PERFORMANCE EVALUATION OF EFFICIENTNETV2 MODELS ON THE CLASSIFICATION OF HISTOPATHOLOGICAL BENIGN BREAST CANCER IMAGES

Oluwasegun A. Abioye [a,] , Abraham E. Evwiekpaefe [a], Awujoola J. Olalekan

[a] Directorate of Information and Communication Technology, Nigerian Defence Academy, Kaduna, Nigeria –
segunabioye@nda.edu.ng
[a] Department of Computer Science, Nigerian Defence Academy, Kaduna, Nigeria – aeevwiekpaefe@nda.edu.ng
[b] Directorate of Information and Communication Technology, Nigerian Defence Academy, Kaduna, Nigeria –
ojawujoola@nda.edu.ng

ABSTRACT:

In the field of breast cancer diagnosis, the precise classification of benign images plays a pivotal role in ensuring effective patient care. This research undertakes a detailed examination of EfficientNetV2 models, specifically focusing on their ability to discern benign histopathology breast cancer images. The dataset were carefully curated to include diverse benign cases such as adenosis, fibroadenoma, phyllodes_tumor, and tubular_adenoma of image level for 40X magnification factor underwent thorough preprocessing before being divided into training and testing sets. Various variants of the EfficientNetV2 model—EfficientNetV2B0, EfficientNetV2B1, EfficientNetV2B2, EfficientNetV2B3, EfficientNetV2S, EfficientNetV2M, and EfficientNetV2L—were trained on the designated dataset. The performance evaluation shows the intricacies of the efficiency of each model. Notably, EfficientNetV2L emerged as a standout performer, boasting impressive metrics such as Accuracy (0.97), Precision (0.97), Recall (0.97), F1-score (0.97). These findings underscore the potential of EfficientNetV2L as a robust tool for accurately discerning benign histopathology breast cancer images. This study contributes significant insights to the field of breast cancer diagnostics, particularly addressing the critical task of classifying benign cases accurately. The gained insights pave the way for improved decision-making in assessments, ultimately enhancing the overall efficacy of breast cancer diagnosis.

KEYWORDS: Histopathology, breast cancer, image classification, efficientNetV2, benign.

1. INTRODUCTION

Cancer is one of the deadliest diseases, annually claiming the lives of millions. Breast cancer is recognized as the predominant cancer and the primary cause of mortality in women (Anastasiadi et al., 2017). According to data from the World Health Organization (WHO), 460,000 individuals die of breast cancer each year out of a total of 1,350,000 reported cases (Wang et al., 2020). Breast cancer is a significant health concern originating from the uncontrolled growth of abnormal cells. It can initiate in various organs or tissues, exceeding their normal boundaries, infiltrating adjacent areas, and potentially spreading to other organs (WHO, 2018). Various imaging methods are employed for detecting breast cancer, including Histopathology (Saha et al., 2018), Computed Tomography (Domingues et al., 2020), Magnetic Resonance Imaging (Murtaza et al., 2020), Ultrasound (Pavithra et al., 2020), Mammograms (Moghbel et al., 2020) and Positron Emission Tomography. Research has demonstrated that histopathological images do not solely provide binary identification and classification but instead facilitate the multiclass identification and classification of different breast cancer subtypes. Given the high mortality rate associated with breast cancer, women are advised to undergo routine screenings, including mammograms and computerized tomography (CT).

In cases where abnormal cells are detected, a biopsy is conducted to assess the irregularity in the breast. Typically, the obtained sample undergoes staining with hematoxylin and eosin (H&E). Hematoxylin interacts with Deoxyribonucleic Acid (DNA), imparting a purple or blue hue to the nuclei, while Eosin reacts with proteins, resulting in a pink coloration in other structures (Bardou et al., 2018). Histopathological image diagnosis stands as the benchmark for diagnosing various cancers, including breast cancer. Nevertheless, this method is a labor-intensive process highly reliant on the pathologist's expertise, subject to factors like fatigue and diminished attention, making it time-consuming and potentially prone to variations. Hence, there is a need for computer-aided diagnosis (CAD) systems to offer an unbiased evaluation to pathologists and enhance diagnostic efficiency (Aresta et al., 2019). Nonetheless, traditional computerized diagnostic methods, spanning from rule-based systems to machine learning techniques, might struggle to effectively address the intra-class variation and inter-class consistency found in histopathology images of breast cancer (Robertson et al., 2018). Furthermore, these methods primarily rely on feature extraction techniques like scale-invariant feature transform (Lowe, 1999), speed robust features (Bay et al., 2006), and local binary patterns (Ojala et al., 2002). These techniques are based on supervised information and may be prone to biased results when classifying histopathology images of breast cancer (Dimitriou et al., 2019).

