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Segmentation and Classification of Breast Cancer Histopathological Image Utilizing U-Net and Transfer Learning ResNet50

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ABSTRACT

Breast cancer is the most common type of cancer among various types of cancer. Approximately 1 in 8 women in the United States die from breast cancer. Early screening and accurate diagnosis are essential for prevention and accelerated treatment intervention. Several artificial intelligence methods have emerged to develop effective segmentation, detection, and classification to determine cancer types. Although there has been progress in automated algorithms for breast cancer histopathology image analysis, many of these approaches still face several challenges. This study aims to address the challenges in breast cancer image analysis. This research method uses the development of the U-Net architecture combined with Transfer Learning using ResNet50. The encoder path aims to improve the model's sensitivity in the segmentation and classification of cancer areas by utilizing deep hierarchical features extracted by ResNet50. In addition, data augmentation techniques are used to create a diverse and comprehensive training dataset, which improves the model's ability to distinguish between different tissue types and cancer areas. The results of this study are U-Net and ResNet50, which show an average IoU of 0.482 and a Dice coefficient of 0.916. This study concludes that integrating U-Net with Transfer Learning ResNet50 improves the segmentation and classification accuracy in breast cancer histopathology images and overcomes the problem of high computational requirements. This approach shows significant potential for improvement in early breast cancer detection and diagnosis.

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1. INTRODUCTION

Breast cancer is the most common type of cancer among other types of cancer and the most prevalent cancer affecting women [1]. About 1 in 8 women in the United States (approximately 13%) die from breast cancer [2]. The prevalence of breast cancer has seen a significant increase, establishing it as one of the leading types of cancer in terms of both incidence and mortality rates [3]. The WHO also notes that breast cancer is the leading cause of cancer-related deaths among women worldwide, which is expected to increase every year [4]. To reduce the mortality rate caused by breast cancer, screening is necessary to prevent and detect breast cancer as early as possible [5], with the potential to reduce the need for surgeries and improve survival rates [6]. Breast imaging techniques are commonly employed to locate cancerous cells or suspicious lesions with high frequency [7]. Currently, several artificial intelligence methods have emerged to build effective segmentation, detection, and classification systems to identify cancer types [8, 9]. Despite the development of automatic algorithms for analyzing breast cancer histopathology images, many of these approaches still face several challenges [10]. Common problems include inaccurate segmentation, insensitive object detection, and non-specific classification, also these segmentation and classification processes require significant computation. Also, finding the right balance between accuracy and efficiency can often be challenging [11]. In other cases, there have been studies producing less satisfactory results due to using datasets with low-resolution images [12]. Additionally, the inability to handle a wide variety of images and the structural complexity of breast cancer tissue also pose obstacles to developing effective solutions [13].

Previous research proposed an algorithm to detect individual cells from a histopathology image. The results showed that the proposed method is suitable for image segmentation processes, although it is quite challenging because traditional methods are still used. Subsequently, the process of histopathology image segmentation using deep learning began to be developed, which has surpassed traditional methods [14]. First proposed an efficient lymph node metastasis segmentation method based on deep learning that can be performed in minutes [15]. Another study proposed an automatic segmentation model to detect breast cancer that represents different histopathology image patterns [16]. A tile-wise technique is used to address the issue of very large image sizes, where the image is divided into several patches representing tiles. These tiles are then applied with a deep convolutional neural network (DCNN) along with an encoder-decoder with separable atrous convolution architecture [17]. Other research stated that nucleus cell segmentation is very important and difficult to perform in histological analysis due to various factors including poor image quality, varying staining, variable cells, and other morphological factors. The study proposed a spatial-channel attention-based modified U-Net architecture combined with Residual Network (ResNet) blocks in the encoder layer [18]. Another research proposes an autoencoder architecture for unsupervised segmentation and a U-Net architecture for supervised segmentation. Several metrics, such as recall, precision, and F1-score, are used for quantitative performance measurement. The results obtained from the proposed approach are highly competitive [19]. This study has quite good quantitative results and performance but only focuses on histopathology image segmentation.

