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RESEARCH PAPER

# Optimized Histopathological Image Classification for Breast Cancer Using Deep Learning Model

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***Abstract*—A significant cause of death very early among women is due to breast cancer. Since invasive ductal carcinoma (IDC) and breast cancer in general continue to be among the most common and fatal illnesses affecting women, prompt identification is crucial. Convolutional neural networks (CNNs), in particular, are particularly notable in automating image processing of breast cancer to the point that the images do not need human interpretation. The proposed project enhances the detection of IDC by creating a reliable diagnostic algorithm, in which deep learning and histopathology image analysis are used. On a large-scale dataset of IDCs containing more than 277,000 image patches, it applied a full preprocessing pipeline, including Otsu thresholding, tissue masking, Hematoxylin channel extraction, CLAHE enhancement, Gaussian denoising and gamma correction to improve image quality. Images with low tissue content were eliminated and SMOTE has been utilized to work on the imbalance of classes. This was a fully fine-tuned ResNet50V2 that was pretrained on ImageNet, and then combined with own dense layers and trained based on Adam optimizer and binary classification. Accuracy (acc) of the model was 88.52%, and precision (pre), recall (rec), and F1-score (F1) were greater than 88%. The effect of various architectural and training setups was studied using ablation and confirmed the efficiency of the chosen model. The comparative analysis yielded better performance in comparison to the existing CNN, CNN-GRU, and DenseNet-based models. The results indicate the possibility of AI-based breast cancer detection to be used in clinical practice, decrease errors in diagnosis, and increase the rate of early diagnoses. Combined application of the state-of-the-art image enhancement, balanced data depiction, and comprehensive study of the ablation using pre-trained CNN models is novel. This adds a high-performing and interpretable, yet clinically relevant, solution to the early diagnosis of breast cancer by using histopathology.**

***Keywords*—Breast Cancer, Invasive Ductal Carcinoma, Deep Learning, CNN, ResNet50V2, Histopathology, Image Classification, Ablation Study.**

## I. INTRODUCTION

Cancer is a global disease that impacts people of all ages and socioeconomic backgrounds [1]. Breast cancer is among the most prevalent cancers in women, despite the fact that there are many different kinds of the disease. The primary cause of mortality for female cancer patients globally is breast cancer. Numerous women are impacted by this serious global issue because of its high frequency and deadly nature. The most common disease, making up over 14% of all malignancies, is breast cancer, which has significant rates of death and morbidity among women globally [2][3]. It affects around 2.1 million women annually and raises their death rate. Estimates for 2020 put the death toll from breast cancer at 6,855,000 women. As the most common method for diagnosing breast cancer, the histopathological examination, breast cancer stands out among the many types of cancer due to its high mortality rate and provide that it is the most prevalent kind of cancer in women globally [4].

IDC is the most common kind of breast cancer that develops when the breast is invaded by ductal carcinoma. Cancer can take many distinct forms. IDC begins in the milky ducts of the breast and accounts for around 80% of all cases of breast cancer [5]. The IDC has the capacity to spread to other areas of the body after infecting lymph nodes. Traditional diagnostic approaches rely heavily on histopathological analysis, where expert pathologists manually examine tissue samples under a microscope. Histopathological images, which are used for disease inquiry and are microscopic pictures of tissues, are the gold standard when it comes to cancer diagnosis. These pictures provide important and useful information that medical professionals may thoroughly examine to determine the patient's current condition. Histopathology images were hard to find and obtain until recently, and the scientific community could not access them [6]. Consequently, the majority of histopathology image studies, particularly those involving breast cancer images, were conducted on very limited datasets. Despite its status as the gold standard, this method is laborious, expert-only, and susceptible to inter-observer variability. To reduce diagnostic delays and improve consistency, AI has become a viable option for illness diagnosis and medical imaging [7].

Software that is backed by AI is necessary for identification of breast cancer to reduce the workload for qualified medical personnel and avoid misinterpretation. This problem remains unsolved in the present state of AI-supported breast cancer diagnostic systems [8]. The use of ML approaches for breast cancer categorization has received a lot of attention within the AI sector. However, the conventional ML techniques tend to rely on manually created features and domain-specific knowledge and this restricts their scalability and versatility across datasets [9]. Such techniques are also not effective when the image is complex and when there are differences in morphology of tissues as is the case in histopathological images. To address the above challenges, scholars have resorted to DL, which is an enhanced section of ML that allows automatic feature extraction and direct representation learning directly on raw images [10]. One technique of ML is referred to as DL and it utilizes neural networks. The neurons in each layer are connected to the other by weighted connections as the intricate structure of the DL

networks involves more than one layer [11]. To speed up these procedures and improve diagnostic accuracy, researchers have put forth a variety of DL models for the detection and classification of breast cancer. The application of DL techniques and CNNs in particular has transformed the medical analysis of images by representing the hierarchies of data space and enhancing the level of accuracy in classification. The annotated datasets and high computational resources required to train deep CNNs are however not always available in the medical domain [12]. Enhancing pre-trained models on a big dataset (like ImageNet) for specific objectives like breast cancer classification has been a well-liked remedy for this problem. The approach improves the generalization of models on small medical data but also accelerates the training [13]. In the study, it uses a DL-based CNN architecture that uses an already-trained transfer learning model with several parameter adjustments to enhance the categorization of images of histological breast cancer.

### *A. Motivation and Contributions*

Breast cancer, especially IDC is a major health problem which needs early and precise diagnosis to be treated. Analysis of histopathological images is a tedious task that is prone to diagnostic errors. The necessity to identify IDC, the most common type of breast cancer, with high precision and promptness is a motivated cause of the research because it significantly increases the outcomes of treatment and survival rates. Traditional methods of diagnosis, such as manual review of histopathology slides, are tedious, subjective, and prone to human error. As more and more data is available on digital pathology platforms, and companies turn to deep learning, the future of automated, objective, and highly accurate diagnostic tools can be hoped. By utilizing convolutional neural networks and, in particular, pre-trained ones, it is possible to extract meaningful features out of complex histopathological images and help the pathologists arrive at a faster and more accurate conclusion. The study in question utilizes such AI capabilities to improve the accuracy of diagnostics, cut down on the workload, and play a role in more effective screening and diagnostics of breast cancer.

### *B. Contributions and Significance of the Study*

The general objective of the research is to assist in early diagnosis and also improve clinical decision-making through the development of a valid and automated DL-based approach that is capable of detecting IDC in breast histopathology images. The key contributions are as:

- This paper presents a new and domain-specific preprocessing pipeline that is specific to histopathological breast tissue images. It combines the pipeline, CLAHE, and denoising which leads to quality image input that can increase the visibility of features and model interpretability.
- The research uses SMOTE to overcome Class imbalance is a prevalent issue in medical datasets. This guarantees the equal representation of IDC-positive and IDC-negative classes, which is important to reduce the model bias and guarantee the high level of classification.
- The main finding is that the ResNet50V2 model that was originally trained on ImageNet was adapted and optimally fine-tuned to IDC in breast histopathology images. The paper has shown that even general-purpose CNNs can be highly accurate in classifying medical images with an appropriate choice of tunings.
- The proposed design incorporates a simplified classification head to the ResNet backbone layers. The design has low chances of overfitting and good learning ability, thus it is applicable in large-scale medical imaging with limited computation capabilities.
- Model performance is completely justified with a set of diagnostic measures such as the Confusion Matrix, F1score, ROC AUC, recall, acc, and pre. This is a multi-level assessment which ensures that the model is transparent and reliable in the decision making of a real diagnostic scenario.