In recent years, there has been a significant surge in developing and applying deep learning models, particularly in biomedical image processing, showcasing remarkable progress in computer vision. This advancement stems from the capability of deep learning models to autonomously learn advanced features directly from images, making them powerful tools across various domains. Researchers are keen on leveraging these models for image analysis and classification challenges. Based on their success, researchers are exploring the application of deep learning models in classifying breast cancer histopathology images. The complex nature of histopathological images which demands an understanding of cellular structures, poses a challenge for traditional methods. Deep learning models, with their ability to automatically discern and learn these features,

* Corresponding author

offer a promising avenue to enhance the accuracy of breast cancer classification. Researchers increasingly utilize these advanced models to contribute to ongoing efforts in improving diagnostic processes for breast cancer pathology (Dimitriou et al., 2019).

In this study, we utilized different versions of the EfficientNetV2 model architecture to efficiently classify breast cancer histopathology. The analysis involved leveraging the BreakHis dataset, specifically focusing on benign subtypes, and employing images captured at a magnification level of 40X. The main contributions of this paper are: first, the augmentation of the images from BreakHis dataset; which helps in expanding the size of the training dataset by generating additional variations of existing images. It's important to note that a larger dataset often leads to more robust models and helps prevent over fitting. Next, we evaluated the performance of EfficientNetV2 models on histopathological images using some standard computational metrics. Fig. (1) shows the breast cancer histopathology benign images with the following; sample A- adenosis, B - fibroadenoma , C - phylodes _tumor and D - tubular_adenoma.
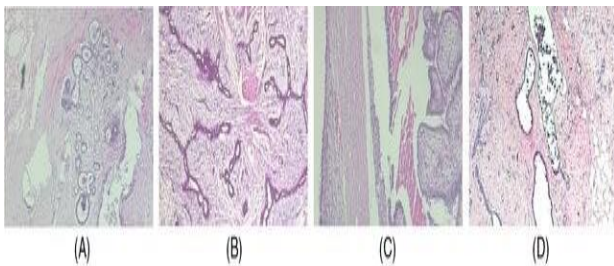

Figure 1: Breast cancer histopathology benign images sample A - adenosis, B - fibroadenoma, C - phylodes tumor, and D - tubular adenoma

The remaining sections of this paper are provided as follows. Section 2 presents related work. Section 3 demonstrates the materials and methods used to conduct this research. Section 4 illustrates the results along with discussion. Finally, Section 5 highlights the conclusion and future direction of this study.

2. LITERATURE REVIEW

Various studies have been conducted, leading to significant advancement in the automated classification of breast cancer histopathological images, the distinctive features of these images, encompassing factors like the inconsistent tissue and cell morphology, occurrences of cell overlapping, variations in the appearance of stained histological sections, and uneven color distribution shows important difficulties in image classification (Loukas et al., 2013).

These difficulties pose significant challenges for the automated and accurate classification of breast cancer pathological images. Additionally, it is important to acknowledge that pathological images have a very high resolution, rendering it impractical to directly apply certain methods that have proven successful in the field of natural images to the domain of pathological images.

Hirra et al. (2021) conducted research on the accurate detection and classification of breast cancer, recognizing its critical importance in medical imaging due to the intricacies of breast tissues. They highlighted the efficacy of deep learning methods in various domains, particularly in medical imaging, owing to their automatic feature extraction capabilities. The study introduced a novel patch-based deep learning approach named Pa-DBN-BC for detecting and classifying breast cancer in histopathology images, leveraging the Deep Belief Network (DBN). Through a combination of unsupervised pre-training and supervised fine-tuning phases, features were extracted from image patches automatically. Logistic regression was then employed to classify patches within histopathology images. The

extracted features served as inputs to the model, which generated a probability matrix indicating positive (cancer) or negative (background) samples. Their proposed model underwent training and testing on a comprehensive dataset of whole-slide histopathology images encompassing images from four distinct data cohorts, achieving an accuracy of 86%. The study concluded that their approach surpassed traditional methods by automatically learning optimal features, demonstrating superior performance compared to previously proposed deep learning methods.

Zhou et al. (2022) presented a novel approach aimed at assisting pathologists in efficiently and accurately diagnosing breast cancer through histopathological analysis. Their method comprises two modules: the Anomaly Detection with Support Vector Machine (ADSVM) method and the Resolution Adaptive Network (RANet) model. The ADSVM method is designed to identify mislabeled patches, thereby enhancing the training performance of the RANet model. Within the RANet model, subnetworks with variable resolutions and depths are utilized to classify images based on their classification difficulty, potentially improving computational efficiency and prediction accuracy. The proposed RANet-ADSVM approach was evaluated using two publicly available datasets: BreaKHis and BACH 2018. Binary and multiclass classifications were conducted at both patient and image levels across different magnification factors on the BreaKHis dataset. The highest accuracies of 98.83% and 99.14% were achieved for binary classification at 200× magnification at the patient and image levels, respectively. For the BACH 2018 dataset, binary and multiclass classifications were performed at patch and image levels. Experimental results revealed the best accuracies for multiclass and binary classifications at the image level to be 97.75% and 99.25%, respectively. Furthermore, comparative experiments demonstrated that the proposed approach significantly improved both classification accuracy and computational efficiency. Compared with similar networks such as ResNet and DenseNet, the proposed method reduced computational time by approximately 50% .Top of Form

