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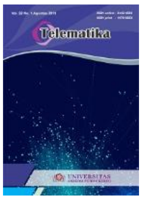

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Deep Learning for Histopathological Image Analysis: A Convolutional Neural Network Approach to Colon Cancer Classification

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ABSTRACT

Colon cancer is a type of cancer that attacks the last part of the human digestive tract. Factors such as an unhealthy diet, low fiber consumption, and high animal protein and fat intake can increase the risk of developing this disease. Diagnosis of colon cancer requires sophisticated diagnostic procedures such as CT scan, MRI, PET scan, ultrasound, or biopsy, which are often time-consuming and require particular expertise. This study aims to classify colon cancer based on histopathological images using a dataset of 10,000 images. This data is divided into 7,950 images for training, 2,000 for testing, and 50 for validation, aiming to achieve effective generalization. The Convolutional Neural Network (CNN) method was applied in this research with a relatively shallow architecture consisting of 4 convolution layers, 2 fully connected layers, and 1 output layer. Research results were evaluated by looking at the accuracy value of 99.55%, precision value of 99.49%, recall of 99.59%, prediction experiments on several images, and loss and accuracy graphs to detect signs of overfitting. However, this research has limitations in determining hyperparameters and layer depth, which was only tested from 1 to 5 convolution layers. Therefore, there are still opportunities for further development, such as applying unique feature extraction before the classification process.

INTRODUCTION

Cancer is a non-communicable disease characterized by the growth of abnormal cells that are uncontrolled and can move and attack between cells in body tissues (Ningrum & Rahayu, 2021). The World Health Organization lists that cancer is one of the main causes of death in the world. Colon cancer attacks the last part of the human digestive system, commonly called the large intestine. 90% of patients are older people over 60 years, although this disease can also attack any age (Rambe, 2019). Based on data from the Global Burden of Cancer (GLOBOCAN) released by the World Health Organization (WHO) stated that in 2020 colon cancer was ranked fourth with the number of cases 1,148,515 cases with a death rate reaching 576,858 people or equivalent to 5.8% (Ferlay J, Ervik M, Lam F, Colombet M, Mery L, Piñeros M, Znaor A, Soerjomataram I, 2020).

The environment and lifestyle influence the increase in the incidence of colon cancer. Diet plays an important role and can lead to colon cancer. The level of consumption of low-fiber foods and high consumption of protein and animal fats are factors that influence the cause of colon cancer or colon cancer (Puspitasari & Waluyo, 2021). General symptoms can usually be seen from changes in bowel habits, abdominal pain, bleeding in the rectum, and iron deficiency anemia, although other gastrointestinal diseases also have these symptoms (Puspitasari & Waluyo, 2021). However, not all patients exhibit the same set of symptoms, and diagnosing the presence of cancer is challenging without comprehensive diagnostic procedures like CT scans, MRIs, PET scans, ultrasounds, or biopsies. In numerous instances, individuals display minimal or no symptoms during the initial stages of cancer, as these become apparent only once the tumor reaches a significant size or the cancer has advanced to neighboring tissues or organs, sometimes making it too late for effective intervention.

Due to this, there is a crucial need for early detection. This implies that the sooner an individual receives a diagnosis, the greater the time available for the doctor to devise a suitable treatment plan, enhancing the patient's prospects of overcoming the illness. Presently, early diagnosis and the implementation of suitable treatments stand as the sole means to decrease the mortality rates associated with cancer. (Cancer-Symptoms and Causes-Mayo Clinic, 2021). This diagnosis can be achieved through X-rays, CT scans, and histopathological images obtained from the biopsy process on colon tissue (Singh & Singh, 2023). From these results, doctors or medical professionals can identify the type of cancer, guiding the subsequent treatment (Naito et al., 2021). However, manual classification is time-consuming, emphasizing the need for technology or systems to streamline the cancer classification process, with Machine Learning being one potential solution.

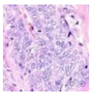
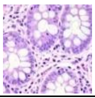
Machine Learning in the computer field has become a trend in information technology and has penetrated various sectors, including health (Fauzi et al., 2023). Machine Learning is applied in the health sector with diverse applications in pathology. These range from disease detection to the development of intelligent systems that, based on patient symptoms, can recommend appropriate medication (Ahmed et al., 2020). As a result, doctors and healthcare professionals can promptly receive the detection outcomes, facilitating quicker actions or interventions in disease management (Patil & Shankar, 2023).