The research is also important in medical imaging and cancer diagnosis because it provides a robust, automated system for detecting IDC in histopathology images. Early and correct diagnosis of breast cancer is linked to better patient outcomes and efficient treatment; however, manual analysis of the data (involving pathologists) can be tedious, subjective, and subject to mistakes. Combining innovative image processing methods with DL, the work helps increase diagnostic accuracy, reduce human input, and facilitate clinical decision-making. In addition, the method is scalable and can be applied to other medical imaging tasks, using publicly available data and methods that can be reproduced, thereby enabling the development of AI-assisted healthcare solutions.

### *C. Novelty and Justification*

The research presents a novel framework of IDC breast cancer detection by using the power of CNN-trained models alongside sophisticated image processing and data balancing. In contrast to the other methods, which usually ignore the effect of low tissue quality or use custom CNNs, this paper specifically combines high-performing pre-trained convolutional networks with fine-tuning to that particular task, i.e., histopathological analysis. Balanced distribution of classes is guaranteed during the use of SMOTE and this increases the robustness of the model and minimizes prediction bias. One of the novelties is also the consideration of a detailed ablation study where every preprocessing method and model architecture is studied in detail. This thorough analysis gives an important rationale to the design decisions, giving openness and understanding of the role played by each component in the performance of the model. This work is a unique and worthy addition to automated breast cancer diagnosis due to the combined efforts of high-quality image processing, pre-trained CNN models and empirical validation.

### *D. Organization of the Paper*

This paper is organized as follows: Related work and current issues are covered in Section II. Section III explains the dataset, preprocessing techniques, and proposed ResNet50V2 model architecture. Experimental findings, assessment criteria, and comparative analysis are presented in Section IV. Section V discusses the findings and what they mean for future research.

## II. Literature Review

The section provides a review of previous research concerning the use of breast cancer prediction with the help of ML and DL models, where high accuracy was achieved on structured data, with some focus on the histopathology images and sophisticated DL architectures.

 

Kaur and Madaan (2024) use the available methods and determine some of the risk factors that lead to breast cancer. Breast cancer risk analysis may be anticipated using machine learning techniques. The approach involves gathering a dataset of patients, pre-processing the dataset to eliminate unnecessary information and reduce dimensionality, normalizing features, and dividing the dataset into training and testing sets. For breast cancer therapy to be successful, early diagnosis is crucial. The proposed work's effectiveness is assessed and validated using the Breast Cancer Surveillance Consortium Dataset. RF exhibited the highest accuracy of 75.2% [14].

Arachchi et al. (2024) early detection of Breast Cancer is essential, and many lives can be spared with effective treatment. The WBCD dataset was examined and utilized in several ML models. SVM, KNN, Naïve Bias model, Logistic Regression (LR), AdoBoost and DT were used for prediction. This paper covers the findings and evaluations of many ML models for Breast Cancer detection. Comparing the results reveals that the AdoBoost model yields the best outcomes. 96% accuracy and logistic regression model is predicted 96% of ROC value. Logistic regression model and AdoBoost, which is better than the previously published approach [15].

Kaur and Gupta (2024) employ Random Forest and DT approaches to use the Breast Cancer Wisconsin data to increase the accuracy of breast cancer diagnoses. These methods investigate thirty features taken from digital images of tiny needle aspirates in order to obtain minute cell nuclei properties. After data collecting, analysis, visualization, and model deployment follows hyperparameter tuning via GridsearchCV. Although the RFC had remarkable accuracy of 93%, indicating resilience in managing complex data, the Decision Tree classifier resulted in 91% accuracy. These results show how well ML techniques might be applied to enhance the diagnosis of breast cancer, therefore providing doctors more precise tools for early identification and better patient treatment [16].

Singh and Kaswan (2024) proposed method in their research are the use of a soft voting classifier for automatic assessment of malignancy or benignancy of breast cancer using three ML algorithms: LR, SVM, and DT. The suggested method is tested and evaluated using the 699-item Breast Cancer Wisconsin dataset (Original). The data is balanced using the random oversampling method to minimize the bias. The methodology that is proposed, gives 0.9708 accuracy, 0.9821 precision, 0.9483 recall, and an F1score of 0.9649 with an AUC of 0.9678 [17].

Alsabry et al. (2023) using SMOTE to fix the dataset's imbalanced target class is the goal of improving BC prediction models. The models are evaluated using two methods: the first makes use of the first, which uses SMOTE to balance the target class in the Breast Cancer Coimbra Dataset (BCCD). The comparison of the two methods' performance shows that using SMOTE considerably enhances the BC prediction models' performance. The Optimized Logit Boost model achieved a 73.9% accuracy rate with SMOTE, whereas AdaBoost with Bayesian Optimization attained a 52.2% accuracy rate. Without SMOTE, the model obtained a rate of 76% [18].

A'la et al. (2023) results in just a tiny fraction of the imbalance dataset being present in the coimbra breast cancer dataset. Nevertheless, this might be problematic for building ML models, since the resulting model can favor the majority and under-predict the minority. This study employs SMOTE in an effort to reduce the class imbalance. Following the SMOTE implementation, a 10-fold cross-validation ML model is constructed using the RF technique. The model is then evaluated for acc, pre, and rec. Results demonstrate an improvement in model acc (from 76.72% to 80.47%), pre (from 76.60% to 80.00%), and rec (from 69.23% to 81.25%) [19].

Anklesaria et al. (2022) sought to integrate various ML algorithms with hyperparameter tweaking that pick features using the RF Feature Importance Method, include ANN, DT, RF, KNN, SVM, LR, and NB. These models were trained using the WDBC dataset, which stands for the Wisconsin Diagnostic Breast Cancer. Additionally, they found that Undersampling produced a superior overall outcome after balancing the dataset using both SMOTE and Undersampling. Specificity, accuracy, sensitivity, F1score, precision, recall, and AUC are performance assessment criteria for the developed model. According to the results, the two most successful models that fitted their dataset were KNN (95.3% accuracy) and SVM Algorithm (95.8% accuracy) [20].

Behera et al. (2022) utilized five distinct ML algorithms on the BC dataset: KNN, SVM, DT, RF, and LSTM. Confusion matrices, precision, F1 scores, recall, and accuracy used to compare the results obtained by the LSTM classifier to those of the KNN, SVM, RF, and DT classifiers. This study's main objective is to identify the best ML algorithm for breast cancer prediction. The LSTM algorithm has the highest accuracy of 96%, as it is demonstrated to be superior to all the other algorithms under review [21].

Ara, Das and Dey (2021) study made use of the Wisconsin Breast Cancer Dataset, which was accessible via the UCI repository. Through data analysis, this study evaluates how well a number of machine learning algorithms predict breast cancer. Here, SVM, LR, DT, KNN, NB, and RF are used as classifiers in determining if a tumor is benign or malignant. The most suitable algorithm is selected by computing and comparing the accuracy of each of the algorithms. The analysis indicates that RF and SVM are superior to other classifiers with a 96.5 percent accuracy level. These classifiers can be applied to develop an automated system for preliminaries of breast cancer [22].

