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Histopathology Grading of Breast Cancer Using Visual Geometry Group Method

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Abstract — Breast cancer continues to rank among the world's leading causes of death for women. Developing successful treatment plans requires a timely and accurate diagnosis. Although histopathological image analysis is still the gold standard for evaluating malignancy, it is prone to inconsistencies and human error. The objective of this research is to use the Visual Geometry Group's (VGG16) deep learning technique to automate the evaluation of breast cancer histology. A collection of breast cancer histopathology images spanning 85 epochs was used to train the VGG16 model, which is well-known for its excellent performance in image classification tasks. For training and testing, the model uses batch sizes of 33 and 64, respectively, and a Stochastic Gradient Descent (SGD) optimizer with a learning rate of 0.01. With an F1 score of 0.98, 89.3% training accuracy, and 98% validation accuracy, the experimental findings show excellent performance. These results indicate that VGG16 is highly effective in distinguishing between different tissue grades of breast cancer. Despite its high performance, challenges remain regarding computational efficiency and interpretability for clinical use. Future research should focus on exploring lightweight architectures, improving model explanations, and validating more diverse and larger datasets to enhance real-world applicability in digital pathology.

Keywords: histopatology breast cancer, grading breast cancer, Deep Learning, CNN, VGG 16.

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1. Introduction

With over 685,000 fatalities and 2.3 million new cases each year, breast cancer remains a serious global health concern [1]. Breast tissue histopathological analysis is still the gold standard for tumor diagnosis and grading, and it is an important factor in treatment planning and prognosis [2]. Expert pathologists carefully grade stained tissue slides using a microscope, paying particular attention to important factors such nuclear pleomorphism, tubule development, and mitotic count [3]. Nevertheless, this manual procedure is subjective and time-consuming, frequently resulting in variability between and within observers [4].

Artificial intelligence (AI), especially deep learning, has been a game-changing technology in computational pathology in recent years. Classification, segmentation, and grading of pictures from breast cancer histopathology are among the medical imaging tasks in which Convolutional Neural Networks (CNNs), including well-known designs like Visual Geometry Group (VGG) networks, have shown notable results [5]–[7]. These models can learn hierarchical features from data and generalize well, making them suitable for complex image analysis in pathology. Most deep learning approaches for breast cancer grading have focused primarily on identifying nuclear structures, tissue patterns, and morphological characteristics of tumor cells [8]–[10].

Recent literature has explored various strategies to enhance grading accuracy and model

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robustness. Kundale et al. [11] combined handcrafted features with deep learning, emphasizing preprocessing and texture descriptors. Guabou et al. [12] proposed an ensemble of CNNs across magnification levels using ResNet, DenseNet, and VGG, demonstrating the strength of transfer learning. Similarly, Albash et al. [13] achieved high classification accuracy using an ensemble model based on VGG16, while Alzubaidi et al. [14] incorporated a hybrid of deep and shallow features to improve performance on underrepresented classes.

Model interpretability has also become a research focus. Aldakhil et al. [10] introduced an attention mechanism to highlight diagnostically relevant nuclei, enhancing clinical trust. Pan et al. [15] developed a multi-task learning framework that jointly performed classification and nuclei segmentation. In a broader comparative study, Hameed et al. [16] evaluated various deep learning models, emphasizing the importance of high-quality, diverse datasets. To address dataset limitations, Ruiz-Casado et al. [17] utilized GANs to generate synthetic histopathology images, enhancing model training through augmentation.

While these advancements have improved grading performance, they largely overlook non-cellular features present in histopathological images. During tissue preparation, artifacts such as crack-like patterns often emerge due to processing, sectioning, or fixation. These cracks are typically dismissed as noise. However, emerging studies suggest that such structural disruptions may contain latent information correlated with tissue integrity, malignancy, and preservation quality [18], [19]. Cracks can exhibit traits like length, density, and orientation that potentially reflect extracellular matrix degradation or cellular cohesion loss in malignant tissues [20].

Some initial studies have explored integrating texture irregularities and edge disruptions using handcrafted features or unsupervised clustering [21], [22]. However, these methods lack robustness and scalability in clinical workflows. No prior work has explicitly modeled crack morphology within a deep learning framework as an auxiliary feature in breast cancer grading.

This work addresses that gap by proposing a novel VGG-based deep learning architecture that integrates crack pattern analysis as a supplementary feature. The approach involves preprocessing to detect and isolate crack-like structures, followed by multi-stream feature fusion with standard histological features. The hypothesis is that combining these cues can enhance model sensitivity to structural degradation associated with high-grade malignancies.

