Transfer Learning-based CNN Model for the Classification of Breast Cancer from Histopathological Images

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***Abstract*—Breast cancer can have significant emotional and physical repercussions for women and their families. The timely identification of potential breast cancer risks is crucial for prompt medical intervention and support. In this research, we introduce innovative methods for breast cancer detection, employing a Convolutional Neural Network (CNN) architecture and Transfer Learning (TL) technique. Our foundation is the ICAIR dataset, encompassing a diverse array of histopathological images. To harness the capabilities of deep learning and expand the model's knowledge base, we propose a TL model. The CNN component adeptly extracts spatial features from histopathological images, while the TL component incorporates pretrained weights into the model. To tackle challenges arising from limited labeled data and prevent overfitting, we employ ResNet152v2. Utilizing a pre-trained CNN model on extensive image datasets initializes our CNN component, enabling the network to learn pertinent features from histopathological images. The proposed model achieves commendable accuracy (96.47%), precision (96.24%), F1-score (97.18%), and recall (96.63%) in identifying potential breast cancer cases. This approach holds the potential to assist medical professionals in early breast cancer risk assessment and intervention, ultimately enhancing the quality of care for women's health.**

***Keywords*—Breast cancer; transfer learning; ResNet152v2; medical image analysis; ICAIR 2018 dataset**

I. Introduction

In our contemporary landscape, cancer has solidified its status as a ubiquitous threat, permeating global communities and emerging as a predominant cause of illness and mortality. A chilling statistic underscores the severity of its impact—over 14.5 million lives have succumbed to cancer worldwide, and an ominous prognosis emerge, suggesting an alarming surge to over 28 million by the year 2030. In the realm of oncology, breast cancer takes center stage, its diagnosis often initiated through the intricate dance of biopsy and subsequent microscopic image analysis [1]. Within the microscopic tapestry of breast tissue, pathologists wield their expertise, navigating the labyrinthine structures and components that hold the key to early detection. Histologically probing the microscopic realm, they unravel the intricate distinctions between normal tissue, benign formations, and the malignant lesions that herald a potential storm [2]. The insights harvested from these histological images are not merely observations; they serve as the bedrock for prognosis assessments, guiding the course of treatment in the relentless pursuit of increased curative outcomes with minimized morbidities.

As the medical landscape continues to evolve, the arrival of Deep Learning (DL) heralds a promising era, transcending traditional boundaries in recognition tasks. DL-based technologies, seamlessly integrated into the workflow of pathologists and clinicians, become instrumental in the perpetual quest for early cancer detection—a steadfast research focus in the expansive field of tumor oncology [3]. A beacon within this evolving narrative is the emergence of Computer-Aided Breast Cancer Diagnosis, an application of paramount importance. Yet, to maintain a grounded perspective on clinical applications, the imperative of multicategory diagnosis becomes evident, recognizing the intricate spectrum of breast cancer manifestations. Motivated by this imperative, the incorporation of deep learning approaches stands as a beacon, promising not just innovation but an elevation in the accuracy of classifiers, further fortifying the arsenal against cancer's relentless assault [4].

The intricate relation between microscopic analysis and biopsy marks the inception of the breast cancer diagnostic journey, unraveling the complex narrative within tissue samples. In the relentless pursuit of early cancer detection, the intersection of radiomics and histopathology emerges as a frontier, promising enhanced insights into tumor characteristics. Emerging technologies such as three-dimensional histopathological reconstruction redefine our approach, offering a holistic visualization of tissue architecture for comprehensive diagnosis. Beyond traditional image-based classification, molecular signatures and genomic profiling usher in a new era of precision medicine, tailoring treatments to individual patients. Ethical considerations in the use of artificial intelligence within pathology underscore the need for responsible and transparent integration into clinical workflows [5].

The integration of blockchain technology into histopathological data management ensures secure, traceable, and interoperable handling of sensitive medical information. The collaboration between pathologists and computational biologists becomes a cornerstone, fostering a symbiotic

relationship for refining algorithms and validating findings [6]. Virtual reality applications in medical education leverage histopathological images, providing immersive learning experiences for the next generation of pathologists. Novel contrast agents in histopathology imaging promise heightened sensitivity, enabling the detection of subtle cellular changes indicative of early-stage malignancies. The burgeoning field of exosome analysis in breast cancer pathology offers a promising avenue, unveiling the potential of liquid biopsy for non-invasive and real-time disease monitoring [7].

However, challenges persist in the current paradigm. The inadequacy of feature representation in existing methods poses a threat to classifier accuracy, highlighting a critical need for improvement [8]. Furthermore, the influence of the magnification factor in acquiring histopathology images introduces a variable that can lead to misclassification, amplifying the urgency for refinement. The deficiencies in accuracy and sensitivity within existing methods underscore the necessity for an overhaul, especially in applications demanding precise classification results [9]. In navigating this complex terrain, the existing classification algorithms grapple with singular features—be it spatial, morphological, or textural. The demand echoes for a comprehensive framework adept at handling multiple feature types, bridging the existing gaps and fortifying the foundation for a new era in cancer diagnosis [10]. As the quest for reliable and precise classification intensifies, the intersection of medical expertise and technological innovation emerges as the crucible where breakthroughs are forged and the relentless pursuit of conquering cancer unfolds.

Moreover, considering the limited availability of labeled data, the study leverages advanced Transfer Learning (TL) methods to enhance the model's adaptability to the specific task under consideration. Following this, the model undergoes a process of fine-tuning and adaptation tailored to the breast cancer detection task. This enables the model to autonomously acquire the ability to discern relevant spatial features from histopathological images. The integration of information from various sources, including disparate imaging and clinical data, into a unified model showcases commendable levels of accuracy, sensitivity, and specificity. In an age where healthcare increasingly embraces data-driven methodologies, this study contributes significantly to the expanding domain of medical image analysis. It underscores the importance of employing TL to overcome the limitations imposed by scarce labeled data. Subsequent sections of this manuscript will delve into the intricacies of the methodology, the careful design of the experimental framework, the presentation of results, and a thorough discussion of the findings.