Karatza et al. (2021) used AI techniques such as RF, NN, and ENN to attain this goal. They offered descriptions and optimization of their behavior, and interpretability, such as Shapley Values (SV), Individual Conditional Expectation (ICE) plots, and the Global Surrogate (GS) approach. The AI algorithms were trained and tested using the WDBC data set from the public UCI repository. The suggested ENN performed best in diagnosing breast cancer, with an acc of 96.6% and an area under the ROC curve of 0.96. By decreasing the AUROC curve to 0.97 and the accuracy of RF, which was 96.49%, to 97.18%, the RF performed better when the features were chosen based on their relevance as determined by the GS model. In addition, feature selection based on the features' relevance as assessed by SV improved the NN's performance (resulting in an increase in accuracy from 94.6% to 95.53% and an AUROC curve from 0.94 to 0.95) [23].

The comparative study of previous research on DL models for breast cancer diagnosis is shown in Table I.

 

TABLE I. COMPARATIVE ANALYSIS OF EXISTING WORK ON DEEP LEARNING MODELS FOR BREAST CANCER DETECTION

| References | Methodology | Dataset | Result | Advantages | Limitations | Recommendations |
|---|---|---|---|---|---|---|
| Kaur and Madaan (2024) | ML with feature extraction, normalization, RF | Breast Cancer Surveillance Consortium (BCSC) | Random Forest: 75.2% accuracy | Integrates risk factors with ML; real-world dataset | Accuracy lower than 80%; lacks deep learning | Explore ensemble DL models and additional biomarkers |
| Arachchi et al. (2024) | SVM, KNN, Naive Bayes, LR, AdaBoost, DT | WBCD (Wisconsin) | AdaBoost: 96%, LR: 96% ROC | Multiple models compared; strong ensemble results | Small dataset; no feature selection mentioned | Use larger datasets, test robustness with noise |
| Kaur and Gupta (2024) | Random Forest, Decision Tree + GridSearchCV | WBCD | RF: 93%, DT: 91% | Hyperparameter tuning; good visual analysis | Doesn't compare with DL models | Include CNN/LSTM or hybrid ensemble comparisons |
| Singh and Kaswan (2024) | Soft Voting Classifier (LR + SVM + DT) | WBCD (Original) | Accuracy: 97.08%, AUC: 0.9678 | Combines classifiers; handles imbalance with oversampling | Dataset size is small; potential overfitting | Try SMOTE-ENN and feature reduction techniques |
| Alsabry et al. (2023) | Multiple tree & SVM models + SMOTE | BCCD (Coimbra) | Best: LogitBoost (88%), others <85% | Detailed SMOTE impact; many algorithms | Low accuracy on small models; imbalance issues | Explore deep networks and domain knowledge-driven features |
| A'la et al. (2023) | Random Forest + 10-fold CV + SMOTE | Coimbra Dataset | Before SMOTE: 76.72%, After: 80.47% | Boost in precision, recall with SMOTE | Still moderate performance (<85%) | Combine SMOTE with ensemble learning for robustness |
| Anklesaria et al. (2022) | SVM, LR, KNN, DT, RF, ANN, NB + Feature Selection | WDBC | Best: SVM: 95.8%, KNN: 95.3% | Feature importance analysis; comparative study | Focus only on WDBC; no time-series methods | Apply temporal/deep learning on sequence data |
| Behera et al. (2022) | KNN, SVM, DT, RF, LSTM | BC Dataset | Best: LSTM: 96% | First use of LSTM; compares with traditional ML | Details on dataset and preprocessing unclear | Benchmark LSTM on other datasets like BCSC, BCCD |
| Ara, Das and Dey (2021) | SVM, LR, KNN, DT, RF, NB | WBCD (UCI) | RF, SVM: 96.5% | Simple comparison; clear performance metrics | No use of balancing or advanced preprocessing | Consider imbalanced dataset handling (SMOTE) |
| Karatza et al. (2021) | RF, NN, Ensembles + SHAP, ICE, Surrogate Models | WDBC (UCI) | ENN: 96.6%, RF: 97.18% | Interpretability + Performance; use of SHAP | Needs more external validation | Apply models to real-world/clinical datasets (BCSC) |

### A. *Research Gaps*

Several research gaps exist in breast cancer prediction despite significant advancements using ML and DL techniques. Current studies have demonstrated promising accuracy using models like SVM, RF, ANN, and ensemble classifiers on structured datasets like WBCD and BCCD. However, limited work has explored high-resolution histopathological image data using advanced CNN architectures. Moreover, class imbalance issues are often under-addressed, and many approaches lack comprehensive preprocessing pipelines. The integration of deep learning with optimized preprocessing and SMOTE-based balancing for IDC detection remains underexplored, particularly in real-world clinical image datasets like the Breast Histopathology Images dataset.

## III. METHODOLOGY

The suggested approach for detecting IDC breast cancer using the Breast Histopathology Images collection is detailed in this section. This approach describes the use of the Breast Histopathology Images collection for IDC breast cancer identification. After collecting data from Kaggle, exploratory analysis identifies class imbalance. Preprocessing, image enhancement, and balances the dataset is then separated into three categories: validation, testing, and training. Labels are one-hot encoded for binary classification. A ResNet50V2 model is evaluated for its performance in using the F1score, recall, accuracy, and precision for feature extraction and categorization. This entire process is shown in Figure 1.

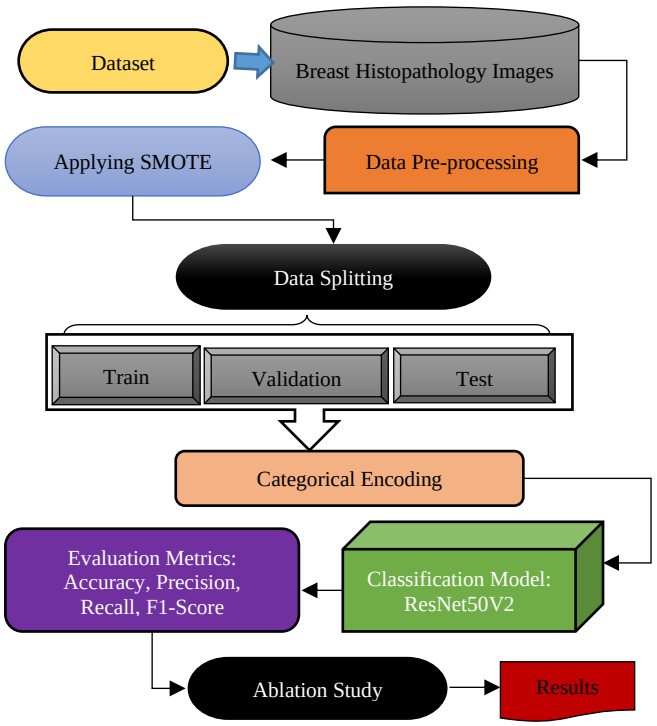


Fig. 1. Data Flow Diagram

The stages of the suggested technique flowchart 1 are described in short below:

### A. *Data Collection*

The "Breast Histopathology Images" dataset, which focusses on IDC, Kaggle provided the most prevalent subtype of breast cancer, which was used in this study. The breast cancer histopathology pictures in the IDC collection are built

up as patches with dimensions of 50 × 50 pixels. With these patches, it may find both IDC positive and negative images. There are 277,524 photos in total, of which 78,786 are IDC positive and 198,738 are IDC negative. Each of these patches has a Magnification Factor of 40×. This research uses a subset of the IDC dataset. Figure 2 displays the example photos from the Breast Histopathology images collection.