Joseph et al. (2022) discussed the importance of breast cancer (BC) classification in biomedical informatics, emphasizing its significant impact on women's health as a leading cause of cancer-related deaths. They highlighted the growing interest in utilizing machine learning techniques, particularly Deep Learning algorithms like Convolutional Neural Networks, for BC detection and monitoring through pathological image analysis. While binary classification methods have been explored, few approaches exist for multi-classification of histopathological images, often limited by inefficient feature extraction and overfitting issues. To address these challenges, Joseph et al. (2022) proposed a method combining handcrafted feature extraction techniques (Hu moment, Haralick textures, and color histogram) with Deep Neural Network (DNN) classifiers, trained on the BreakHis dataset. Augmentation of data is employed to mitigate overfitting. Their approach achieves superior performance in breast cancer multi-classification, with accuracy scores of 97.87% for 40x, 97.60% for 100x, 96.10% for 200x, and 96.84% for 400x magnification-dependent histopathological images. The results underscore the effectiveness of their method in comparison to existing literature, highlighting the crucial role of data augmentation in enhancing classification accuracy.

Alkassar et al., (2021) tackled the pressing need for improved breast cancer diagnosis, particularly emphasizing early detection given its high fatality rate among women. They underscored the efficiency of histopathology slides over traditional screening methods, despite challenges in the diagnostic process due to human errors during slide preparation. To overcome these obstacles, they proposed a novel method for

diagnosing breast cancer, categorizing it into benign or malignant classes using magnification-specific binary (MSB) classification. Moreover, their approach further refines classification by subdividing each type into four subclasses using magnification-specific multi-category (MSM) classification.

The method involves stain normalization to enhance color separation and contrast, followed by the extraction of deep and shallow features using DenseNet and Xception-based deep structure networks. They employed a multi-classifier method based on the maximum value to optimize performance. Evaluation on the BreakHis histopathology dataset demonstrates promising diagnostic accuracies of 99% for MSB and 92% for MSM, surpassing recent state-of-the-art methods in the literature.

Zewdie et al. (2021) tackled the pressing issue of improving breast cancer diagnosis, given its status as the most prevalent and fatal cancer among women globally. They underscored the critical role of advancements in screening and early detection to bolster survival rates. While clinical examination and imaging techniques aid in diagnosis, pathological assessment remains the gold standard due to its ability to discern cancer type, sub-type, and stage. However, current diagnostic methods relying on visual inspection of microscopic images are time-consuming, laborious, and subjective, potentially resulting in misdiagnosis.

To surmount these challenges, the authors proposed a multi-class classification system based on deep learning. By harnessing histopathological images from various sources and magnifications and applying pre-processing techniques to enhance image quality, they employ a pre-trained ResNet 50 model. This system adeptly categorizes breast cancer into binary (benign and malignant) and multi-classes (sub-types) while also identifying cancer grade for invasive ductal carcinomas. Test results showcased impressive accuracy rates, including 96.75% for binary classification, 96.7% for benign sub-type classification, 95.78% for malignant sub-type classification, and 93.86% for grade identification. The proposed method serves as a decision support system, particularly valuable in resource-constrained settings, facilitating early and precise cancer detection, thereby contributing to a reduction in breast cancer mortality rates.

Behar et al. (2021) addressed the urgency of breast cancer detection, highlighting its status as a leading cause of female mortality. Their study introduces a convolutional neural network (CNN)-based model for automatic classification of histopathology images into malignant and benign tumours. Leveraging transfer learning with the ResNet50 architecture, the model achieves remarkable training, validation, and test accuracies of 99.70%, 99.24%, and 99.24%, respectively. Compared to recent studies, the model demonstrates enhanced classification accuracy, average precision, F1 score, and receiver operating characteristic (ROC) area, reaching 99.1%. This reliable and accurate CNN model offers significant potential for improving breast cancer diagnosis and treatment outcomes.

Wang et al., (2021) proposed a novel approach, FE-BkCapsNet, for automatic classification of breast cancer histopathological images. This method combines the strengths of convolutional neural networks (CNN) and capsule networks (CapsNet) to enhance classification performance. By integrating semantic features from CNN and spatial features from CapsNet into new capsules, the model extracts more discriminative information. The authors introduced a dual-channel structure to extract convolution and capsule features simultaneously. Additionally, they optimize routing coefficients adaptively by modifying the loss function and embedding the routing process into the entire optimization process. Testing on the BreaKHis dataset yields promising results, with classification accuracies of 92.71% (40×), 94.52% (100×), 94.03% (200×), and 93.54% (400×). These findings underscore the efficiency of FE-BkCapsNet for breast cancer classification in clinical settings.