By seamlessly combining the capabilities of hybrid neural network architectures with sophisticated TL techniques, this research aims to establish a more refined approach to breast cancer risk assessment. These pioneering efforts are expected to have a substantial impact on healthcare outcomes and usher in a new era of enhanced women's health. The major contribution of the research work includes:

- Enhancing the accuracy of breast cancer classification from histopathological images by leveraging transfer learning-based CNN models.
- Effectively extract relevant features for breast cancer classification, reducing the annotation burden and potentially speeding up the diagnostic process.
- Transfer learning-based CNN models offer increased generalizability across different datasets and scalability to handle larger volumes of data. This allows the developed model to be applicable across diverse clinical settings and potentially assist in automating the analysis of histopathological images on a larger scale, thus improving the efficiency of breast cancer diagnosis and treatment.

II. Literature Review

The emergence of Computer-Aided Breast Cancer diagnosis signifies a pivotal milestone in clinical applications, amplifying the need for a realistic perspective that incorporates multicategory diagnosis. The incorporation of DL approaches in breast cancer diagnosis holds the ability to enhance the accuracy of classifiers by delivering more robust foundation for clinicians and pathologists. Existing methods face challenges related to feature representation, affecting the overall accuracy of classifiers, thereby necessitating a drive for improved methodologies. The influence of the magnification factor in acquiring histopathology images introduces variability, potentially leading to misclassification—a factor that demands standardized protocols and careful consideration. Current breast cancer classification algorithms often focus on singular features, such as spatial, morphological, or textural characteristics, highlighting the need for a comprehensive framework capable of handling multiple feature types. Existing methodologies contribute uniquely to the evolving landscape of breast cancer detection, encompassing advancements in DL, challenges in feature representation, and the quest for a more comprehensive diagnostic framework.

Xie et al. [11] introduced a convolutional neural network (CNN) architecture tailored for breast cancer grading, demonstrating exceptional performance across diverse datasets and illustrating the model's adaptability to different staining techniques and tissue variations. The research elucidates the interpretability of the deep learning model, utilizing attention mechanisms to highlight regions crucial for accurate grading, fostering trust and understanding among clinicians. This work delves into the transferability of the trained model to different institutions, addressing concerns of model generalizability and promoting wider adoption in diverse clinical settings. Expanding on morphological features, Wei et al. [12] conducted an in-depth analysis of the discriminatory power of specific morphological descriptors, emphasizing the significance of nuclear shape, glandular arrangement, and stromal characteristics. This study explored the correlation between morphological features and clinical outcomes, establishing potential links between specific histopathological patterns and prognosis. The computational efficiency of morphological feature extraction methods is crucial for real-time applications in clinical settings.

Zewdie et al. [13] introduced texture analysis methods, including gray-level co-occurrence matrices and Gabor filters, evaluating their effectiveness in capturing subtle textural nuances indicative of different breast cancer subtypes. They

explored the impact of preprocessing techniques on texture analysis outcomes, shedding light on the importance of standardized image preparation for robust classification results. Moreover, the research investigates the reproducibility of texture features across multiple institutions, addressing concerns related to dataset variability and ensuring the reliability of the proposed classification approach. Aswathy et al. [14] introduced a novel spatial feature integration method, considering not only local but also global contextual information for improved classification accuracy. They explored the impact of spatial feature incorporation on the model's ability to differentiate between intertumoral heterogeneity and distinct tumor subtypes. They discussed the potential applications of spatial feature-based classification in guiding targeted therapies and predicting treatment response based on spatial tumor characteristics.

Building on ensemble learning model, Hameed et al. [15] systematically evaluated various ensemble strategies, including bagging and boosting, to discern their impact on breast cancer diagnosis accuracy. They investigated the robustness of ensemble models against noisy or imbalanced datasets, providing insights into the models' performance in real-world clinical scenarios. They discussed the scalability of ensemble learning approaches, exploring their feasibility for large-scale deployment in healthcare institutions. Yan et al. [16] introduced a multimodal fusion paradigm, which showcased the synergy between histopathological images and complementary data sources, such as gene expression profiles or clinical information. The added value of multimodal fusion helped in resolving ambiguous cases, demonstrating the potential for more confident and accurate breast cancer subtype classification. Challenges related to data integration, emphasizing the importance of harmonized datasets for meaningful fusion and collaboration across different domains were discussed.

Xue et al. [17] extended the application of transfer learning to histopathological image classification, leveraging pre-trained models on large datasets to enhance the efficiency and generalizability of classifiers. The impact of domain adaptation techniques in mitigating domain shift issues were addressed along with the challenges related to variations in staining techniques and image acquisition protocols. This work transferred knowledge from other medical imaging domains, offering insights into the broader applicability of histopathological image analysis. Hussain et al. [18] integrated explainable AI techniques and evaluated the effectiveness of explainability methods, such as saliency maps and attention mechanisms, in enhancing the transparency and trustworthiness of histopathological image classifiers. Hameed et al. [19] introduced and evaluated a suite of quantitative metrics specific to histopathological image classifiers, ensuring comprehensive and standardized performance assessment. The research addressed the limitations of traditional metrics, proposing novel measures tailored to the intricacies of histopathological images, including inter-observer agreement and sensitivity to rare subtypes. The importance of benchmark datasets with ground truth annotations is evaluated by facilitating fair and meaningful comparisons between different classification models.

III. Materials and Methods

This section serves as the foundation of our endeavor to advance breast cancer classification by combining state-of-the-art technologies. As we navigate through the intricate details of our approach, our goal is to elucidate the systematic framework that forms the foundation for the development and evaluation of our breast cancer detection model. Within this section, we delineate the essential steps, techniques, and tools utilized in our research, shedding light on the trajectory toward unlocking the full potential of transfer learning and CNN architectures. Breast cancer, posing a significant challenge to women's health globally, calls for innovative solutions in early detection [20]. Our methodology aims to bridge the gap between the intricacies of breast cancer diagnosis and the capabilities of artificial intelligence, specifically tailored for the ICIAR 2018 histopathological dataset—an invaluable repository of histopathological images and clinical data. In the subsequent sections, we will meticulously detail our data preprocessing strategies, the architectural framework of our transfer learning model and the intricacies of the training and validation procedures. The proposed methodology is crafted not only to make a meaningful contribution to the field of breast cancer classification but also to serve as a blueprint for future research endeavors focusing on unlocking the potential of artificial intelligence in healthcare diagnostics.