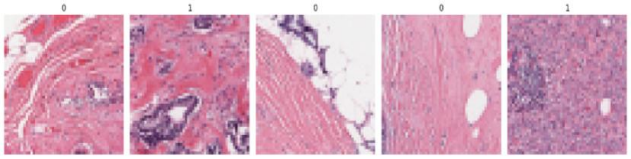


Fig. 2. Sample Images of Breast Histopathology Images dataset

### *B. Exploratory Data Analysis (EDA)*

The Breast Histopathology Images dataset for IDC classification was well explored with exploratory data analysis (EDA). First, it was found that the dataset provided a major imbalance between the Positive and Negative images of IDC, as indicated in Figure 3. A rich preprocessing pipeline was carried out in order to improve data quality, as shown in Figure 4, where data was resized, then masked for tissues, stains were extracted, followed by contrast and noise post-processing. Figure 5 presents some of the outputs of the pre-processed images, which are clear and consistent enough to be used as model input. Lastly, Figure 6 shows the SMOTE effect, which balances the classes, solving the data imbalance issue to train a better model.

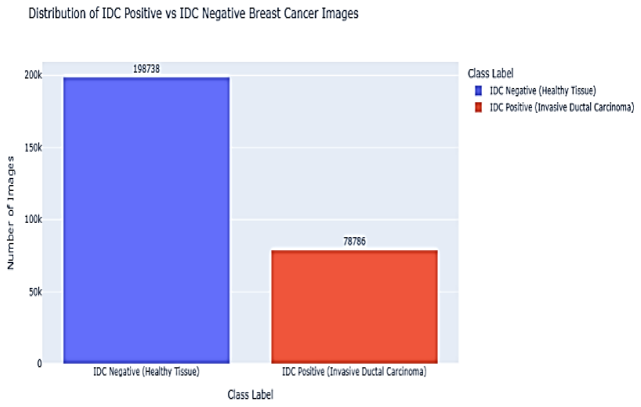


Fig. 3. Distribution of IDC Positive vs IDC Negative Breast Cancer Images

The class distribution of the Breast Histopathology Images dataset for IDC classification is shown in Figure 3. It reveals a significant imbalance, with 198,738 images labeled as IDC Negative (healthy tissue) and only 78,786 images labeled as IDC Positive (invasive ductal carcinoma). This disparity highlights a common challenge in medical image classification tasks class imbalance, which can affect model performance and bias predictions. To overcome this imbalance through such techniques as SMOTE is critical to achieve robust and fair classification in Breast Cancer detection systems.

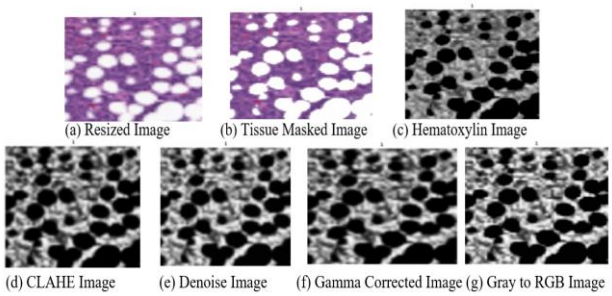


Fig. 4. Preprocessing Stages for Breast Histopathology Image Enhancement

The steps of sequential preprocessing of breast cancer histological pictures are shown in Figure 4. It starts with resizing (a), masking tissues (b) to isolate regions of interest and extraction of the Hematoxylin stain (c). CLAHE (d) is used to enhance contrast and denoising (e) is used to reduce noise. Photo-adjustment (f) enhances brightness and contrast with gamma correction and the resulting (g) is translated into the RGB format that is uniform to input the ResNet50V2 classification model.

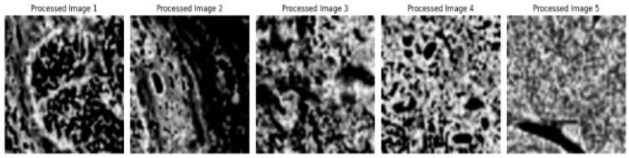


Fig. 5. Sample Output of Preprocessed Histopathology Images Used for IDC Classification

Five sample histopathology image patches as the result of the full preprocessing pipeline appeared in Figure 5. Every processed image demonstrates a signal increase in contrast and better cellular structures, which allow better feature extraction. These are high clarity, standardized images, which are fed to the CNN model to provide homogenous information representation when performing IDC classification.

### *C. Data Preprocessing*

Deep learning methods use histopathology images as inputs, thus preprocessing is essential in ensuring that the images can be used in such models, as well as, extracting the best out of the models in terms of image quality, variety, and accuracy [24]. The preprocessing involves seven major processes namely: image resizing, tissue masking, hematoxylin imaging, CLAHE imaging, Denoised Imaging, Gama Corrected Images, Grey to RGB Images.

- **Image Resizing:** Image patches of all the histopathology are resized to 124×124 pixels to normalize the input size of the model.
- **Tissue Masking:** Background Masking is the method used to isolate tissue regions by threshold-based masking to isolate only the tissue.
- **Hematoxylin Imaging:** The Hematoxylin channel is removed to highlight the structures of nuclei by using colour deconvolution.
- **CLAHE Imaging:** A method called Contrast Limited Adaptive Histogram equalization may boost local contrast and highlight features.
- **Denoised Imaging:** Denoised Imaging removes artifacts and background noise to enhance clarity of cellular structures in images.

- **Gamma Corrected Images:** Brightness and contrast are adjusted via gamma correction for better image normalization.
- **Gray to RGB Images:** Processed grayscale images are converted back to RGB format for compatibility with CNN models.

### *D. Applying SMOTE*

The Python scikit-learn module was used to implement the SMOTE, which was aimed at addressing the class imbalance [25]. To balance the dataset used to train the algorithms, it creates artificial samples of the minority class. A balanced dataset with 140,463 images in each class (IDC Negative and IDC Positive) is displayed in the output following the application of the SMOTE technique. To ensure consistent input dimensions for DL model training, the image and label arrays are appropriately reshaped.

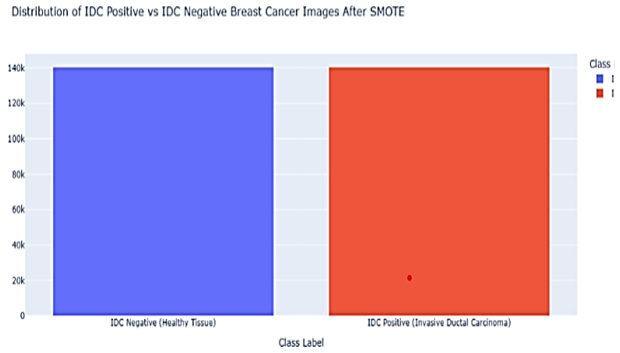


Fig. 6. Class Distribution of IDC Positive and Negative Samples After SMOTE Balancing Technique

The class distribution of IDC positive and IDC negative breast cancer images after applying the SMOTE method as shown in Figure 6. The graph shows that the two classes have been equalized to around 140,000 samples apiece correcting the previous disproportion in the classes. This balanced dataset allows all the classes to get equal representation in the deep learning model so that it better at generalizing, less biased to majority class and better at classification used in detecting IDC.

### *E. Data Splitting*

To guarantee that the DL models are completely trained, validated, and tested, Training, validation, and test sets are the three divisions of the dataset [24]. The dataset, consisting of 280,926 images after the application of SMOTE is divided into three subsets by an 80-10-10 ratio: 80% (224,740 images) to be used in the model training, 10% (28,093 images) to validate the hyperparameters and track the overfitting, and 10% (28,093 images) to be used in the final test. This split ensures effective model learning, evaluation, and generalization on unseen breast cancer histopathology images.