Wakili et al. (2022) addressed the complexities of breast cancer analysis, emphasizing its prevalence and the challenges it poses for experts. Despite the potential of deep learning in histopathological image classification, current methods are computationally intensive and prone to overfitting. Through a survey, the authors identified an optimal training-testing ratio of 80%:20%, outperforming the common 70%:30% split. They introduced DenTnet, leveraging transfer learning with DenseNet as a backbone model to overcome feature extraction challenges. DenTnet achieves detection accuracies of up to 99.28% on the BreaKHis dataset, showcasing superior generalization and computational efficiency.

Hameed et al. (2020) introduced an ensemble deep learning approach for the accurate classification of non-carcinoma and carcinoma breast cancer histopathology images, leveraging a newly collected dataset. Four distinct models were trained based on pre-trained VGG16 and VGG19 architectures. The initial phase involved 5-fold cross-validation for each model, encompassing fully-trained VGG16, fine-tuned VGG16, fully-trained VGG19, and fine-tuned VGG19 models. Subsequently, an ensemble strategy was employed, averaging the predicted probabilities. The ensemble of fine-tuned VGG16 and fine-tuned VGG19 exhibited competitive classification performance, particularly in the carcinoma class, achieving a sensitivity of 97.73% and an overall accuracy of 95.29%. Additionally, it yielded an F1 score of 95.29%.

In the majority of literature reviews considered, the emphasis lies in crafting a model for classifying both benign and malignant breast cancer histopathological images. However, the main aim of this research paper is to narrow the focus solely on benign breast cancer histopathological images. The objective is to conduct a performance evaluation on the proposed images using EfficientNetV2 models.

3. MATERIAL AND METHOD

The aim of this study is to perform the evaluation of EfficeintNetV2 models on histopathological breast cancer benign images. This section encompasses aspects such as data collection, dataset description, and data pre-processing which includes data augmentation operations, evaluation metrics, as well as the study's procedure and methodology. Fig. (2) shows the architecture of the proposed models.
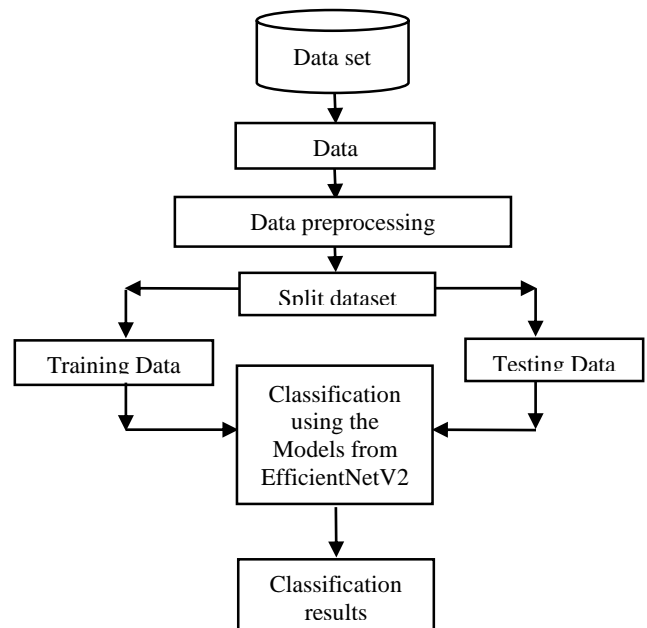

Figure 2: The architecture of the proposed models

3.1 Dataset Description

The BreakHis dataset for breast cancer histopathological image classification comprises 9,190 microscopic images of breast tumor tissue obtained from 82 patients, utilizing various magnification levels (40X, 100X, 200X, and 400X). It encompasses 2,480 benign and 5,429 malignant samples, each with dimensions of 700X460 pixels, presented in a 3-channel RGB format with b-bit depth in each channel, and saved in PNG format. This collaborative effort involved the P&D Laboratory – Pathological Anatomy and Cytopathology in Parana, Brazil. In this study, we utilized benign breast cancer images at a magnification level of 40X. To optimize the effectiveness of our proposed models, augmenting the limited set of benign images was considered. The BreakHis dataset provides only a limited number of benign images, necessitating data augmentation to prevent over fitting. Table 1 presents the number of both the original benign images and the augmented images for magnification level 40X used in the study.

Table 1: Shows the number of both original and augmented benign images for magnification level 40X

No	Benign Types	Total Benign Original Images	Total Benign Augmented Images
1.	Adenosis	114	1,026
2.	Fibroadenoma	253	1,076
3.	Phylodes Tumor	109	1,100
4.	Tubular Adenoma	149	1,057

3.2 Data Augmentation Operations

During the process of augmenting the original benign images with magnification level of 40X collected from the BreakHis dataset. The parameters used for the generating of the augmented images are contained in the table below. Table 2 shows the parameter settings for each operation used in the data augmentation.