A. Dataset Description

Utilized in our experimental investigations, the ICIAR 2018 breast cancer histopathological dataset offers a comprehensive exploration of breast cancer pathology through Hematoxylin and Eosin (H&E) stained microscopy images [21]. These images, categorized as normal, benign, in situ carcinoma, or invasive carcinoma, present a diverse spectrum of breast cancer types. The dataset's credibility is ensured by the meticulous annotation conducted by doctors, with any annotation discrepancies leading to the exclusion. To provide visual context, Fig. 1 offers illustrative examples derived from the ICIAR 2018 dataset, granting a preview of the varied histopathological presentations contained within the dataset.

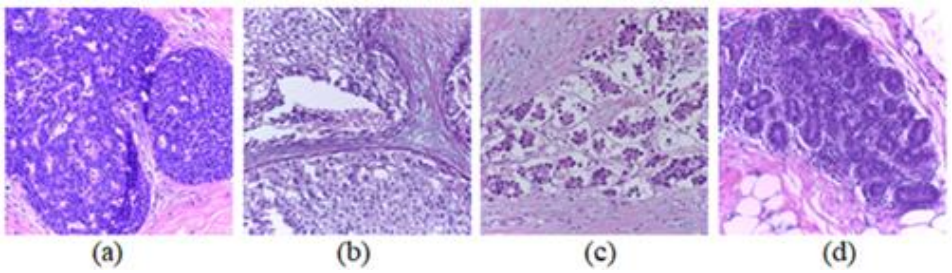

Fig. 1. Images from ICIAR 2018 dataset (a) Benign, (b) Carcinoma-in-situ, (c) Carcinoma-invasive, (d) Normal.

Employing the Red-Green-Blue (RGB) color model, the dataset captures intricate cellular details. Each image boasts a resolution of 2048 x 1536 pixels, enabling microscopic insights. With a memory space requirement of 10-20 MB per image, the dataset strikes a balance between richness of information and computational efficiency. The image-wise labeling approach contributes to a holistic understanding of breast cancer pathology, offering valuable insights for researchers and clinicians alike. Table I furnishes a thorough breakdown, shedding light on the distribution of different image classes within the given dataset. This classification facilitates the methodical analysis of breast cell properties, serving both research and diagnostic objectives.

TABLE I. IMAGES IN ICIAR 2018 DATASET

Sl. No	Image Class	Total	Train	Test
1	Benign	1000	800	200
2	Carcinoma-in-sit	1000	800	200
3	Carcinoma invasive	1000	800	200
4	Normal	1000	800	200

The strategic use of data augmentation is implemented to address overfitting concerns in CNNs while concurrently improving the accuracy of disease detection. Fig. 2 provides a visual depiction of images within the dataset and a comprehensive overview of the image distribution.

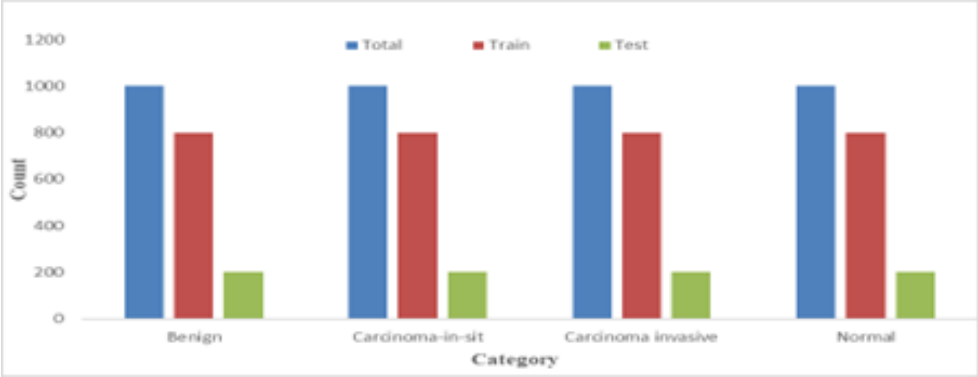

Fig. 2. Distribution of various categories in dataset.

B. Breast Cancer Classification using Transfer Learning

While dealing with histopathological images, the utilization of ResNet-152v2 stands as a pivotal advancement in leveraging deep learning for enhanced diagnostic accuracy. ResNet-152v2, renowned for its depth and skip-connection architecture, proves instrumental in capturing intricate patterns and subtle features crucial for discerning between cancer categories [22]. This classification model benefits from its ability to mitigate vanishing gradient issues, allowing for effective training of deep networks using TL technique. This approach facilitates a more nuanced understanding of the complex structures present in histopathological images, empowering the model to provide precise and reliable identification of breast cancer pathology. The proposed model incorporating ResNet-152v2 and TL is illustrated in Fig. 3.