### *F. Categorical Encoding*

A collection of finites and collected categories with components that are mutually exclusive determine how categorical variables are encoded. A CNN input picture for each subclass is represented by a numerical value vector [26]. A two-dimensional vector representing each label is used to correspond to the two classes: IDC Negative and IDC Positive, enabling compatibility with the binary classification output layer in the neural network. This transformation was performed on all three datasets, training, validation, and test—resulting in label shapes (224740, 2) for training, preparing the data for the softmax-style classification layer of the deep learning model.

### *G. Classification Model for Breast Cancer*

This section discusses the analysis and classification of DL model ResNet50V2 that explained in below:

#### *1) ResNet50V2*

CNN with outstanding performance across a range of computer vision applications is ResNet50V2. The deterioration issue in deep networks is addressed by this variation of the ResNet design, which employs skip connections. The 50-layer ResNet50V2 was pre-trained using ImageNet and other large-scale image datasets [27]. The network is able to learn residual mappings and deeper models may be trained with the help of residual blocks. Another manner in which skip connections enhance training is by enabling the direct passage of gradients from earlier to later layers. Because of its feature extraction capabilities, the ResNet50V2architecture finds use in breast cancer detection, particularly in cases where the patterns are complex and hierarchical. Deep layers in ResNet50V2 learn abstract representations of breast tissue textures, forms, and features that are critical for malignant vs benign tissue classification. The benefit of transfer learning (TL) is brought about by using the pre-trained ResNet50V2 model, which has learnt generic characteristics from a large-scale image dataset like ImageNet. ResNet50V2 is able to obtain broad image representations by pre-training, which may then be refined for the diagnosis of breast cancer. The Breast Cancer detection system may benefit from the taught features from ResNet50V2 in terms of both accuracy and functionality. ResNet50V2 adopts a modified residual block with pre-activation. The residual mapping is defined as Equation (1):

$$y = x + \mathcal{F}(ReLU(BN(x))), \{W\} \quad (1)$$

Where, x = input to the residual block, y = output of the block, BN(·) = batch normalization, ReLU(·) = activation function, F(·) = series of convolutions with weights{W}. This equation reflects the pre-activation structure of ResNet50V2, where normalization and activation precede the convolutional operations within the residual path.

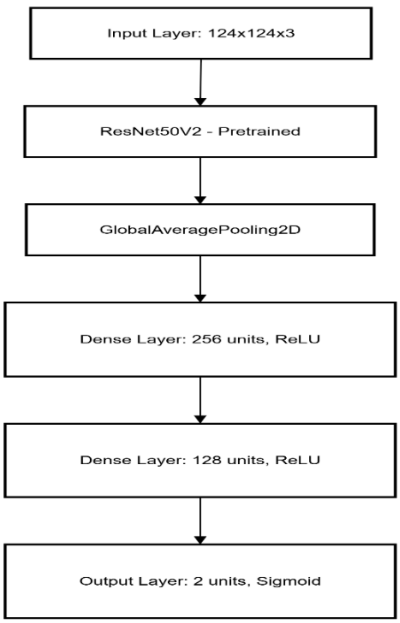


Fig. 7. Architecture of ResNet50V2 Model

The architecture of the suggested DL model for IDC Breast Cancer classification, which is based on ResNet50V2, is displayed in Figure 7. The ResNet50V2-based model utilizes a robust transfer learning strategy to classify histopathology image patches into IDC-positive (cancerous) or IDC-negative (non-cancerous) categories. The input layer processes RGB images resized from 50×50 to 124×124×3 to match the expected dimensions of the pretrained model.

The ResNet50V2 architecture imported in include top=false with ImageNet weights initialized is a potent feature extractor that is optimized for medical imaging. This is followed by GlobalAveragePooling2D layer that summarizes spatial information without cutting the most prominent features, which decreases the occurrence of overfitting relative to flattening techniques. The resulting features are then run through two fully connected layers, the first layer being a Dense layer of 256 and ReLU-activated units to refine complex features and followed by the second layer of a Dense layer of 128 and ReLU-activated units to refine the high-level features. The last layer is the Dense(2, activation='sigmoid') which does binary classification by returning the class probability of IDC and non-IDC. This model can be adjusted to histopathology data because ResNet50V2 base is set to be trainable which is essential. An Adam optimizer with a binary cross-entropy loss and a learning rate of 0.0001 is used to build the model. In binary classification issues (such as IDC vs. non-IDC in breast cancer diagnosis), binary cross entropy is a frequently used loss function. The objective is to divide the data into two distinct categories. It compares a discrepancy between true labels ($y$) and model predictions($\hat{y}$). The binary cross-entropy loss of binary classification problems is defined by Equation (2):

$$L = -\frac{1}{N}\sum_{i=1}^{N}(y_i.log(\hat{y}_i) + (1-y_i).\log(1-\hat{y}_i)) \quad (2)$$

Where:

- $N$ = Total number of samples
- $y$ : true label (0 or 1).
- $\hat{y}_i$: Forecasted probability of the +ve class ($0 \leq \hat{y}_i$).
- log = Natural logarithm

The training is performed with a Batch Size of 32 and 10 epochs, with independent validation set to measure the performance of generalization. The parameters like accuracy and loss are tracked throughout the stages of training and validation to make sure the model converges as much as possible and is discriminative in the identification of breast cancer.

The research analyzed the ResNet50V2 model's ability to classify breast histopathology pictures in binary using a variety of training and architectural changes. In the case of removing the Dense (128) layer, the model demonstrated a reduction in its accuracy, which shows that this layer that is fully connected is a critical component of acquiring high-level features of cancerous tissue. Making the Global Max Pooling instead of Global Average Pooling also resulted in greater sensitivity to dominant features at the expense of generalization with a further risk of overfitting. Replacing the optimizer with Adam with SGD, instead of making the optimization process faster, led to worse final accuracy, which suggests that SGD with fixed learning rate and nonadaptive momentum discourages the optimal weight changes in this medical imaging example. Lastly, the application of categorical cross-entropy instead of a sigmoid cross-entropy on the output layer with the use of only the rather erratic performance on binary classification was brought on by a SoftMax function, which performs poorly with two-class probabilities.. These findings collectively emphasize the critical roles of the Dense(128) layer, Global Average Pooling, adaptive optimizers like Adam, and the sigmoid activation function in achieving optimal classification performance with the ResNet50V2 backbone.

### *H. Model Evaluation*

An important part of creating a successful deep learning model is model evaluation. The performance of the trained model is evaluated by applying it to the test photographs for classification after image pre-processing, training, and validation. Many metrics are used for assessment, including the area under the ROC curve (AUC), the ROC, cross-validation, and the confusion matrix. Commonly utilized to construct evaluation metrics are the following concepts in confusion metrics: true negative (TN), i.e., the classifier's prediction and the test instances were both negative; true positive (TP), i.e., the results of the test cases and the classifier's prediction were both positive; false negative (FN), i.e., the classifier forecast a negative result even if the test examples were positive; and lastly, false positive (FP), i.e., the results of the tests were negative, yet the forecast came out positive [28]. The model's classification performance is frequently assessed using the confusion matrix's accuracy, pre, rec, and F1. These measures are briefly summarized in the next paragraphs.