Choosing an effective model in machine learning technology cannot be underestimated because this directly impacts prediction accuracy. This research aims to recommend an approach that adopts Convolutional Neural Network (CNN), a Deep Learning technique specifically designed for analyzing digital images. CNN has received wide recognition, especially in image classification, since 2012 (Felix et al., 2020). Several studies have shown that CNN is often used for image classification processes, such as (Anand et al., 2023; George et al., 2024; Hossain et al., 2023; Kumar & Panda, 2023; Oyelade et al., 2022; M. Zhang et al., 2024; S. Zhang et al., 2023). This fact is one of the main reasons for applying CNN in this research. Several studies have been conducted regarding colon cancer, including (Bhattacharya et al., 2023; Fahami et al., 2021; Gao et al., 2023; Gerwert et al., 2023; Kaya et al., 2022; Murugesan et al., 2023; Rajput & Subasi, 2023; Rathore et al., 2015; Talukder et al., 2022; Toğaçar, 2021). This research uses a dataset obtained from the Kaggle repository, consisting of 10,000 histopathology images, with 5000 images of Colon Adenocarcinoma (colon aca) and 5000 images of Benign Colon (colon n) (Lung and Colon Cancer Histopathological Images | Kaggle, n.d.). The image processing process is done by changing the image dimensions to 50x50 pixels to speed up the image recognition process. Next, this dataset was divided into 7,950 images for training, 2,000 for testing, and 50 for validation, aiming to achieve effective generalization in data classification. The results showed that the developed model successfully classified colon cancer accurately.

RESEARCH METHODS

The data used in this study is secondary data (public data) obtained from the Kaggle Repository, known as the LC25000 dataset. This dataset, created by Andrew A. Borkowski and colleagues and collected at the James A. Haley Veterans Hospital located in Tampa, Florida, has 10,000 images with 2 classes of colon cancer, and each class has 5,000 images with 768 x 768 pixels in size and in jpeg file format. The datasets were generated from original samples from appropriate sources and validated by the Health Insurance Portability and Accountability Act (HIPAA).

Table 1. Colon Cancer Dataset

No	*Image*	*Class*	*Amount*
1		Colon Adenocarcinomas	5.000
2		Colon Benign	5.000
		Total Dataset	*10.000*

The research stages started with data collection, image calling, preprocessing, dataset sharing, building CNN architecture, determining hyperparameters, conducting model training, model evaluation, and model implementation. This is done to get the suitable model in classifying colon cancer using histopathological images. The stages of the research can be seen in Figure 1.

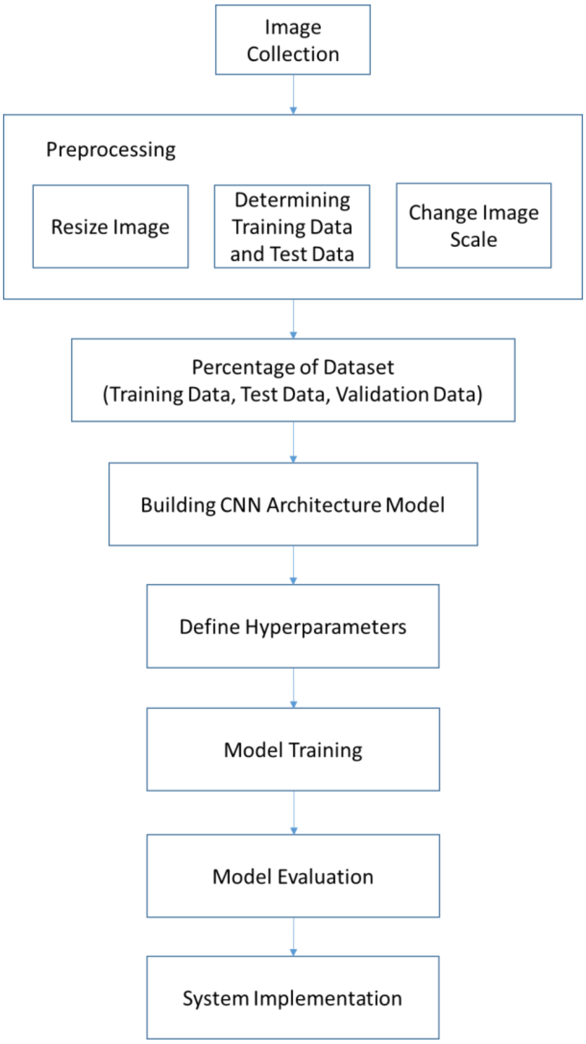


Figure 1. Research Stages

Based on the Figure 1, the stages of the research can be explained as follows:

1. **Image Collection**

The initial step in retrieving the images involves identifying the storage directory for the dataset to be utilized. This dataset comprises two classifications of colon cancer: Colon Adenocarcinoma and Colon Benign. Subsequently, all the necessary libraries for constructing the architectural model are imported. These include modules such as OS, pandas, glob, cv2, numpy, matplotlib, sklearn, tensorflow, hard, and others.

2. **Preprocessing**

This phase comprises three key steps. First, the image size is adjusted to 50x50 pixels, a measure taken to reduce the image dimensions and expedite the image recognition process during the modeling phase. Subsequently, the next step involves determining the proportion of training data to test data, with an 80:20 ratio. This signifies that 80% of the data is allocated for training, while the remaining 20% is reserved for testing. The final step entails modifying the scale of the image values. This adjustment is essential to represent the image as a 3D array or tensor, often referred to as a tensor, with values ranging between 0 and 255.