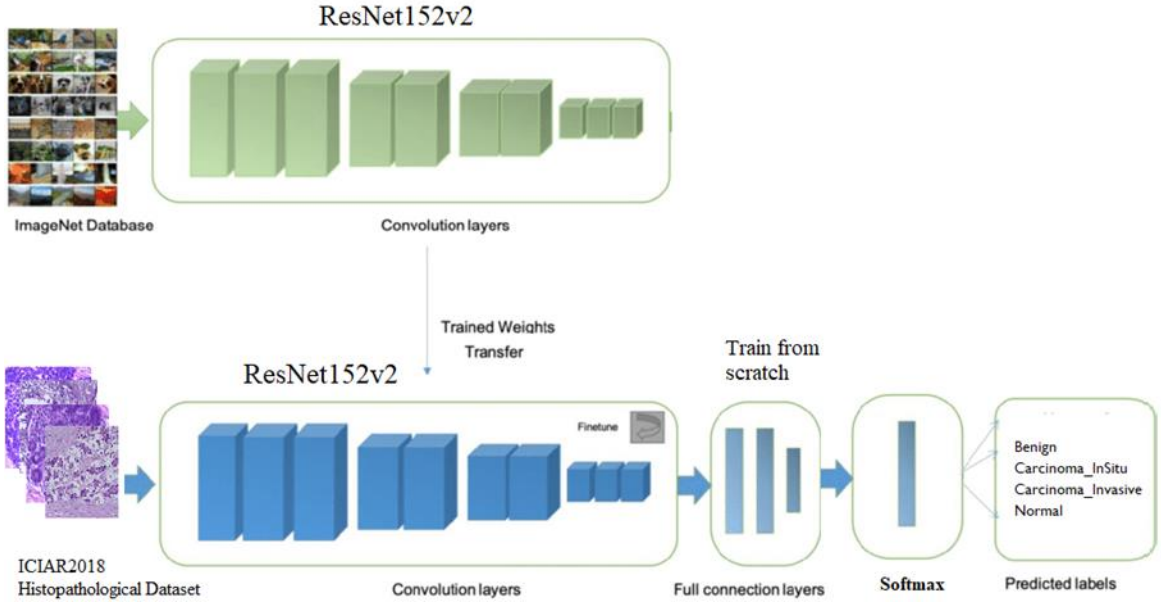

Fig. 3. Proposed transfer learning model.

To address the challenges associated with vanishing or exploding gradients during training, researchers introduced the concept of Residual Blocks. In the architecture of these Residual Networks (ResNets), a crucial technique called skip connections is employed. Skip connections establish links between the activations of one layer and subsequent layers by bypassing certain intermediary layers. This design creates what is known as a residual block, which is a fundamental building block of ResNets. The strength of ResNets lies in their ability to stack these residual blocks together, forming a deep and interconnected network. By incorporating skip connections, ResNets facilitate the flow of information across layers, mitigating the issues of vanishing gradients and enabling the training of exceptionally deep neural networks. This design principle has proven effective in improving the optimization process and fostering the successful training of deep model. The process flow and working of the skip connections is illustrated in Fig. 4.

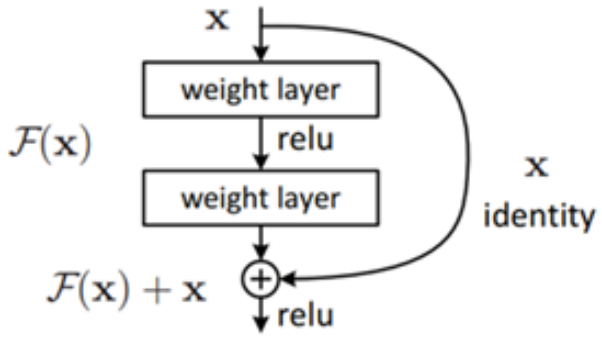

Fig. 4. Skip (Shortcut) connections.

The methodology employed in this network diverges from conventional layer-wise learning of the underlying mapping. Instead, we enable the network to adapt to the residual mapping. Thus, rather than expressing it as H(x), the initial mapping, we encourage the network to adjust according to Eq. (1) and Eq. (2).

$$F(x) = H(x) - x \tag{1}$$

$$H(x) = F(x) + x \tag{2}$$

The residual block in the proposed architecture is expressed using Eq. (3). This equation provides an insight about the output of the network. Here, x is the input to the block, Wi represents the learnable parameters, and F is a residual function implemented by a series of convolutional layers. The output y is the sum of the residual function and the input, allowing for the bypass of information is expressed as in Eq. (3).

$$y = F(x, \{W_i\}) + x \tag{3}$$

The inclusion of skip connections offers a notable benefit: if a particular layer negatively impacts the architecture's performance, regularization allows it to be bypassed. Consequently, this permits the training of extremely deep neural networks without encountering issues related to vanishing or exploding gradients. The ResNet architecture pioneered the concept of employing deeper networks [23]. The skip connection technique facilitates the training of highly deep networks, contributing to enhanced model performance. By preserving acquired knowledge during training, residual connections expedite the training process, effectively amplifying the network's capacity.

ResNet152V2 stands out as a residual network comprising an impressive 152 layers. Its primary function involves feature extraction from images by training input images based on pre-existing weights [24]. The architectural makeup of this model encompasses various layers, including reshape, flatten, the first dense layer, dropout, the second dense layer, and an activation layer dedicated to predicting image classes. Given its considerable depth and a multitude of parameters, ResNet152V2 proves particularly well-suited for intricate tasks, especially in scenarios where datasets are extensive and diverse. It's important to highlight that initiating training for ResNet152V2 from scratch demands a substantial amount of labeled data and significant computational resources. This proves especially beneficial when confronted with limited data or computational resources. The proposed architecture, as illustrated in Fig. 5, encapsulates the key components of this sophisticated model.

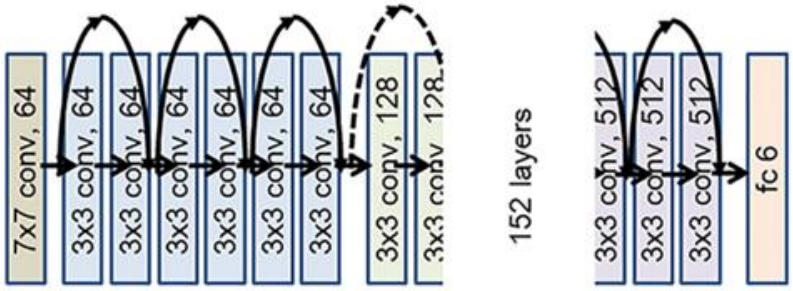

Fig. 5. ResNet152 V2 architecture.

The architecture of proposed classifier within the context of multi-classification comprises of two distinct components: the reduction path and the classifier head. The reduction path follows conventional convolutional network design principles, incorporating repeated convolutions and max-pooling operations to facilitate down sampling [25]. This process involves iteratively applying three stages, collectively termed a "block," multiple times, contributing depth to the network. The sequence concludes with fully connected layers that form the classifier. Critical to this architecture are the convolutional layers, pivotal in computing local weighted sums, commonly known as 'feature maps,' at each layer. These feature maps are generated by the repeated application of filters across the entire dataset, significantly enhancing training efficiency. The

iterative application of these processes contributes to the network's depth and its ability to capture intricate patterns in the data. In the concluding stage, an activation function, specifically the softmax function, is employed to categorize the outputs of the model into different classes, covering various aspects of breast cancer cases. This crucial step equips the model with the ability to make nuanced and precise predictions, ultimately enhancing its diagnostic capabilities. Table II provides a detailed examination of the network's structure, encompassing the arrangement of layers and corresponding parameters.