#### *1) Accuracy*

The accuracy score of the computation of a model involves dividing the total number of forecasts by the proportion of accurate predictions. It only shows the predictions for normal patients and the diagnoses for abnormal breast cancer patients as a percentage. Equation (3) provides a definition for the accuracy.

$$Accuracy = \frac{\text{TruePositive+TrueNegative}}{Total} \quad (3)$$

#### *2) Precision*

The true positive results, including those that the classifier misidentified, are divided by the actual positive results to calculate precision. Equation (4) may be used to express precision.

$$Precision = \frac{\text{TruePositive}}{\text{TruePositive+FalsePositive}} \quad (4)$$

#### *3) Recall*

The ratio of TP findings to TP samples that ought to have been identified is the measure of rec. Both rec and pre should be good when diagnosing medical images after decreasing the number of patients who are misdiagnosed as malignant. Equation (5) may be used to calculate the rec.

$$Recall = \frac{\text{TruePositive}}{\text{TruePositive+FalseNegative}} \quad (5)$$

#### *4) F1-Score*

The F1-score is a measure of the acc of each class's model. When the dataset is unbalanced, the F1measure is often used. Comparing two models with high Sn and low Pre is helpful. Equation (6) may be used to define it.

$$F1 - Score = 2 \times \frac{precision \times recall}{precision + recall} \quad (6)$$

 

*5) ROC_AUC*

The ROC curve visually represents performance across thresholds, with AUC providing a summary of the model's class-distinction capabilities.

*I. Algorithm: IDC Breast Cancer Classification*

**Input: Breast Histopathology Images Dataset (Kaggle)**
**Output: Trained ResNet50V2 model capable of classifying IDC and non-IDC patches.**

1. **Import Libraries**:
   - Import Python libraries: NumPy, Matplotlib, OpenCV, Seaborn, PIL.
   - Import TensorFlow and Keras modules (e.g., tensorflow.keras, Image Data Generator).
   - Import imblearn for SMOTE.
   - Import sklearn metrics and preprocessing tools.
2. **Load Dataset**:
   - Download and extract the Breast Histopathology Images dataset from Kaggle.
   - Load image patches (50x50) and their labels (IDC positive = 1, IDC negative = 0).
   - Visualize sample patches and class distribution.
3. **Exploratory Data Analysis (EDA)**:
   - Analyze class imbalance.
   - Visualize IDC-positive vs. IDC-negative patch counts.
   - Plot sample tissue images and perform pixel distribution analysis.
4. **Data Preprocessing:**
   - Resize all patches to 124×124 pixels.
   - Apply tissue masking to remove background.
   - Extract hematoxylin stain via color deconvolution.
   - Apply CLAHE for local contrast enhancement.
   - Denoise images to reduce artifacts.
   - Perform gamma correction for brightness normalization.
   - Convert grayscale images to RGB format.
5. **Data Balancing with SMOTE:**
   - Use SMOTE to synthetically oversample IDC-positive class.
   - Balance both classes to ~140,000 samples each.
6. **Split Dataset:**
   - Divide data into Train (80%), Validation (10%), and Test (10%) sets.
   - Shuffle and stratify samples for balanced representation.
7. **Encode Labels:**
   - Apply one-hot encoding for binary classification (IDC = [0,1], non-IDC = [1,0]).
8. **Model Building (ResNet50V2):**
   - Load pretrained ResNet50V2 with ImageNet weights.
   - Customize model: Add GlobalAveragePooling2D, Dense(256), Dense(128), and final Dense(2) with sigmoid.
   - Compile with Adam optimizer and categorical cross-entropy loss.
9. **Model Training**:
   - Train model on training set for 10 epochs.
   - Use validation data for monitoring accuracy and loss.
   - Implement early stopping to prevent overfitting.
10. **Model Evaluation**:
    - Evaluate performance on test set.
    - Compute Accuracy, Precision, Recall, F1-Score.
    - Generate confusion matrix, classification report, and ROC curve.
    - Visualize prediction outcomes on sample test images
11. **Ablation Study:**
    - Modify architectural parameters: remove dense layer, change pooling, switch optimizer.
    - Compare performance metrics across configurations.
12. **Comparative Analysis:**
    - Compare ResNet50V2 against CNN, CNN-GRU, DenseNet121.
    - Tabulate accuracy, precision, recall, and F1-score results.

## IV. Result Analysis and Discussion

The findings of the suggested model for the DL model-based categorization of breast cancer are presented in this section. This research was conducted and evaluated in an experimental environment using a system equipped with an Intel Core i5-8250U CPU at 1.8 GHz, 12 GB of RAM, and running Windows 10 Professional 64-bit. Python 3 was used to implement the DL models for IDC classification. The study also includes a comparative study of several models, including CNN, CNN-GRU, DenseNet-121, and the proposed ResNet50V2, using the Breast Histopathology Images dataset.

### *A. Experiment results*

This section presents the experimental outcomes of the proposed ResNet50V2 model for IDC classification using the Breast Histopathology Images dataset. Table II highlights the model's effectiveness in accurately identifying cancerous and non-cancerous tissue through key performance metrics.

TABLE II. Results of the ResNet50V2 model on Breast Histopathology Images dataset for IDC classification

| Matrix | ResNet50V2 Model |
|---|---|
| Accuracy | 0.8852 |
| Precision | 0.8847 |
| Recall | 0.8859 |
| F1-Score | 0.8853 |

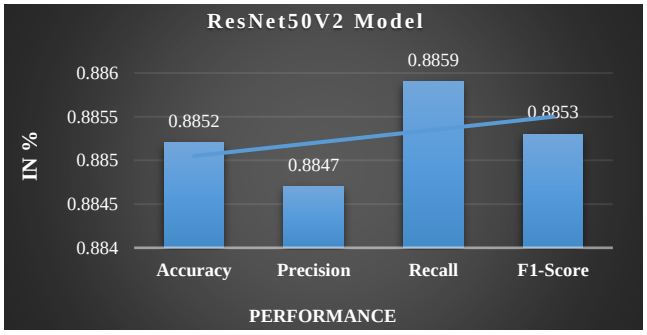


Fig. 8. ResNet50V2 Model Performance on IDC Breast Cancer dataset

The bar chart presents the ResNet50V2 model's performance on the Breast Histopathology Images dataset for IDC classification as shown in Figure 8 and Table II. The model shows consistent and high evaluation metrics with 88.52% accuracy, 88.47% precision, 88.59% recall, and an F1-score of 88.53%, indicating effective and reliable classification performance with minimal variance among the metrics. For Breast Histopathology Images dataset, the classification outcomes is according to IDC or non-IDC patch.

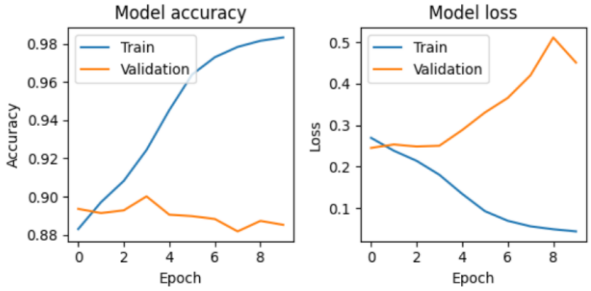


Fig. 9. Accuracy and Loss Curve of ResNet50V2 Model

The ResNet50V2 model's training and validation performance across 10 epochs are shown in Figure 9. The training accuracy steadily increases, ultimately reaching a high of 98.60%, while the validation accuracy stabilizes around 88.52%, indicating strong learning on the training data but limited generalization. Similarly, after epoch 2, the validation loss rises to 0.4507 and peaks close to epoch 8, whereas the training loss sharply declines to 0.0376, indicating a widening difference between training and validation measures. This overfitting is made evident by this divergence, in which the model is overfitting the training data at the expense of its performance on unseen data.