Some research developed segmentation and classification in histopathological images. First, a HoVer-Net model is proposed for simultaneous segmentation and classification of nuclei using Kumar, CPM-17, CoNSep, CRCHisto, and TNBC datasets. The study uses ResNet50 as an encoder and has three independent decoders that produce masks, feature maps, and class output. The training stage of the study takes around 380 minutes in total and reaches a good result for Dice of more than 0.70 and mPQ for more than 0.5 [20]. The second study proposed a modified HoVer-Net model with augmentation techniques and SeResNext101 encoder to improve performance. The study stated that the process of cell segmentation and classification is challenging in pathology. The study uses PanNuke and GIas datasets and reached a good result that overcoming HoVer-Net with mPQ reach 0.4997 [21]. Another study introduces a new method for automatic instance segmentation and classification in histopathological images using a Vision Transformer-based deep learning architecture using PanNuke, MoNuSeg, and CoNSep datasets. The study claims that their method is faster by 1.85 times than HoVer-Net [22]. The last is a study that proposed HoVer-UNet that combines U-Net and Mix Vision Transformer backbone to encode the distilled knowledge from Hover-Net. The study uses the PanNuke and CoNSep datasets and states that their inference times are three times lower than Hover-Net. For the classification results, Hover-Unet outperformed HoVer-Net for some nuclei [23]. A gap that remains unresolved in previous study is the low classification accuracy, which requires significant improvement. Additionally, many existing methods face the challenge of high computational demands.

The difference between this study and the previous study is that this study proposes a U-Net model based on a convolutional neural network architecture to obtain accurate segmentation, optimize the understanding of spatial context and feature hierarchy, and reduce computational complexity in histopathology images. The u-Net model is designed to be efficient while maintaining high segmentation accuracy and reducing computational complexity, making it suitable for deployment in environments with limited resources. U-Net is combined with Transfer Learning ResNet50, a deep learning model known for its powerful feature extraction capabilities as an encoder to achieve accurate segmentation and classification and to optimize the understanding of spatial context and feature hierarchy in histopathology images. This integration enhances the model's sensitivity in detecting cancerous areas by leveraging the deep hierarchical features extracted by ResNet50. The model is also accompanied by augmentation to increase the

diversity of the training dataset. Augmentation also improves the model's ability to distinguish between different types of tissue and cancerous regions, resulting in more specific and accurate classifications. Using U-Net based on the architecture performs very well on different biomedical image segmentation applications [24]. The use of U-Net, which retains both coarse and fine features in the image, provides a solution to the variety of cell images [18]. This paper introduces an approach for the segmentation and classification of breast cancer histopathology images, leveraging the strengths of the U-Net architecture and the transfer learning capabilities of ResNet50 [25]. The proposed methodology aims to address the critical challenges in accurate and efficient analysis of histopathological images, which are pivotal for the early detection and diagnosis of breast cancer.

The objective of this study is to integrate U-Net for precise segmentation, and ResNet50 for robust classification, exploiting the advantages of deep learning in medical imaging, ensuring high performance and reliability. By utilizing transfer learning, the model benefits from pre-trained weights, enhancing its ability to generalize across diverse datasets, improving classification accuracy, and decreasing the computational learning time. Preliminary results indicate that this study contributes to achieving significant improvements in segmentation, classification, and performance, with better classification results than previous research [20, 24].

The subsequent chapters will delve into the detailed methodology, experimental setup, and comprehensive evaluation of the proposed model. The promising results thus far underscore the potential of deep learning techniques in advancing the field of breast cancer histopathology image analysis.

2. RESEARCH METHOD

The research methodology chapter outlines this study's systematic approach and procedures to investigate the segmentation and classification of breast cancer histopathology images. This study follows a quantitative research design, focusing on the numerical analysis and evaluation of the obtained results. This chapter provides a comprehensive description of the research design, data collection, preprocessing techniques, image augmentation, model development, evaluation metrics, and validation procedures employed in this study that will be explained in sub-section 2.1 until 2.5. The details of the research methodology conducted in this study are shown in Figure 1.

