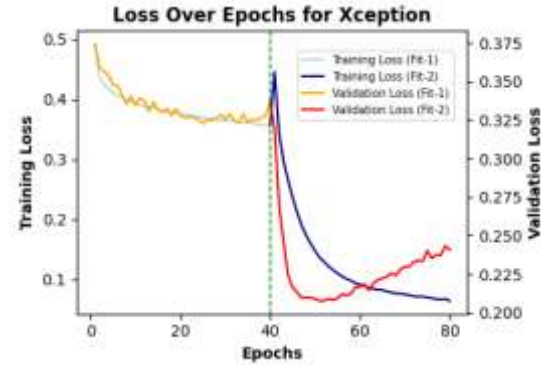
(A)



(B)



(C)



(D)

Figure 4. Loss over Epochs Curves for (A) DenseNet121 (B) InceptionResNetV2 (C) VGG19 (D) Xception

Table 4 illustrates the comparison with the prior research work in the classification of breast cancer using the same dataset. This showcases the superiority of the proposed

model's outcomes, surpassing the results obtained in previous research endeavors.

Table 4. Comparison with previous research works

Year	References	Methodology	Accuracy (%)
2019	(Kassani et al., 2019)	Ensemble Model	94.64
2022	(Lyu, 2022)	DenseNet	91.82
2022	(Alruwaili & Gouda, 2022)	ResNet50	89.5
2023	(Rohila et al., 2023)	ResNet50	95.2
2023	(Rahman et al., 2023)	ResNet50	93.0
2024	Proposed	DenseNet121, VGG19, InceptionResNetV2, Xception	95.70 96.53 93.01 93.76

5. CONCLUSION

Breast cancer treatment and detection benefit significantly from histopathological images, which provide detailed visual information about tissue samples, aiding pathologists in diagnosing abnormalities like tumour cells. Observing the current trends in AI and its increasing utilization in the healthcare domain to improve efficacy, precision, and timely treatment, we have integrated transfer learning models into our approach. These models are leveraged to detect breast cancer from histopathological images using a 2-step transfer learning approach. VGG19 is the outstanding performer with highest accuracy (96.53%), precision (97.12%), recall (94.22%), f1-score (95.65%) and area

under the curve (98.84%). The other models also gave neck-to-neck competition.

The novel 2-step verification approach proved beneficial by effectively boosting model accuracy, reducing loss, and enhancing performance in breast cancer detection. This method optimally leverages pre-trained knowledge in the initial phase and fine-tunes task-specific features in the subsequent stage, leading to improved generalization, mitigated risk of overfitting, and efficient utilization of computational resources.

Although the models demonstrated promising outcomes, it is essential to recognize the potential limitations, including dataset biases and the necessity for external validation. Future endeavours involve expanding the dataset, exploring diverse architectures, and ensuring seamless integration of AI tools into existing clinical workflows.

6. FUTURE SCOPE

Although the models demonstrated promising outcomes, it is essential to recognize the potential limitations, including dataset biases and the necessity for external validation. Future endeavors might involve expanding the dataset, exploring diverse architectures, and incorporating explain ability measures for enhanced clinical acceptance.

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