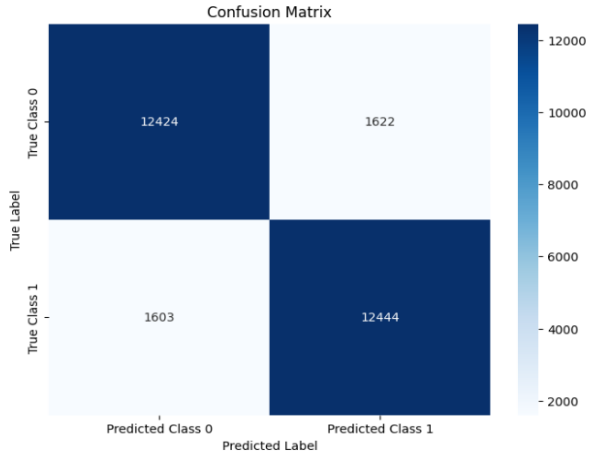


Fig. 10. Confusion matrix of ResNet50V2 Model

A Confusion Matrix, which is presented in Figure 10, shows that the ResNet50V2 model is capable of classifying samples of breast cancer: IDC. The model was right in its classification of 12,424 Class 0 and 12,444 Class 1. Nevertheless, it wrongly categorized 1,622 samples of Class 0 as Class 1 and 1,603 Class 1 as Class 0. The fact that the ratio between TP and TN is almost equal to 1 suggests that the model has a high and stable classification capability, has low FP and FN rates, which indicates that the model is effective and reliable in separating cancerous and non-cancerous samples.

Classification Report:

| | precision | recall | f1-score | support |
|---|---|---|---|---|
| Class 0 | 0.89 | 0.88 | 0.89 | 14046 |
| Class 1 | 0.88 | 0.89 | 0.89 | 14047 |
| accuracy | | | 0.89 | 28093 |
| macro avg | 0.89 | 0.89 | 0.89 | 28093 |
| weighted avg | 0.89 | 0.89 | 0.89 | 28093 |

Fig. 11. ResNet50V2 Model Classification Report

Figure 11 displays the ResNet50V2 model's classification performance, with a balanced precision, recall and F1scores of 0.89 in Class 0 and Class 1. The algorithm is both consistent and effective at distinguishing between malignant and non-cancerous cases, with a general acc of 89%. In the case of Breast Histopathology Images dataset, the classification outcomes is based on IDC or non-IDC patch.

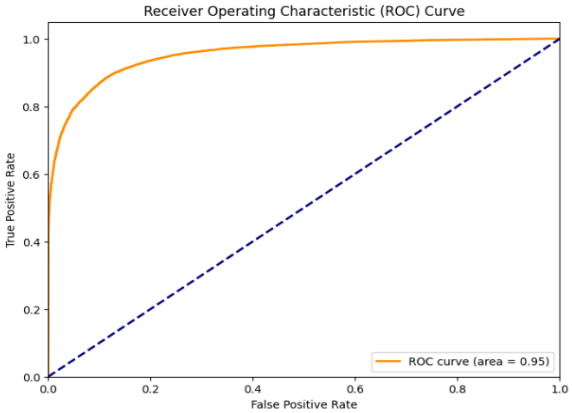


Fig. 12. ROC analysis ResNet50V2 Model

Figure 12 shows that the ResNet50V2 model analyzed by the ROC performs well in classification. The ROC curve indicates high TPR across all FPR, and it is strongly tilted towards the upper-left corner. The AUC stands at 0.95, Which indicates that the model's differentiation between the positive and negative classes is effective. The shape of the curve and high AUC score of the model indicate the effectiveness and strength of the model in the IDC Breast Cancer cases and hence is very effective and reliable in binary classification in medical imaging.

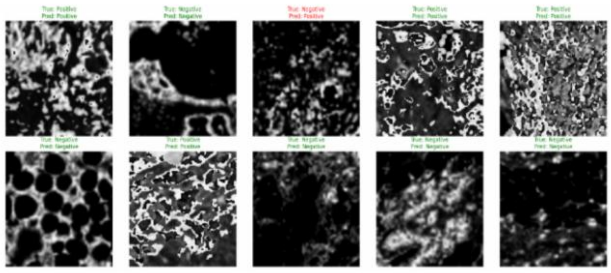

Fig. 13. Prediction Images of ResNet50V2 Model

Figure 13 represents the visual prediction results obtained by the ResNet50V2 model on the histopathological images of IDC breast cancer, detailing different results in classification. The figure contains TP, TN, FP, and FN, and the labels of them show ground truth and model predictions. The majority of the predictions are consistent with the actual labels, particularly of positive cases, meaning that the model is rather reliable. Some misclassifications are found (marked in red), indicating some difficulty in some difficult or ambiguous tissue structures. This graphical interpretation supports the efficiency of the model in practical image classification works as well as underlines the necessity of further optimization or augmentation procedures to decrease the quantity of incorrect forecasts and enhance this model's overall diagnostic performance in the most important medical imaging procedures.

### *B. Ablation Study*

The ablation study inspects the effect of given architectural and training manipulations on the ResNet50V2 model's performance with the dataset of Breast Histopathology Images. The study endeavors to comprehend the impact of components of the model, like dense layers, pooling strategies, optimizers and activation functions, on model behavior and generalization. Strauss curves of accuracy

and loss of every configuration indicate training dynamics, stability and possible overfitting. This methodical assessment give an idea of the most promising design options which would help to optimize and refine CNN models to be more reliable and applicable in real-life medical imaging scenarios.

TABLE III. ABLATION STUDY RESULTS WITH DIFFERENT PARAMETERS AND LAYERS OF RESNET50V2 MODEL ON THE TEST SET

| Methods | Accuracy | Precision | Recall | F1-Score |
|---|---|---|---|---|
| ResNet50V2 + No Dense (128) | 89 | 89 | 89 | 89 |
| ResNet50V2 + GlobalMaxPooling | 87 | 88 | 87 | 87 |
| ResNet50V2 + SGD Optimizer | 87 | 88 | 87 | 87 |
| ResNet50V2 + Only Softmax | 89 | 89 | 89 | 89 |

Table III presents the results of the ablation study evaluating the performance of the ResNet50V2 model across different architectural and optimization configurations. The baseline setup with the Dense (128) layer removed and the one with only the Softmax layer yielded the best acc, prec, rec, and F1 of 89%. In contrast, Global Max Pooling and SGD optimizer had a minimal impact on the metrics, and the accuracy and recall went down to 87%, indicating that these changes might restrict the ability of the model to learn intricate spatial features or to be effective. Altogether, the ablation analysis indicates that, although simple structures can also achieve similar performance, the selection of architectures and optimizers is essential to ensure the best model generalization and predictive accuracy.

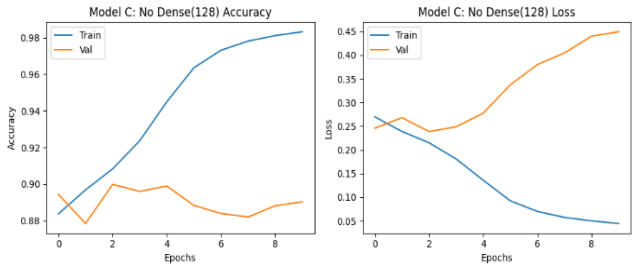


Fig. 14. Accuracy and Loss Curves of ResNet50V2 Model with No Dense (128)

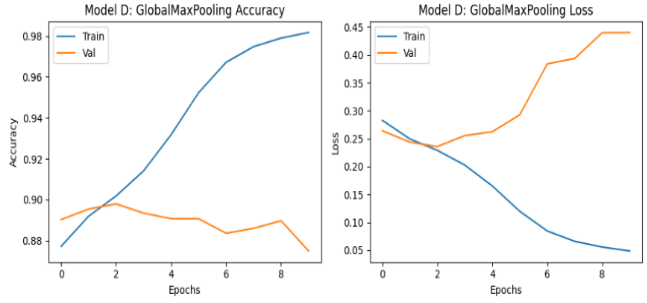


Fig. 15. Accuracy and Loss Curves of ResNet50V2 Model with Global Max Pooling.