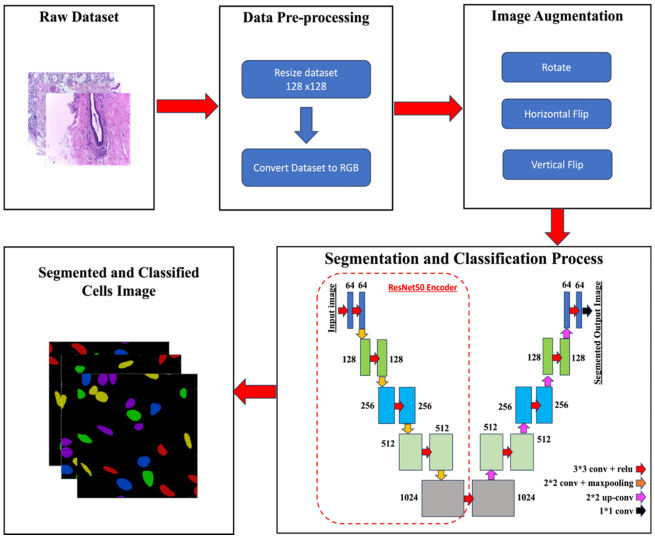

Figure 1. Research Methodology

2.1. Data Collection

During the data preparation stage, the collection of the dataset to be used in the research was carried out. The dataset used is the publicly available PanNuke dataset [26]. This dataset consists of 19 types of cell tissues, one of which is the type of breast cancer case with malignant tumors. This dataset is used to classify the histological structure of breast cancer that has been stained with hematoxylin and eosin (H&E) into five classes automatically: neoplastic, epithelial, inflammatory, connective, and dead cell. The image sample from PanNuke dataset is shown in Figure 2.

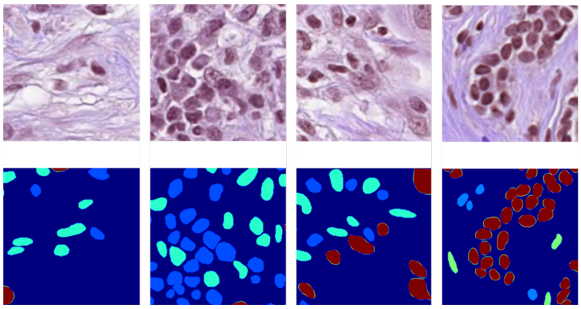

Figure 2. Sample images and ground truth from PanNuke dataset

2.2. Data Pre-processing

Effective data preprocessing is a critical step in any machine learning and deep learning project, as it ensures that the dataset is in the best possible condition for training models. This study's data preprocessing stage involves adjusting the images according to the U-Net architecture used. The first step is to standardize the resolution of the entire dataset to ensure uniformity. In this study, all datasets will be adjusted to a resolution of 128×128 because the previous data is not good in bigger resolution. After the resolution adjustment stage, the images are also converted to RGB as it is expected to provide a more optimal image representation that can be beneficial in distinguishing different objects or features within the images. Converting the images to RGB helps enhance color contrasts and detail, improving the model's performance in identifying and segmenting various cell types and structures.

2.3. Data Augmentation

Image augmentation is a powerful technique used to increase the diversity of the training dataset [27], which helps the model learn more effectively and generalize better. This process prevents overfitting and enhances the model's performance on new, limited data. In this study, given the limited size of the dataset, image augmentation is employed on the segmented images to create variations in the dataset without altering the actual labels. Various augmentation techniques include rotations of 90^o, 180^o, and 270^o, and image flipping. These methods generate multiple versions of the original images, thereby enriching the training data and enabling the model to recognize and adapt to different orientations and perspectives of the histopathological features. Table 1 details the number of data images before and after augmentation.