This research is innovative due to the formal integration of crack morphology—previously regarded as a nuisance variable—into the deep learning framework for histopathological grading. The urgency arises from the growing digitization of pathology workflows and the necessity for more resilient, interpretable AI technologies capable of functioning well in substandard picture settings. Additionally, research by Yan et al. [23] and Jiang et al. [24] emphasize the significance of integrating multi-scale and multi-modal aspects, hence reinforcing the methodology of our work, which merges crack features with traditional tissue-level indicators.

2. Method

This study uses a modeling method, where in this work models using VGG16 method where in this study breast cancer cell data with three grade levels will be used. The cancerous tumor arises from the aberrant proliferation of cells that infiltrate adjacent tissues within the human body [25]. The model was created using PyTorch with the Python programming language with the block diagram as shown in ”Figure 1”.

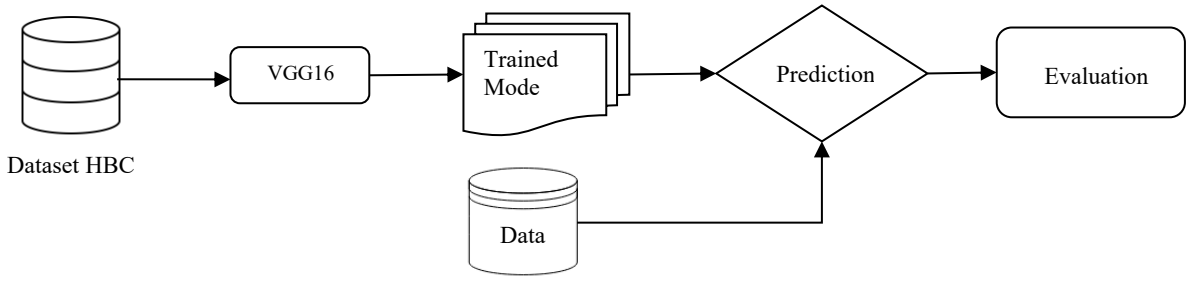


Figure1. Block Diagram

2.1 Dataset

The area of the body affected by breast cancer comprises the glands and milk ducts responsible for milk transport. Breast cancer frequently metastasizes to other organs, rendering them malignant [26]. In this research, we are going to use the breast cancer dataset with 13 classes and three grades. This means that in these 3 grades there are types, such as grade 1 has 3 types, grades 2-3 have 5 types, so the total class is 13.

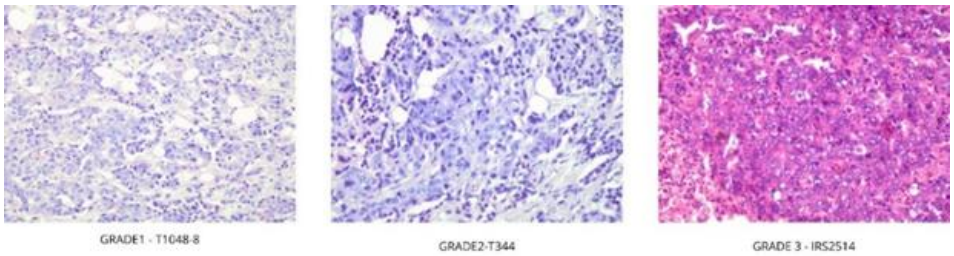


Figure 2. The Pictures of 3rd-Grade Breast Cancer

"Figure 2" exemplifies the dataset utilized for training and testing the model, sourced from the Anatomical Pathology Laboratory of Dr. Soetomo Hospital in Surabaya. We will utilize the dataset for a classification task.

2.2 Preprocessing

This work involves picture preprocessing before to and during image utilization. The image will undergo an augmentation process to enhance the dataset, as it is widely recognized that more data availability improves the efficacy of machine learning algorithms [27], [28]. The initial dataset comprised 140 photos, which was expanded to 1,429 images through the application of Random Horizontal Flip and Random Vertical Flip augmentation techniques. Horizontal or vertical flipping: Inverts the image along the horizontal or vertical axis to get a mirrored representation. This technique may replicate various observation angles and mirror symmetry, hence enhancing data variety [8]. Upon completion of model augmentation, it is prepared for bifurcation into two segments: training and testing, with the training dataset comprising 796 images and the testing dataset containing 633 images. The image undergoes further processing during training or testing, specifically by shrinking it to 100 × 100 pixels and normalizing it.

$$norms = \frac{\left(x_{ch} - \left(\frac{1}{n}\sum_{i=0}^{n} x_{ch_i}\right)\right)}{\sigma(x_{ch})} \quad (1)$$

"Formula 1" is used to normalize the image per channel x_ch. To normalize the image, we need to calculate the mean from the image channel $\left(\frac{1}{n}\sum_{i=0}^{n} x_{ch_i}\right)$ and standard deviation σ(x_ch); for

example, an image has three channel RGB (Red, Green, Blue), when we convert the image into an array or a Tensor, we gonna get a shape like (3, 30, 30) this shape is represented as (channel, high, wide), so each channel x_ch has shape (1, 30, 30).