Table 2: The parameter settings for each operation used in data augmentation

No	Operations	Parameters	Setting Values
1.	**Rotate**	Probability	0.7
		Max_left_rotation	25
		Max_right_rotation	25
2.	**Zoom_Random**	Probability	0.5
		Percentage_area	0.8
3.	**Flip_Left_Right**	Probability	0.5
4.	**Random_Contrast**	Probability	0.5
		Min_factor	0.8
		Max_factor	1.2
5.	**Random_Brightness**	Probability	0.5
		Min_factor	0.7
		Max_factor	1.3

3.3 EfficientNetV2 Model

EfficientNetV2 is a novel convolutional network family designed for faster training and enhanced parameter efficiency compared to its previous models. It is an improved version of EfficientNet. The primary objective is to further optimize both training speed and parameter efficiency. In the initial layers of the network architecture, the speed of depthwise convolutional layers (MBConv) were slow. The depthwise convolutional layers typically have fewer parameters than regular convolutional

layers, but its performance on modern accelerators was below standard. To address this issue, EfficientNetV2 uses a combination of MBConv and Fused MBConv, for faster training without increasing the number of parameters (Tan & Le, (2021).

3.4 Method

The initial steps involve setting up the model by loading the EfficientNetV2 architecture for each model. Subsequently, a new input layer is created, preprocessing is applied to input images, and features are extracted using the base model. The model is then designed with a GlobalAveragePooling2D layer for feature aggregation and a fully connected layer for classification, considering the specific number of classes in the histopathological dataset. The dataset is prepared by loading and preprocessing both training and testing images and labels. The images are loaded from Google Drive, resized to the specified dimensions, and converted to the required color format. Labels are encoded from text to integers. The model is then trained using the training dataset with defined epochs, batch size, and validation data. During training, key metrics such as loss, accuracy, and validation metrics are monitored and plotted to assess the model's convergence. After training, the model is evaluated on the test set, and various performance metrics are calculated, including accuracy, precision, recall, F1-score, and ROC-AUC. The confusion matrix and a detailed classification report provide insights into the model's performance for each class. The entire process is documented to share the methodology, code, and results, fostering community collaboration and contribution. This comprehensive approach ensures a systematic and transparent workflow for breast cancer histopathology image classification using EfficientNetV2.

4. RESULT AND DISCUSSION

The research work measured the performance of EfficeintNetV2 models on histopathological benign breast cancer images using the following metrics; accuracy, precision, recall, f1-score, kappa_score, sensitivity and false negative ratio. Table 3: shows the classification report of EfficientNetV2 models on histopathological benign breast cancer images.

Table 3: The classification report of EfficientNetV2 models on histopathological benign breast cancer images.

Model	Acc	Prec	Recall	F1-Score
EfficientNetV2B0	0.95	0.95	0.95	0.95
EfficientNetV2B1	0.96	0.96	0.96	0.96
EfficientNetV2B2	0.96	0.96	0.96	0.96
EfficientNetV2B3	0.96	0.96	0.96	0.96
EfficientNetV2L	**0.97***	**0.97***	**0.97***	**0.96***
EfficientNetV2M	0.94	0.94	0.94	0.94
EfficientNetV2S	0.96	0.96	0.96	0.96

The classification report provides a detailed breakdown of the performance metrics for various models under the EfficientNetV2 architecture, each denoted by a specific identifier (e.g., EfficientNetV2B0, EfficientNetV2B1, etc.). The metrics evaluated include Accuracy (Acc), Precision (Prec), Recall, and F1-Score. The models EfficientNetV2B0 through EfficientNetV2B3 exhibit consistent and high performance across all metrics. They achieve an Accuracy of 0.95 to 0.96, indicating their overall correctness in making predictions. Precision, Recall, and F1-Score are also consistently at 0.96, reflecting the models' ability to make accurate positive predictions, correctly identify relevant instances, and strike a balance between precision and recall. EfficientNetV2L stands out in the classification report with slightly higher values across all metrics compared to its counterparts. The model achieves an

Accuracy of 0.97*, denoting potential superiority in overall correctness. Precision, Recall, and F1-Score are reported as 0.97*, 0.97*, and 0.96*, respectively. The asterisks imply additional information or conditions associated with these values, suggesting a nuanced aspect to the model's performance. EfficientNetV2M and EfficientNetV2S, while still performing well, demonstrate slightly lower values compared to EfficientNetV2L. EfficientNetV2M achieves an Accuracy of 0.94, with Precision, Recall, and F1-Score at 0.94. EfficientNetV2S, similar to the other models, reports an Accuracy of 0.96 and consistent scores of 0.96 across Precision, Recall, and F1-Score. In conclusion, the classification report offers a comprehensive evaluation of the EfficientNetV2 models, highlighting their performance across key metrics. EfficientNetV2L emerges as a potentially superior choice, marked by slightly higher scores in overall correctness, precision, recall, and the harmonic balance of precision and recall. These insights aid in selecting the most suitable model based on specific classification requirements.