Table 1. Number of images before and after augmentation

Images Type	Before Augmentation	After Augmentation
Cell Image	2351	7053
Ground Truth	2351	7053

2.4. Data Training

The process of breast cancer histopathology image segmentation using the U-Net architecture involves applying a technique proven effective in machine learning to identify and separate cancerous areas from pathology images. U-Net architecture is renowned for achieving high segmentation accuracy, even with limited training data [1]. Its flexibility allows depth adjustments, crucial for handling specific segmentation complexities typical in histopathology images [28]. Furthermore, Transfer Learning techniques are often applied in this context to enhance model performance and flexibility. Transfer Learning enables leveraging pre-learned knowledge from large and diverse datasets to improve segmentation outcomes. By transferring pre-trained representations, the model can expedite convergence when trained on the specific breast cancer dataset, which is typically smaller and disease-specific. The combination of the robust U-Net architecture and ResNet50 techniques facilitates the development of efficient and accurate solutions in histopathology image analysis to support breast cancer diagnosis. The U-Net dan ResNet50 model implemented in this study is shown in Figure 3.

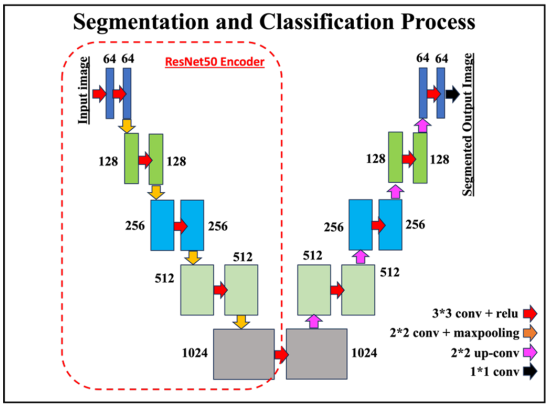

Figure 3. U-Net and Transfer Learning architecture

Figure 3 shows that the U-Net architecture consists of two paths: an encoder on the left side and a decoder on the right side. The encoder is used to capture feature information from the input image and reduce its dimensionality. In contrast, the decoder path captures feature information from the encoder output and is the location where segmentation results emerge. The encoder path begins with double 3×3 convolution layers and ReLU activation functions, resulting in 64 feature maps. This is followed by 2×2 max pooling. In this study, the encoder path employs transfer learning, leveraging pre-trained models to capture rich feature representations from diverse datasets. Transfer learning is integrated across each activation layer. Several transfer learning models combined with U-Net in this study are shown in Table 2. Next, the process continues to the decoder path, starting with 2×2 upsampling, followed by the same structure as the first block but without max pooling. The decoder path in this study uses four convolution blocks, where the number of feature maps in each block is halved to match the original number. The final step in this path involves a 1×1 convolution layer and categorical cross entropy activation function used to produce segmented images.

Table 2. Transfer learning techniques utilized

Transfer Learning Technique	Weight
ResNet50	Imagenet
EfficientNetB0	Imagenet
EfficientNetV2M	Imagenet
MobileNetV2	Imagenet
VGG19	Imagenet

2.5. Matrix Evaluation

The testing and analysis were conducted by comparing the breast cancer histopathology image datasets used in the study. The model's performance was assessed using several matrix evaluations to ensure accuracy and reliability. These evaluations play a crucial role in determining the classification algorithms' effectiveness. In this context, each matrix was carefully selected to provide insights into different aspects of the model's performance. The matrix evaluations performed in this study are as follows:

1. **IoU (Intersection over Union)**: This metric measures the extent to which the segmentation area produced by the algorithm overlaps with the actual area of the segmented object. It is widely used in image segmentation tasks to evaluate the accuracy of predicted boundaries. The IoU score ranges from 0 to 1, where a value of 1 indicates a perfect overlap between the predicted and actual regions. A higher IoU score signifies better performance in identifying and segmenting the target area. The formula for calculating IoU is shown in 1.

$$IoU = \frac{\text{Intersection Area}}{\text{Union Area+Intersetion Area}} \tag{1}$$

2. **Dice Coefficient**: This metric measures the overlap between the segmentation and actual areas, similar to IoU but with a slightly different approach. It is particularly useful in medical imaging tasks where precise segmentation is crucial. The Dice Coefficient ranges from 0 to 1, with a value closer to 1 indicating a higher degree of overlap between the predicted and true areas. A key advantage of the Dice Coefficient is its sensitivity to small structures. The formula for calculating the Dice