TABLE II. PROPOSED TRANSFER LEARNING MODEL SUMMARY

Layers	Type	Output Shape	Parameters
Input Layer	Dense	256 x 256 x 3	-
ResNet152v2	Feature Transfer	8 x 8 x 2048	58331648
Convolution Layer	Conv2D	8 x 8 x 64	131136
Max pooling layer	Maxpooling2D	4 x 4 x 64	0
Convolution Layer	Conv2D	4 x 4 x 32	2080
Convolution Layer	Conv2D	4 x 4 x 64	2112
Dense	Dense	4 x 4 x 32	4160
Dense	Dense	4 x 4 x 64	2080
Flatten	Flatten	512	0
Dense	Dense	4	2052
Total			58,475,268
Trainable			143,620
Non-Trainable			58,331,648

The initial step involves transferring features and weights from a pre-trained ResNet152v2 model, originally trained on the ImageNet dataset. Following this, the data undergoes a series of processing steps, including convolutional operations, max-pooling, dense layers, flattening, and hidden layers. These operations result in a final output comprising six distinct classes, facilitating individual class predictions. During the model's training and validation, a batch size of 128 and a total of 25 epochs were utilized. 25 epochs are the optimal value required for the TL model to converge. It was noted that at this epoch count, both the loss and accuracy metrics stabilize, yielding the most favorable and consistent results. Fig. 6 provides a visual representation of the proposed TL model tailored for the ICAIR 2018 dataset. This schematic diagram provides an overview of the model's architecture, initiating with six distinct classes and setting the stage for robust classification.

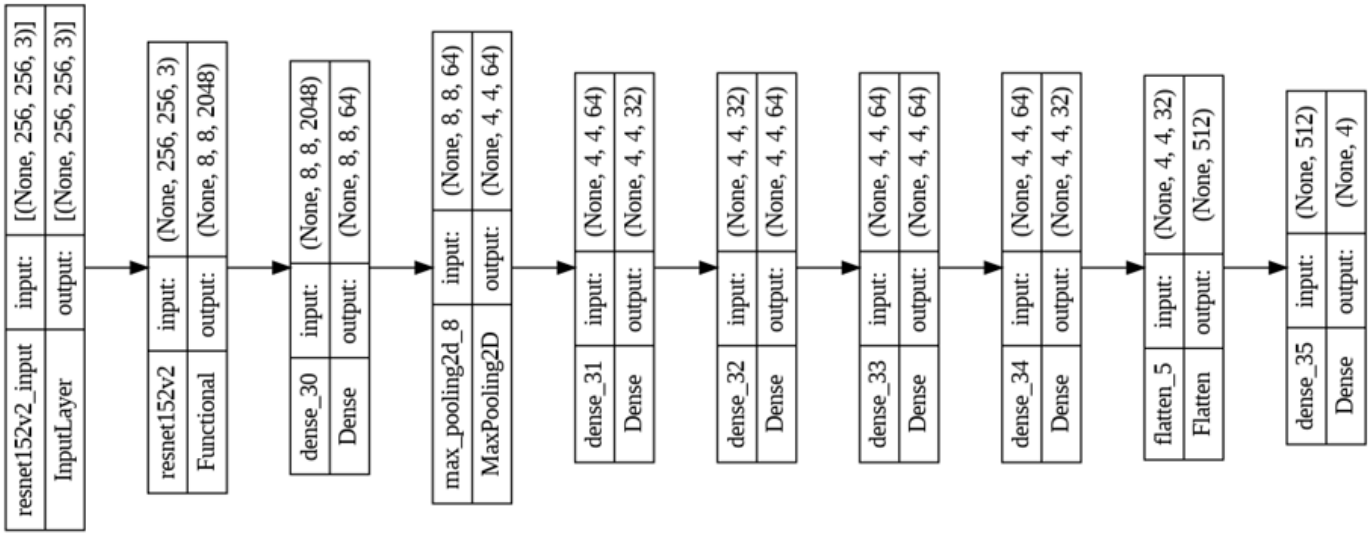

Fig. 6. Proposed transfer learning model.

IV. RESULTS AND DISCUSSION

The systematic investigation involves the extraction of features from various levels within the CNN, placing a specific focus on evaluating the granularity of these features in relation to their performance in classification tasks. This process includes utilizing different layers of the CNN to obtain these features. An integral part of the research revolves around

identifying the optimal CNN layer that produces the most distinctive features for the classification of histopathological images into distinct categories. This holds particular significance considering the training of the TL-CNN model on the ICAIR 2018 dataset. The primary objective of the study is to unveil the CNN layer that offers the most valuable insights for distinguishing between different classes of breast cell images, ultimately enhancing the overall efficiency of the model.

In our suggested methodology, our emphasis lies specifically on the profound layers of the model, leveraging their output features to train the classifier, while maintaining the immobility of the layers leading up to this depth. This approach effectively trims down the number of trainable components, although a considerable number of features remain viable. Our training approach involves an 80% allocation for training and a 20% allocation for testing. Furthermore, for result comparison with previous studies, we ensure consistency by employing the same parameters in cross-validation and fixed partitioning methodologies. The development of the proposed model is executed using Python on the Google Colab platform. We have implemented a learning rate of 1x10-4 for this work, accompanied by a minimized batch size of 128 and a total of 25 training epochs. The loss the model needs to be reduced after each epoch. The loss becomes low and constant after 7 epochs. The accuracy also turns out to be constant after 7 epochs. Fig. 7 provides a graphical representation of the training and validation performance of the proposed TL-CNN classifier.