4.1 Visual Evaluation Metrics for EfficientNetV2L Model on Histopathological Benign Breast Cancer Images

In the research work, EfficientNetV2L presents the best performing result in its evaluation on histopathology benign breast cancer images with magnification level 40X. This section shows the various visual evaluation metrics for EfficientNetV2L on breast cancer images; accompanied with explanations. Figure 3 shows the Confusion Matrix of EfficientNetV2L on Histopathological breast cancer images.
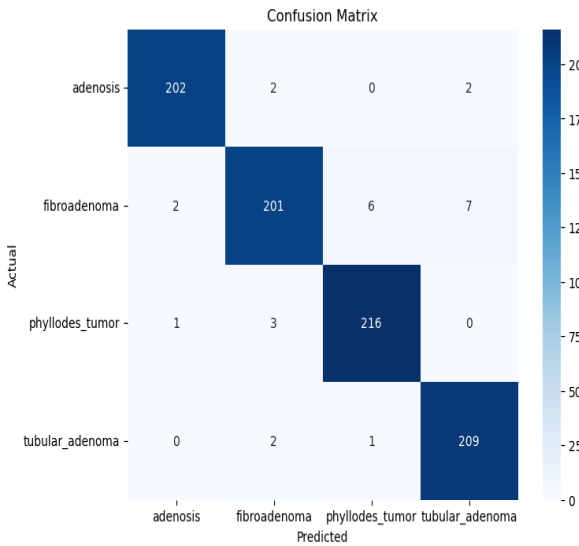

Figure 3: The confusion matrix of EfficientNetV2L on histopathological benign breast cancer images

The provided confusion matrix in Figure 3 represents the result of a classification model using EfficientNetV2L across four different classes: Adenosis, Fibroadenoma, Phyllodes_tumor, and Tubular_adenoma. Each cell in the matrix indicates the count of instances based on the true class (rows) and the predicted class (columns). In the first row corresponding to the true class "Adenosis," the model correctly classified 202 instances as Adenosis (True Positives). However, there were 2 instances misclassified as Fibroadenoma and 2 instances misclassified as Tubular_adenoma, resulting in False Negatives. Moving to the second row, representing the true class "Fibroadenoma," the model correctly predicted 201 instances as Fibroadenoma (True Positives). However, there were 2 instances misclassified as Adenosis (False Positives), 6 instances misclassified as Phyllodes_tumor, and 7 instances misclassified

as Tubular_adenoma (all False Negatives). For the true class "Phyllodes_tumor" in the third row, the model performed well by correctly classifying 216 instances (True Positives). However, there was 1 instance misclassified as Adenosis and 3 instances misclassified as Fibroadenoma, resulting in False Positives. Finally, the last row corresponds to the true class "Tubular_adenoma," with the model correctly predicting 209 instances (True Positives). Nevertheless, there were 2 instances misclassified as Adenosis and 1 instance misclassified as Fibroadenoma, resulting in False Positives. This confusion matrix provides a detailed breakdown of the model's performance for each class, highlighting where misclassifications occur and offering valuable insights into the strengths and weaknesses of the classification model.
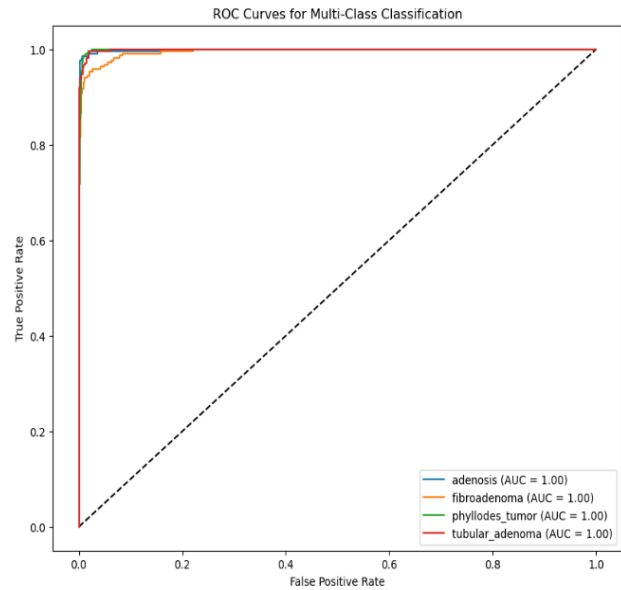