Coefficient is shown in Equation 2.

$$DiceCoefficient = \frac{\text{2*(Intersection Area)}}{\text{Total Area of Prediction + Total Area of Ground Truth}} \quad (2)$$

3. **Recall and Precision**: Recall measures the algorithm's ability to detect all areas that should be segmented, providing insight into how well the model captures the true positive regions. A higher recall indicates fewer false negatives, meaning the model successfully identifies more of the actual object areas. On the other hand, precision measures how much of the area labeled as an object by the algorithm is actually the object. This metric reduces false positives, ensuring that the predicted areas are relevant and accurate. Both recall and precision are crucial for evaluating segmentation performance, as they balance sensitivity and specificity. The recall and precision formulas are shown in Equations 3 and 4.

$$Recall = \frac{TP}{TP + FN} \quad (3)$$

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

4. **F1-Score**: The F1-Score is the harmonic mean of precision and recall (sensitivity), combining both metrics into a single performance measure. It provides a balanced evaluation by considering false positives and negatives, making it especially useful when there is an uneven class distribution. A higher F1-Score indicates a model performing well in detecting relevant areas (recall) and minimizing incorrect predictions (precision). This metric is particularly valuable when optimizing for both precision and recall is necessary. The formula for the F1-Score is shown in Equation 5.

$$F1 - Score = \frac{2 * (Precision * Recall)}{Precision + Recall} \quad (5)$$

The evaluation was conducted by comparing the segmentation and classification results with and without augmentation. This study deliberately separates the segmentation and classification processes to understand better how image augmentation influences the outcomes. By isolating these processes, the impact of augmentation on both segmentation accuracy and classification performance can be more clearly observed. The use of augmentation aims to enhance the model's generalizability by introducing variability in the training data. A detailed comparison of results, both with and without augmentation, helps to highlight its effectiveness in improving overall performance.

3. RESULT AND ANALYSIS

In this chapter, we present the outcomes of our experiments and provide a detailed analysis of the results. We evaluate the performance of our U-Net-based segmentation and classification model, enhanced with transfer learning on breast cancer histopathology images. The metrics used for assessment include mean IoU, IoU per class, accuracy, precision, recall, and the Dice coefficient. Additionally, we discuss the implications of these findings and compare our results with previous studies to highlight the effectiveness and improvements of our approach. The U-Net model itself is already reliable in medical image segmentation. This is evidenced by a fairly good mean IoU score of 0.364 for the U-Net model without augmentation and 0.417 for U-Net with augmentation. Meanwhile, combining the U-Net model with transfer learning as an encoder also has a significant impact. Several transfer learning methods used, such as VGG19, ResNet50, MobileNetV2, and DenseNet201, improved the quantitative results obtained. However, in this study, some methods were less suitable for combining with U-Net, such as EfficientNetB0. The training process was conducted using transfer learning techniques combined with the U-Net architecture. The optimizer used was Adam, and the weights were initialized with ImageNet weights. The training process was run in two scenarios for each model: without augmentation and with augmentation. The goal was to determine the impact of augmentation on the image segmentation and classification process in this study. The graphical representations of training and validation accuracy and training and validation loss between U-Net + EfficientNetB0 and U-Net + ResNet50 can be seen in Figure 4 and Figure 5. The segmentation results measured in Mean IoU and Dice Coefficient are shown in Table 3. Meanwhile, the classification results for each class are shown in Table 4.