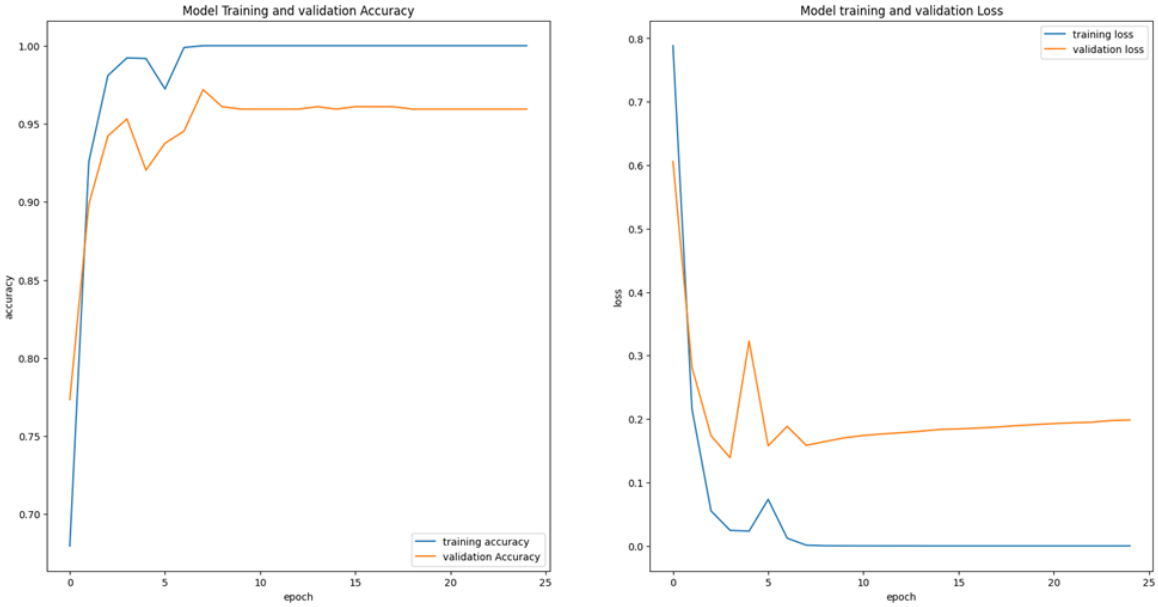

Fig. 7. Accuracy plot and loss plot of proposed model.

To comprehensively evaluate the effectiveness and operational efficiency of the model we suggest, we utilize a suite of four pivotal metrics: F1-score, accuracy, precision, and recall. In defining these metrics, we incorporate the terms False Positive (FP), False Negative (FN), True Negative (TN), and True Positive (TP), which are fundamental for evaluating model performance. These performance parameters are expressed mathematically as in Eq. (4), (5), (6) and (7).

$$Precision = \frac{TP}{TP+FP} \quad (4)$$

$$Recall = \frac{TP}{TP+FN} \quad (5)$$

$$Accuracy = \frac{TP+TN}{TP+FP+TN+FN} \quad (6)$$

$$F1-Score = 2 \times \frac{Precision \times Recall}{Precision+Recall} \quad (7)$$

Beyond the 7th epoch in the proposed ResNet152v2 based CNN classifier, the performance metrics consistently display a commendable level of accuracy. This stability in performance can be credited to the effective application of TL techniques, addressing challenges inherent in categorization tasks. Within the training process, the consideration of errors, often referred to as loss, is crucial. In our case, the observed loss is merely 0.3, indicating an exceptionally low level of error. To comprehensively evaluate the model, the entire test image dataset was employed. The mean accuracy achieved by our suggested TL-CNN model reaches an impressive value of 96.47%. Additionally, the mean values for precision, recall, and F1-score showcase strong performance, measuring at 96.24%, 96.63%, and 97.18%, respectively. Table III provides the classification report for the proposed multiclass classification model.

TABLE III. CLASSIFICATION REPORT OF PROPOSED CLASSIFIER

Category	Precision (%)	Recall (%)	F1-Score	Accuracy (%)
Benign	96	96	96	95
Carcinoma-in-Situ	97	92	95	97
Carcinoma-Invasive	96	97	97	96
Normal	95	98	96	97

The effectiveness of the proposed model is notably impressive in accurately identifying the breast cancer classes. Moreover, it maintains a minimum accuracy of 95% with benign class. This model provides maximum accuracy of 97% with carcinoma-in-situ and normal classes. Precision analysis reveals that the model attains its peak value of 97% for carcinoma-in-situ class. The lowest precision, still notably high at 95%, is observed in the normal class. Moving on to recall, the model reaches a maximum value of 98%, for the normal class. The lowest recall of 92% is noted in carcinoma-in-situ class. F1-score achieves a maximum value of 97% for the carcinoma-invasive class and maintains a minimum value of 95% for the carcinoma-in-situ class. In summary, the classification report underscores the superior performance across all classes. The proposed model demonstrates particular proficiency in identifying various classes within the given dataset. For a detailed perspective on the performance of individual classes, (see Fig. 8). Additionally, Fig. 9 illustrates the confusion matrix generated for the proposed classifier, offering a comprehensive visualization of the classification performance across various breast cancer categories.