Figure 4: The reciever operating characteristics Curve of EfficientNetV2L on histopathological benign breast cancer images
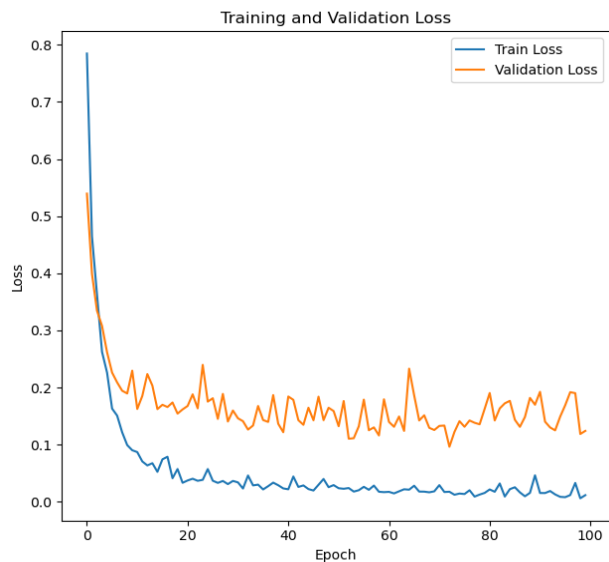

Figure 5: The training and validation loss of EfficientNetV2L on histopathological benign breast cancer images
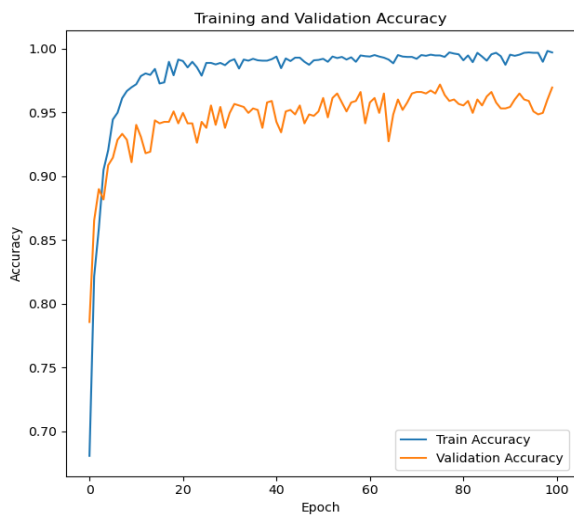
Figure 6: The training and validation loss of EfficientNetV2L on histopathological benign breast cancer

CONCLUSION

The research work provides a comprehensive assessment of EfficientNetV2 models, with EfficientNetV2L emerging as a potentially superior choice, marked by slightly higher scores in overall correctness, precision, recall, and the harmonic balance of precision and recall. These insights offer valuable guidance for selecting the most suitable model based on specific classification requirements, emphasizing the significance of nuanced considerations in model evaluation.

REFERENCES

Anastasiadi, Z., Lianos, G. D., Ignatiadou, E., Harissis, H. V., & Mitsis, M. (2017). Breast cancer in young women: an overview. Updates in surgery, 69, 313-317.

Araújo, T., Aresta, G., Castro, E., Rouco, J., Aguiar, P., Eloy, C., Polónia, A., Campilho, A., & Mendonça, A. M. (2017). Classification of breast cancer histology images using convolutional neural networks. PLoS One, 12(6), e0177544.

Aresta, G., Araújo, T., Kwok, S., Chennamsetty, S. S., Safwan, M., Alex, V., ... & Aguiar, P. (2019). Bach: Grand challenge on breast cancer histology images. Medical image analysis, 56, 122-139.

Bardou, D., Zhang, K., & Ahmad, S. M. (2018). Classification of breast cancer based on histology images using convolutional neural networks. IEEE Access, 6, 24680-24693.

Bay, H., Tuytelaars, T., & Gool, L. V. (2006). SURF: Speeded Up Robust Features. In Proceedings of the Computer Vision—ECCV 2006, Lecture Notes in Computer Science, Graz, Austria, 7–13 May 2006, 404–417.

Bayramoglu, N., Kannala, J., & Heikkilä, J. (2016). Deep learning for magnification independent breast cancer histopathology image classification. In 2016 23rd International Conference on Pattern Recognition (ICPR) (pp. 2440-2445).

Behar, N., & Shrivastava, M. (2022). ResNet50-Based Effective Model for Breast Cancer Classification Using Histopathology Images. CMES-Computer Modeling in Engineering & Sciences, 130(2).

Dimitriou, N., Arandjelović, O., & Caie, P. D. (2019). Deep learning for whole slide image analysis: an overview. Frontiers in Medicine, 6, 264.

Domingues, I., Pereira, G., Martins, P., Duarte, H., Santos, J., & Abreu, P. H. (2020). Using deep learning techniques in medical imaging: A systematic review of applications on CT and PET. Artificial Intelligence Review, 53, 4093-4160.

Doyle, S., Agner, S., Madabhushi, A., Feldman, M., & Tomaszewski, J. (2008). Automated grading of breast cancer histopathology using spectral clustering with textural and architectural image features. In 2008 5th IEEE International Symposium on Biomedical Imaging: From Nano to Macro (pp. 496-499). IEEE.

Hameed, Z., Zahia, S., Garcia-Zapirain, B., Aguirre, J. J., & Vanegas, A. M. (2020). Breast cancer histopathology image classification using an ensemble of deep learning models. Sensors, 20(16), 4373.