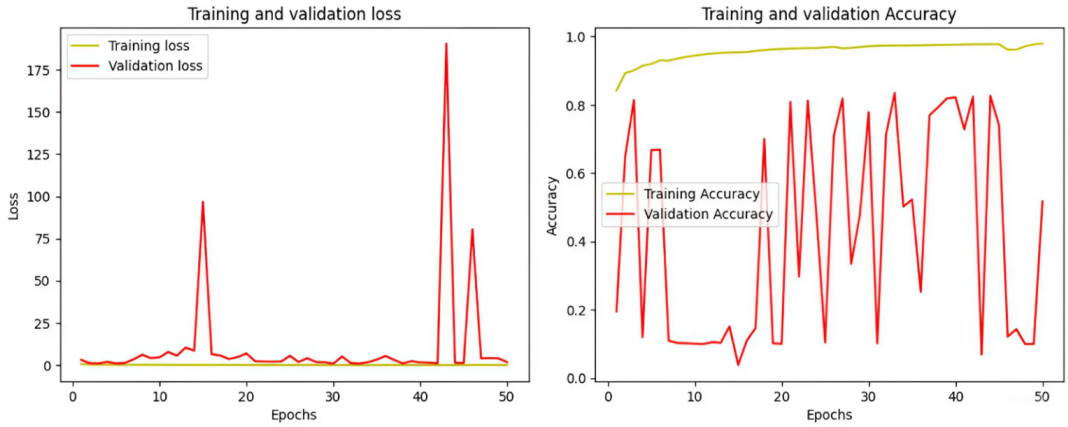

Figure 4. Graphical result of training and validation accuracy and training and validation loss U-Net + EfficientNetB0

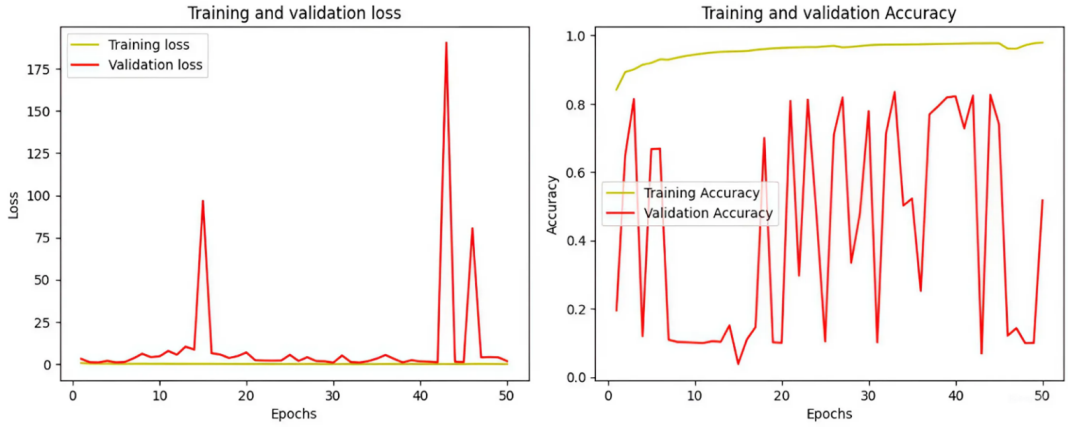

Figure 5. Graphical result of training and validation accuracy and training and validation loss U-Net + ResNet50

Table 3. Segmentation results

Techniques	Without Augmentation		With Augmentation	
	Mean IoU	Dice Coefficient	Mean IoU	Dice Coefficient
U-Net	0.364	0.860	0.417	0.880
U-Net + ResNet50	**0.456**	**0.889**	**0.482**	**0.916**
U-Net + EfficientNetB0	0.110	0.501	0.120	0.803
U-Net + EfficientNetV2M	0.015	0.093	0.330	0.857
U-Net + MobileNetV2	0.452	0.884	0.457	0.889
U-Net + VGG19	0.430	0.873	0.447	0.885

Based on the segmentation results presented in Table 3, the U-Net model is already quite reliable in performing image segmentation tasks. The addition of suitable transfer learning as an autoencoder has enhanced the segmentation results. In these findings, the U-Net + ResNet50 model achieves higher Mean IoU and Dice coefficient scores in both scenarios, with and without augmentation. Furthermore, it is observed that the EfficientNet model is less suitable when combined with U-Net in this study. Two testing scenarios were conducted in this research: without augmentation and with augmentation, indicating that augmentation can improve segmentation performance, although not significantly.