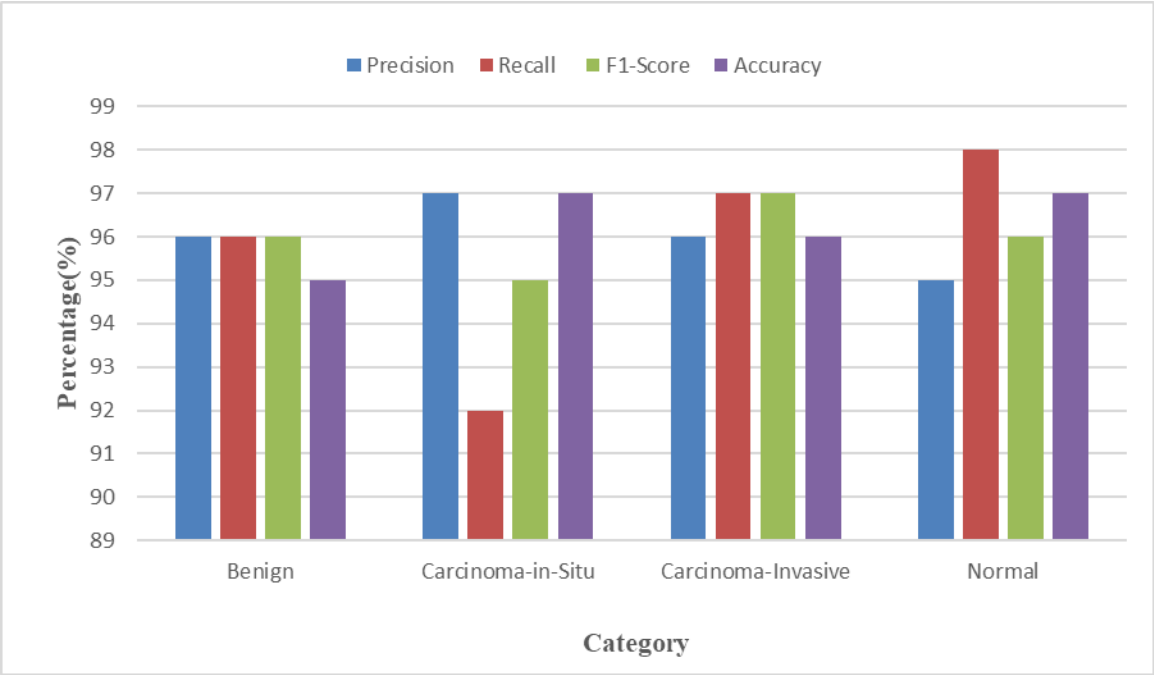

Fig. 8. Category wise classification performance of proposed classifier.

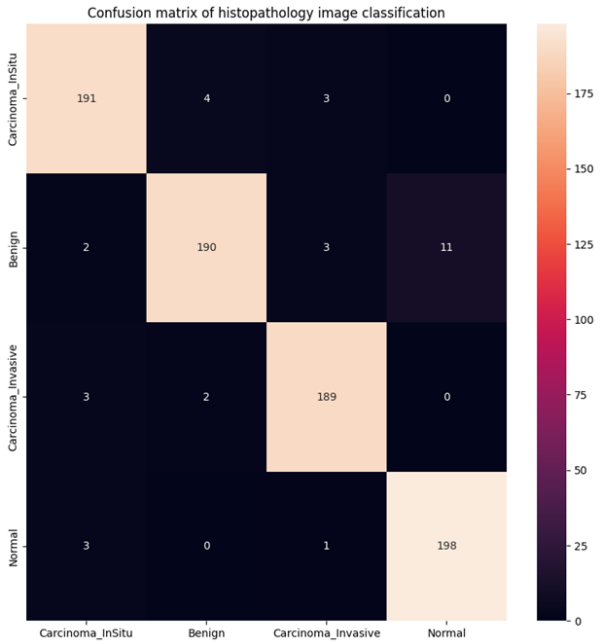

Fig. 9. Confusion matrix of proposed classifier.

In evaluating the effectiveness of the constructed model, it is imperative to conduct a thorough comparison of their classification performance. The assessment of the proposed TL models' classification performance is conducted across diverse datasets. Table IV analyzes of the efficiency of existing models using the selected performance metrics.

TABLE IV. PERFORMANCE COMPARISON

Model	Precision (%)	Recall (%)	F1-score (%)	Accuracy (%)
AlexNet	93.71	95.32	94.35	94.14
GoogleNet	88.44	89.45	86.65	89.42
ResNet 50	92.14	91.67	92.36	92.36
VGG16	93.86	93.83	94.12	93.15
Inception v3	89.31	87.61	88.38	86.11
ResNet152v2-CNN (Proposed)	96.24	96.63	97.18	96.47

In the assessment of classification accuracy, the proposed model distinguishes itself with the highest score of 96.47%. Noteworthy among the pre-trained models are VGG16 with an accuracy rate of 93.15%, ResNet50 at 92.36%, and AlexNet demonstrating a performance of 94.14%. Turning to precision, the proposed model excels with an impressive precision rate of 96.24%. In contrast, AlexNet achieved 93.71% precision, ResNet50 recorded 92.14%, and VGG16 obtained 93.86%. Proposed model attains an outstanding recall value of 96.63%, outperforming all other models in this metric. In comparison, VGG16 achieved a recall rate of 93.83%, ResNet 50 reached 91.67%, and AlexNet recorded 95.32% in recall. Remarkably, the proposed model's recall surpasses other TL models by a significant margin, demonstrating its superiority in capturing and correctly identifying relevant instances. Furthermore, in assessing the F1-score, the proposed model once again takes the lead with a score of 97.18%. There is a noticeable difference between the F1 score of proposed model and existing TL approaches, underscoring the proposed model's overall effectiveness in achieving a good balance between precision and recall. Overall, the proposed model not only exhibits the highest accuracy for breast cancer categorization but also emphasizes the crucial role of specific parameters, particularly TL, in mitigating overfitting and elevating classification accuracy. For a visual comparison of the proposed model with existing classifier (see Fig. 10).