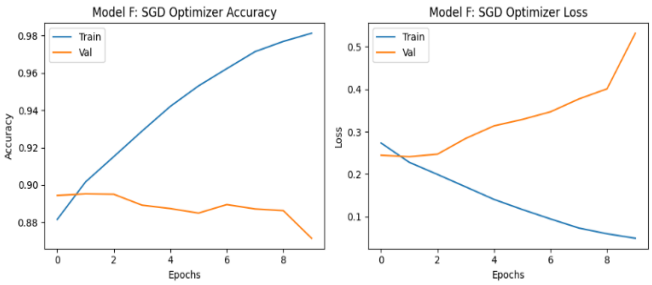


Fig. 16. Accuracy and Loss Curves of ResNet50V2 Model with SGD Optimizer

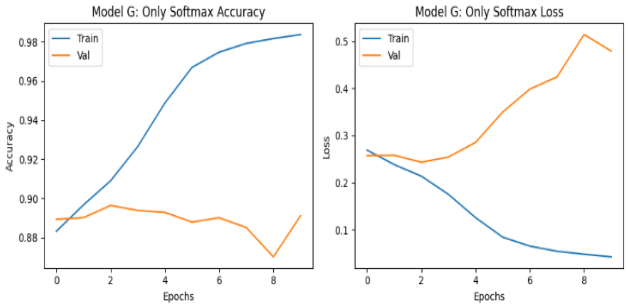


Fig. 17. Accuracy and Loss Curves of ResNet50V2 Model with Only Softmax with accuracy

Figures 14 to 17 illustrate the comparative analysis of diverse architectural and optimization changes made to the ResNet50V2 model. Figure 14 removes the Dense (128) layer and the training accuracy of the model is 98.59% with a slightly improved validation accuracy of 89.03% considering that simplification of the model can increase the generalization. Figure 15 demonstrates that the application of Global Max Pooling leads to a slight decline in performance, and validation accuracy is 87.49% and higher training loss (0.0468), which means that the feature extraction is less effective. Figure 16 also shows that when using SGD optimizer, performance decreases further with the weakest validation accuracy (87.15%) and the highest validation loss (0.5316) similar to the low optimization ability of Adam. In the meantime, Figure 17 shows that the highest validation accuracy (89.11%) and similar training results are attained by a single Softmax layer, which suggests that a more simplistic output setup can be used to successfully perform classification. The findings provide evidence of the significance of the architectural and optimization decisions, and the dense layer and Adam optimizer have a beneficial impact on the training and generalization of balanced training.

### *C. Comparative Analysis*

The comparison of the important demonstration indicators for the proposed ResNet50V2 model and the other deep learning models in the IDC breast histopathology dataset are listed in Table IV. According to its acc, pre, rec, and F1, the ResNet50v2 model outperforms the baseline models in detecting IDC-positive and IDC-negative instances.

TABLE IV. COMPARATIVE ANALYSIS OF DEEP LEARNING MODELS FOR IDC BREAST CANCER CLASSIFICATION

| Reference | Models | Accuracy | Precision | Recall | F1-Score |
|---|---|---|---|---|---|
| Proposed Model | ResNet50V2 | 88.52 | 88.47 | 88.59 | 88.53 |
| Base Paper[29] | CNN Model 3 | 87 | 84 | 84 | 88 |
| [30] | CNN-GRU | 86.21 | 85 | - | 86 |
| [31] | CNN | 83 | 84 | 83 | 83 |
| [32] | DenseNet-121 | 79.64 | 79.97 | 79.40 | 79.68 |

Table IV presents the comparative analysis of the suggested ResNet50V2 model and a number of baseline models were employed in the IDC categorization. The proposed model has the highest total accuracy of 88.52%, and balanced precision (88.47%), recall (88.59%), and the F1-score (88.53%) values. ResNet50V2 has better performance in all measures than CNN Model 3 (87%) and CNN-GRU (86.21%). Conventional CNN and DenseNet-121 seems to be worse in their results, with the lowest accuracy by DenseNet-121 (79.64%). This data illustrations how well the proposed ResNet50V2 architecture performs in classifying images of breast cancer.

This research is able to show a strong deep learning pipeline of IDC breast cancer identification based on histopathology images with high performance of 88.52. The most outstanding is probably the implementation of a complete preprocessing pipeline with tissue filtering, Hematoxylin channel enhancement, and image denoising, which has greatly enhanced the quality of images and diagnostic accuracy. The fact that a fully fine-tuned ResNet50V2 model was used with a comprehensive ablation experiment indicates the strengths of the architecture and its best settings in detecting IDC. The inclusion of SMOTE to solve the problem of class imbalance provides fairness and better generalization of the model. The proposed approach demonstrates better results compared to the current models, like CNN, CNN-GRU, and DenseNet121, which proves its clinical relevance. This unified framework does not only increase the accuracy of classification, it also forms the basis of the interpretable, scalable, and automated diagnostic systems in digital pathology.

### *D. Limitations and Future Work*

Despite the promising outcomes achieved by the proposed ResNet50V2-based model for IDC classification, this study has certain limitations. It is also limited to one dataset, and this fact might not be applicable to different imaging settings and patients. Although SMOTE can be used to deal with class imbalance, synthetic patterns are introduced, which do not necessarily reflect actual histological variations. Moreover, the model is not yet interpretable which is an important feature of the model to be adopted in clinical settings. Future directions will be to increase validation on multi-center and heterogeneous data, incorporate XAI procedures, such as Grad-CAM or SHAP to improve transparency, and hybrid models combining deep and traditional machine learning classifier (RF or SVM) to improve performance and interpretation. Furthermore, the idea of creating lightweight or compressed model versions will be discussed to be able to use them in clinical environment with limited resources.

## V. CONCLUSION

In Breast cancer, early identification and treatment are critical for positive outcomes. Breast cancer is a disease originating in the breast cells and can be regarded as one of the first causes of death among women. The most common and aggressive type of breast cancer is Invasive Ductal Carcinoma (IDC) and this type of cancer necessitates early and accurate diagnosis in order to be treated. The study used the collection of breast histopathology images to examine automated IDC categorization using DL algorithms. The ResNet50V2 architecture was the most successful in the performance with an acc of 88.52% and balanced values of pre, rec, and F1. A study of ablation also indicated the importance of a wide range of architectural and training parameters on the model effectiveness. The high performance and strength of ResNet50V2 were demonstrated by comparative analysis with the baseline models, including CNN, CNN-GRU, and DenseNet-121. On the whole, the paper presents the promise of DL and the use of ResNet50V2 specifically in helping histopathological IDC detection and provide better diagnostic processes in the field of medical imaging. However, compared to traditional DL approaches, transfer learning performs better in small datasets, making it the preferable method. This approach will significantly demonstrate that technology can transform people's lives and might be utilized in the medical profession to identify tumors early and accurately. Future work will involve applying advanced regularization methods, enhancing model generalization and reducing overfitting with the use of ensemble learning and substantial data augmentation.

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