Table 4. Classification results

Techniques	Neoplastic			Epithelial			Inflammatory			Connective			Dead Cell		
	P_N	R_N	$F1_N$	P_N	R_N	$F1_N$	P_N	R_N	$F1_N$	P_N	R_N	$F1_N$	P_N	R_N	$F1_N$
U-Net	0.66	**0.77**	0.71	0.76	0.20	0.31	0.31	0.42	0.36	0.45	0.43	0.44	**0.30**	0.04	0.07
U-Net + ResNet50	0.79	**0.77**	0.78	0.70	0.70	0.70	0.50	0.39	0.44	0.58	0.39	0.47	0.23	0.07	0.11
U-Net + EfficientNetB0	0.15	0.33	0.26	0.00	0.00	0.00	0.61	0.00	0.01	0.20	0.00	0.00	0.00	0.00	0.00
U-Net + EfficientNetV2M	0.09	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
U-Net + MobileNetV2	0.72	0.78	0.75	0.74	0.65	0.69	0.52	0.34	0.41	0.56	0.48	0.52	0.21	0.09	0.11
U-Net + VGG19	0.70	0.79	0.74	0.62	**0.71**	0.66	**0.62**	0.26	0.37	0.53	0.44	0.48	0.31	0.04	0.07
U-Net + Aug	0.82	0.62	0.70	0.66	0.67	0.66	0.61	0.26	0.37	0.51	0.46	0.48	0.27	0.02	0.04
U-Net + ResNet50 + Aug (Proposed)	**0.83**	0.73	**0.79**	**0.84**	0.67	**0.75**	0.60	**0.55**	**0.57**	0.59	0.55	**0.57**	0.20	**0.23**	0.21
U-Net + EfficientNetB0 + Aug	0.27	0.27	0.27	0.44	0.00	0.00	0.38	0.01	0.02	0.17	0.00	0.01	0.00	0.00	0.00
U-Net + EfficientNetV2M + Aug	0.60	0.66	0.63	0.72	0.13	0.22	0.40	0.32	0.36	0.52	0.34	0.41	0.15	0.04	0.06
U-Net + MobileNetV2 + Aug	0.75	0.77	0.76	0.76	0.66	0.70	0.49	0.36	0.42	**0.62**	0.45	0.52	0.20	0.06	0.09
U-Net + VGG19 + Aug	0.81	0.71	0.76	0.76	0.66	0.70	0.58	0.29	0.39	0.42	**0.67**	0.51	**0.30**	0.02	0.04
Hover-UNet [23]	-	-	0.64	-	-	0.62	-	-	0.53	-	-	0.48	-	-	0.18
HoVer-Net [20]	-	-	0.62	-	-	0.56	-	-	0.54	-	-	0.49	-	-	**0.31**

In Table 4, segmentation results are presented. The scenarios were conducted with and without augmentation. There are five classes in the PanNuke dataset: Neoplastic, Epithelial, Inflammatory, Connective, and Dead Cell. The metrics measured in this classification process are Precision (P), Recall (R), and F1-Score (F1). The results show considerable variation, but the U-Net + ResNet50 model with augmentation often outperforms other models. Additionally, upon closer inspection, MobileNetV2 and VGG19 also show potential for better performance. The dead cell class has the lowest scores due to class imbalance and its significantly lower quantity than other cells, an issue that augmentation has not yet resolved. Based on the quantitative results obtained, the study also presents segmentation and classification predictions of histopathology images. This research demonstrates that segmentation results significantly influence classification outcomes. The U-Net + ResNet50 model performs well in segmentation tasks, but there are still some errors in image classification. The following section will display sample prediction results of breast cancer histopathology images. Figure 6 shows the results from the U-Net + EfficientNetB0 model, which are less accurate, and Figure 7 shows the results from the U-Net + ResNet50 model, which are the best and most outperformed the previous study [20, 23].