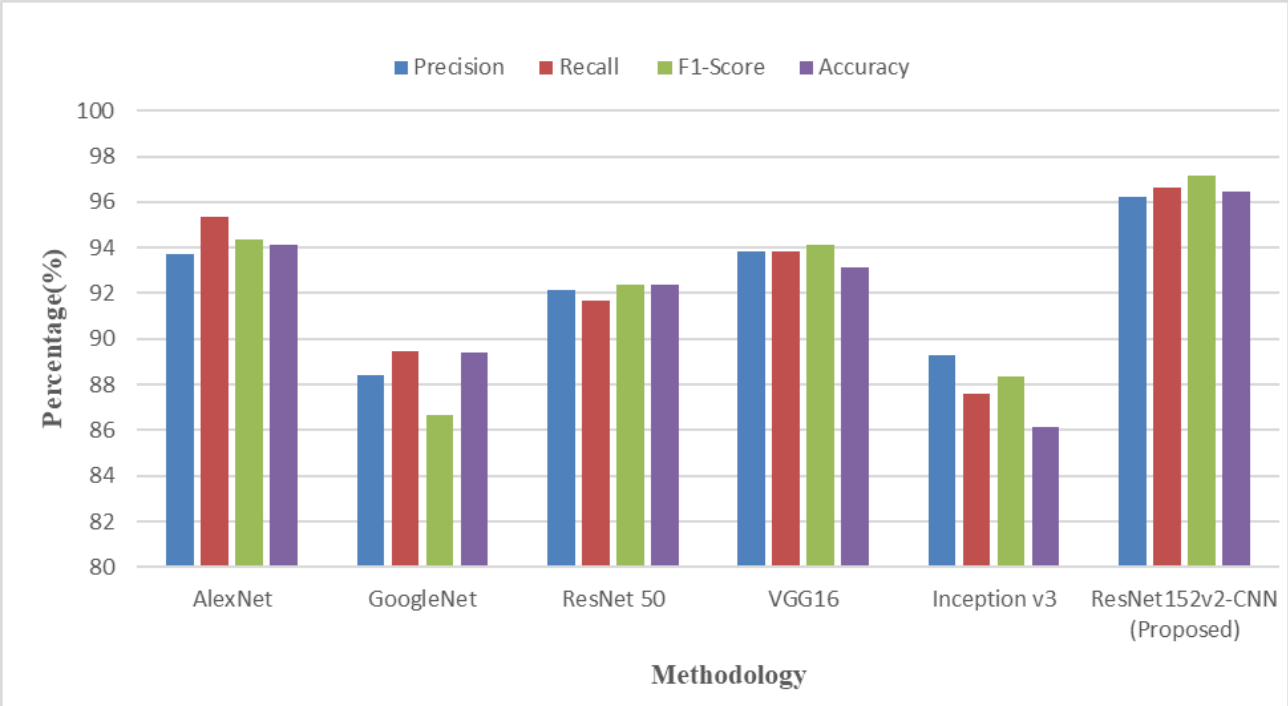

Fig. 10. Performance comparison.

Primary among the benefits is the complete automation of the classification process, eliminating the necessity for manual intervention. Tasks such as feature extraction, noise filtering, delineation of regions, and selection become obsolete. As a result, the predictions provided by the proposed model not only become automated but also consistently reproducible, free from any inherent bias. The prediction results generated by the proposed model along with the ground truth are provided in Fig. 11.

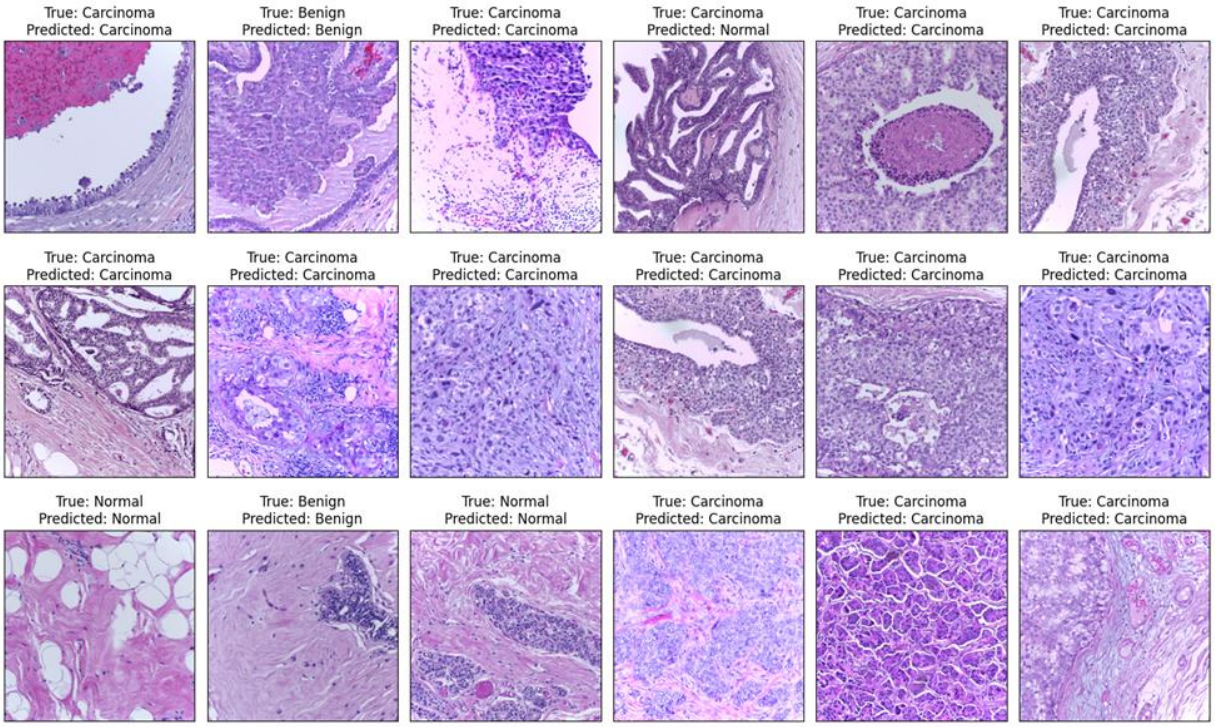

Fig. 11. Prediction outputs.

V. Conclusion

This study focused into the efficacy of TL in the classification of breast cancer through the analysis of histopathological images. The integration of TL with CNN structures proved to be an exceptionally efficient strategy, resulting in peak recognition rates. Notably, the ResNet152v2-CNN model proposed in this research achieved remarkable accuracy (96.47%), precision (96.24%), F1-score (97.18%), and recall (96.63%) in the identification of potential breast cancer cases. One notable advantage of the proposed model lies in their capacity to diminish or even eliminate the need for extensive pre-processing stages, surpassing existing techniques in this aspect. Interestingly, when contrasted with the proposed model, the pre-trained AlexNet classifier demonstrated inferior performance across various performance metrics. Future research endeavors will focus on optimizing the deployment of the proposed model on mobile platforms, addressing computing complexity issues. Additionally, there will be an exploration of further fine-tuning methods and strategies, promising ongoing advancements in histopathological image classification.

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