Hirra, I., Ahmad, M., Hussain, A., Ashraf, M. U., Saeed, I. A., Qadri, S. F., ... & Alfakeeh, A. S. (2021). Breast cancer classification from histopathological images using patch-based deep learning modeling. *IEEE Access*, *9*, 24273-24287.

Joseph, A. A., Abdullahi, M., Junaidu, S. B., Ibrahim, H. H., & Chiroma, H. (2022). Improved multi-classification of breast cancer histopathological images using handcrafted features and deep neural network (dense layer). Intelligent Systems with Applications, 14, 200066.

Loukas, C., Kostopoulos, S., Tanoglidi, A., Glotsos, D., Sfikas, C., & Cavouras, D. (2013). Breast cancer characterization based on image classification of tissue sections visualized under low magnification. Computational and Mathematical Methods in Medicine.

Lowe, D. G. (1999, September). Object recognition from local scale-invariant features. In Proceedings of the seventh IEEE international conference on computer vision (Vol. 2, pp. 1150-1157). Ieee.

Moghbel, M., Ooi, C. Y., Ismail, N., Hau, Y. W., & Memari, N. (2020). A review of breast boundary and pectoral muscle segmentation methods in computer-aided detection/diagnosis of breast mammography. Artificial Intelligence Review, 53, 1873-1918.

Murtaza, G., Shuib, L., Abdul Wahab, A. W., Mujtaba, G., Nweke, H. F., et al. (2020). Deep learning-based breast cancer classification through medical imaging modalities: State of the art and research challenges. Artificial Intelligence Review, 53, 1655-1720.

Ojala, T., Pietikainen, M., & Maenpaa, T. (2002). Multiresolution gray-scale and rotation invariant texture classification with local binary patterns. IEEE Transactions on Pattern Analysis and Machine Intelligence, 24, 971–987.

Pavithra, S., Vanithamani, R., & Justin, J. (2020). Computer-aided breast cancer detection using ultrasound images. Materials Today: Proceedings, 33, 4802-4807.

Robertson, S., Azizpour, H., Smith, K., & Hartman, J. (2018). Digital image analysis in breast pathology—from image processing techniques to artificial intelligence. Translational Research, 194, 19-35.

Saha, M., Chakraborty, C., & Racoceanu, D. (2018). Efficient deep learning model for mitosis detection using breast histopathology images. Computerized Medical Imaging and Graphics, 64, 29-40.

Spanhol, F. A., Oliveira, L. S., Petitjean, C., & Heutte, L. (2015). A dataset for breast cancer histopathological image classification. IEEE Transactions on Biomedical Engineering, 63(7), 1455-1462.

Tan, M., & Le, Q. (2021). Efficientnetv2: Smaller models and faster training. In Proceedings of the International

Conference on Machine Learning (ICML), July 2021 (pp. 10096-10106). PMLR

Vesal, S., Ravikumar, N., Davari, A., Ellmann, S., & Maier, A. (2018). Classification of breast cancer histology images using transfer learning. In Image Analysis and Recognition: 15th International Conference, ICIAR 2018, Póvoa de Varzim, Portugal, June 27–29, 2018, Proceedings (pp. 812-819). Springer International Publishing.

Wakili, M. A., Shehu, H. A., Sharif, M. H., Sharif, M. H. U., Umar, A., Kusetogullari, H., ... & Uyaver, S. (2022). Classification of breast cancer histopathological images using DenseNet and transfer learning. Computational Intelligence and Neuroscience, 2022.

Wang, K., Franch-Expósito, S., Li, L., Xiang, T., Wu, J., & Ren, G. (2020). 34P Comprehensive clinical and molecular portraits of grade 3 ER+ HER-breast cancer. Annals of Oncology, 31, S27.

Wang, P., Wang, J., Li, Y., Li, P., Li, L., & Jiang, M. (2021). Automatic classification of breast cancer histopathological images based on deep feature fusion and enhanced routing. Biomedical Signal Processing and Control, 65, 102341.

World Health Organization. (2018). Latest global cancer data: Cancer burden rises to 18.1 million new cases and 9.6 million cancer deaths in 2018. International Agency for Research on Cancer, Geneva, pp. 1-4.

Zewdie, E. T., Tessema, A. W., & Simegn, G. L. (2021). Classification of breast cancer types, sub-types and grade from histopathological images using deep learning technique. Health and Technology, 11(6), 1277-1290.

Zhang, B. (2011, October). Breast cancer diagnosis from biopsy images by serial fusion of Random Subspace ensembles. In 2011 4th International Conference on Biomedical Engineering and Informatics (BMEI) (Vol. 1, pp. 180-186). IEEE.

Zhou, Y., Zhang, C., & Gao, S. (2022). Breast cancer classification from histopathological images using resolution adaptive network. IEEE Access, 10, 35977-35991.