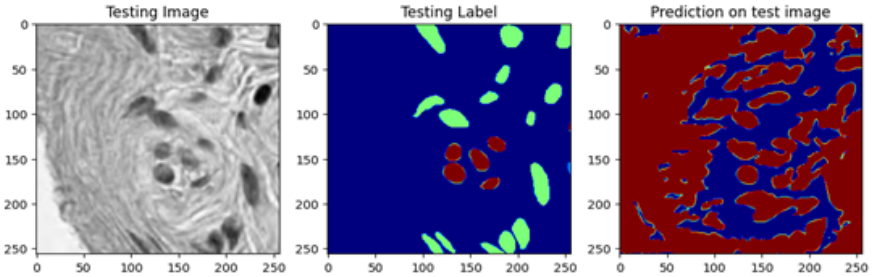

Figure 6. Prediction result U-Net + EfficientNetB0

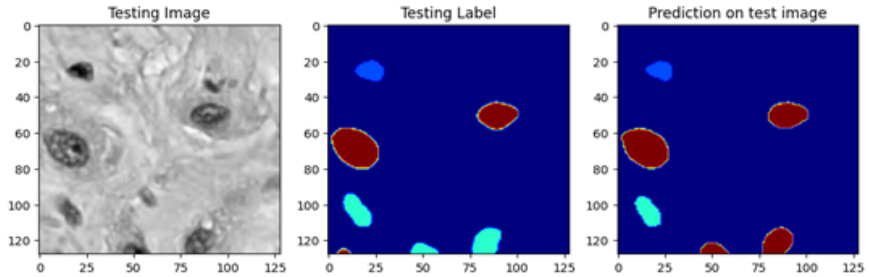

Figure 7. Prediction result U-Net + ResNet50

The study's findings indicate that U-Net + ResNet50 with augmentation outperformed the other models in the segmentation and classification tasks conducted in this study. The results show that U-Net + ResNet50 with augmentation also outperformed the previous study [20, 23]. **In line with Research** [20, 23]. A U-Net model based on a convolutional neural network architecture optimizes the understanding of spatial context and feature hierarchy in histopathology images. Furthermore, the use of ResNet50 plays a crucial role in improving overall accuracy while also addressing the issue of high computational demands by leveraging a pre-trained network.

4. CONCLUSION

In this chapter, we summarize the key findings of our study and discuss their implications. We reflect on the performance of our proposed methods, including the U-Net architecture and transfer learning techniques, in segmenting breast cancer histopathology images. Additionally, we highlight the strengths and limitations of our approach and suggest potential areas for future research further to enhance the accuracy and efficiency of medical image segmentation.

First, the U-Net model has proven to be quite reliable in the segmentation and classification of images. However, the results are significantly improved when combined with transfer learning techniques such as the encoder. Second, in this study, the segmentation results are already quite good. Nevertheless, the classification results for individual cell classes sometimes exhibit misclassifications due to imbalanced data, particularly in the Dead Cell class. Third, combining U-Net with transfer learning has accelerated the training process. Fourth, the augmentation process in this study impacted the results obtained, although not significantly. Lastly, all models performed well, and with more in-depth data pre-processing and addressing the issue of class imbalance, performance could likely be further enhanced.

In conclusion, our study has shown that leveraging U-Net in conjunction with transfer learning offers substantial benefits in medical image analysis. Future work should focus on further refining data preprocessing techniques and balancing the dataset to minimize classification errors and enhance model robustness. By addressing these areas, the potential for even greater advancements in medical image segmentation and classification is significant.

For future research, techniques such as oversampling, undersampling, SMOTE, and others can be applied to address class imbalance. By handling the class imbalance, segmentation performance can be improved, and classification errors can be reduced. Additionally, exploring advanced augmentation techniques and incorporating more diverse datasets may enhance the model's robustness and accuracy. Future work could also further investigate the integration of ensemble learning methods to improve the performance of segmentation and classification tasks in histopathology image analysis.

5. ACKNOWLEDGEMENTS

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6. DECLARATIONS

AUTHOR CONTIBUTION

Nella; Conceptualization, Methodology, Data collection, Implementation, Writing – Original Draft Preparation. Chastine; Conceptualization, Methodology, Writing – Review and Editing.

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COMPETING INTEREST

The authors declare there is no conflict of interest.

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