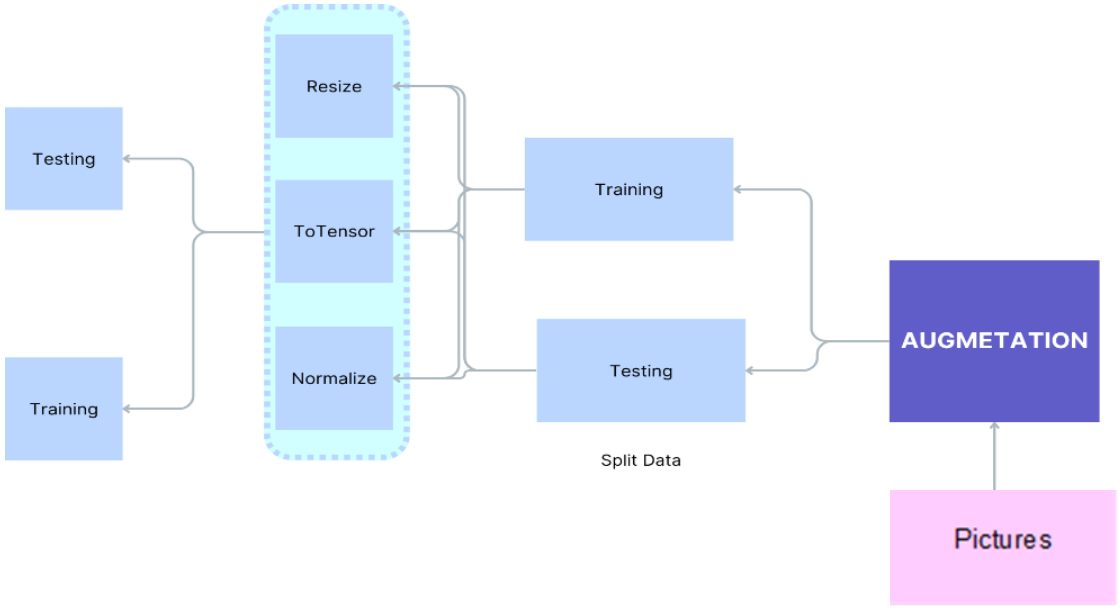


Figure 3. Preprocessing Flow Diagram

In "Figure 3," the data is divided into two sections: Training and Testing. The training data will be utilized for model training, while the testing data will be employed for model evaluation.

2.3 VGG16

VGG16 is a convolutional neural network architecture frequently employed for classification due to its superior performance. According to Taha [29], the integration of two 3x3 convolutional layers results in an effective receptive field of 5x5, encompassing a collection of learnable filters (or kernels), with each unit in the layer obtaining inputs from a localized neighborhood of units in the preceding layer. VGG16 comprises 13 convolutional blocks and 3 FC (Fully Connected) Layer. In this study, we used Pytorch to create VGG16 (not a pre-trained model). Pytorch is a Python library for creating deep learning models to solve specific problems. Resulting in substantial computational costs due to its extensive parameter requirements for training the architecture of VGG16 is seen in "Figure 4".

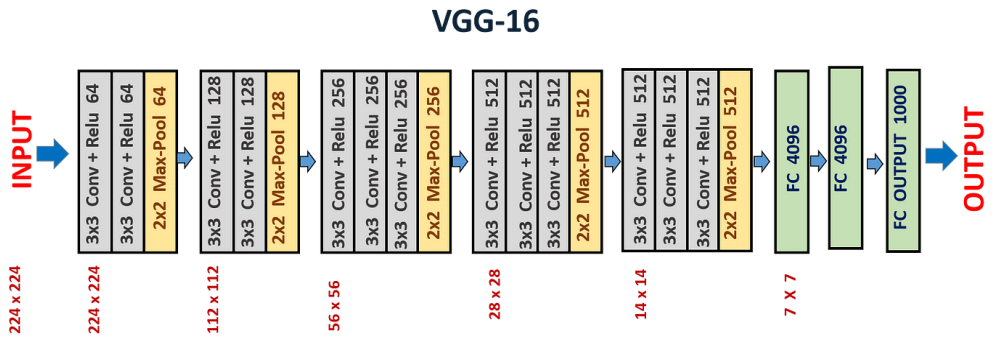


Figure 4. VGG16 Architecture

The VGG16 model underwent training for 60 epochs utilizing the Stochastic Gradient Descent (SGD) optimizer and a learning rate of 0.001, a standard setting for deep neural network training. The

utilized batch sizes were 32 for training and 64 for testing, facilitating quick weight updates and precise evaluation. The documented training duration was 0.498 sec/iteration , indicating that the training procedure was comparatively swift and effective. The integration of parameters with the VGG16 architecture yielded highly precise classification outcomes with little processing demands, rendering it ideal for cancer detection in medical imaging.

3. Result and Discussion

Experiments using the VGG 16 method obtained the following results :

Table 1. Average evaluation and training results

Metric	Value
Training Accuracy	0.9132589285714287
Loss Training (Cross-entropy)	0.25101307
Validation Accuracy	0.8517817982456141
Validation loss (Cross-entropy)	0.48813564
Execution Time	0.498 sec
Validation Precision	0.8181271803593233
Validation Recall	0.8487206423484619

The VGG16 model showed superior efficacy in categorizing the malignancy grade of breast cancer utilizing histological images. These results are evident in the recall and precision metrics, which indicate the model's ability to produce accurate positive predictions, table 1 show average recall and precision score are around 0.84 and 0.81, which this model can correctly predict the class of cancer image in around 0.84 and and the model can be trusted when model predict the class around 0.81. The average training accuracy attained 0.913, signifying that the model effectively learned patterns from the training data. Despite a relatively elevated average cross-entropy loss of 0.25 during training, the model's generalization capability remained unaffected, evidenced by a high validation accuracy of 0.851 and a minimal validation loss of 0.488. The results indicate that the model did not overfit and showed strong performance on novel data.

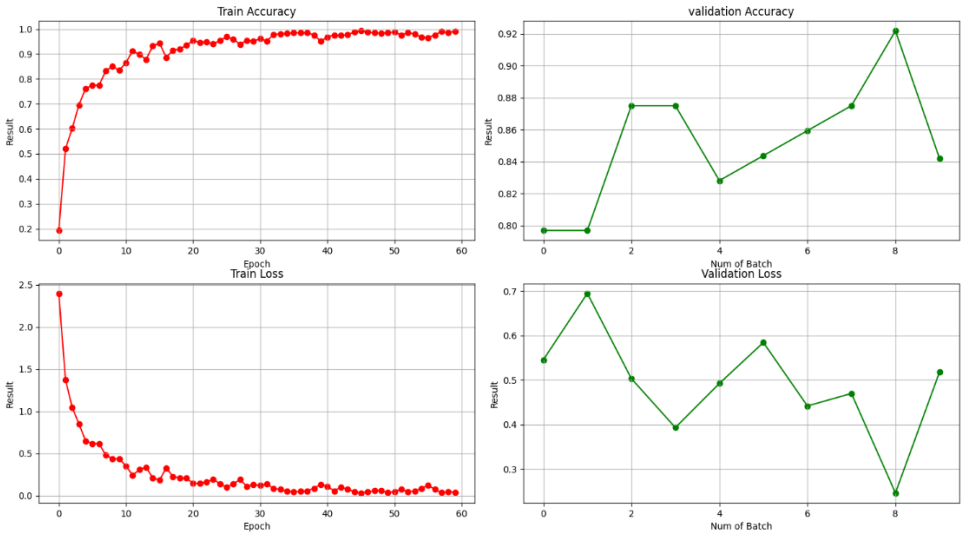


Figure 5 , Visualization of Training and Testing VGG 16 per batch

In figure 5, it can be seen that the VGG16 model can converge (approaching the global maximum), where the loss during training decreases significantly and the accuracy score increases significantly. This shows that the loss and accuracy converge in harmony. In figure

5, during validation, the loss and accuracy run in parallel, where there is no loss that is higher than the accuracy value during validation.

4. Conclusion

The use of the VGG16 method in this work has proven to be highly relevant for the task of histopathological breast cancer grading. The deep convolutional layers proficiently identified complex patterns and morphological characteristics in tissue samples, resulting in enhanced performance measures including elevated accuracy, precision, and recall. This model's capacity for effective generalization, despite a moderately high training loss, further supports its suitability for medical image analysis where diagnostic reliability is critical. VGG16's established architecture, pre-trained weights, and compatibility with transfer learning also make it a practical and accessible choice for research and clinical applications.

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