3. **Dataset Sharing**

During this phase, the dataset undergoes division into training, test, and validation sets, maintaining the predetermined distribution percentage of 80:20 for training and test data established in the earlier stage. This step is crucial to ensure effective generalization of the classifier. Consequently, the data is categorized into training, testing, and validation. Each category comprises 7950 training data samples, 2000 test data samples, and 50 validation data samples drawn from the overall pool of training data.

4. **Building Model**

During this phase, the process involves specifying the number of architectural layers to be employed, commencing with defining the parameters for the input layer. This layer receives image data transformed into a three-dimensional matrix, with each dimension corresponding to the red, blue, and green values (Felix et al., 2020). The quantity of convolution layers constitutes the central component of CNN. The operations mimic traditional convolution processes commonly employed in image processing, involving a kernel and sub-images. In CNN, the typical size of the kernel is 3x3. Subsequently, a convolution operation is executed for each sub-image matching the size of the kernel (Nugroho et al., 2020). The pooling layer follows the convolutional layer in the CNN architecture. This layer comprises filters with specific sizes and strides. The shift for each operation is defined by the number of steps intended to traverse the feature map or activation map area (D. Zhang et al., 2020). The fully connected layers represent a classification process within a multi-layer perceptron (MLP). In these layers, every neuron establishes complete connections with all activations from the preceding layer (Candra & Prapanca, 2020) and output layers. The steps involved in making the CNN model are described in more detail in Table 2.

Table 2. CNN Architecture

Layer		*Size and Filters*	*Kernel Size*	*Activation*	*Pooling size*
1	Image	50 x 50 x 3	-	-	-
	Convolution	16x16	2x2	relu	-
	Max pooling	-	-	-	2x2
2	Convolution	32x32	2x2	relu	-
	Max pooling	-	-	-	2x2

Layer		*Size and Filters*	*Kernel Size*	*Activation*	*Pooling size*
3	Convolution	64x64	2x2	relu	-
	Max pooling	-	-	-	2x2
4	Convolution	128x128	2x2	relu	-
	Max pooling	-	-	-	2x2
Flatten		-	-	-	-
Dropout		0,2			
Dense		200		relu	
Dropout		0,3			
Dense		500		relu	
Dropout		0,4			
Dense		2		sigmoid	

The research was conducted using four convolution layers with an image input of 50x50 pixels according to the image size that had been initiated earlier. All convolution operations on each layer use a 2x2 kernel size starting from the first layer to the last layer, but with different filter sizes for each layer starting from filter 16 for the first layer, filter 32 for the second layer, filter 64 for the third layer and filter 128 for the fourth layer. As for the activation at each convolution layer, it used ReLu activation and pooling layer using max pooling with a size of 2x2.

Furthermore, zero-padding is applied to each convolutional process, involving the addition of zero values on all sides of the input. The resulting output from max pooling is transformed into a two-dimensional vector following the convolutional process. The hidden layer employs dense with a vector size of 200 and a dropout rate of 0.2, alongside another dense layer with a vector size of 500 and a dropout rate of 0.3, utilizing the ReLU activation function. The output layer has as many dense layers as there are classes in the dataset (2 in this case), accompanied by a dropout rate of 0.4 and a sigmoid activation function. The architectural development of the CNN model is illustrated in the figure 2.

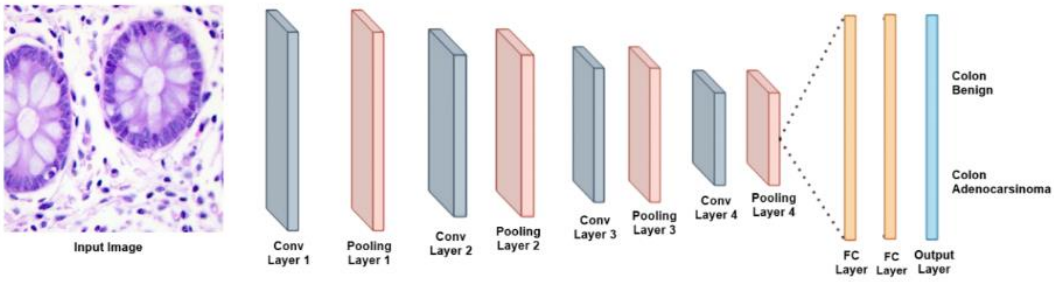


Figure 2. CNN Architecture Model

5. Determination of Hyperparameter

At this stage, hyperparameters are determined for the architectural model being built, but these parameter settings are carried out outside the construction of the CNN architectural model, such as determining the type of optimization, type of probabilistic loss, and measurement of the evaluation model to be used. In this research, hyperparameter determination was carried out using many experiments until high accuracy results were found.

6. Model Training

During the model training phase of the constructed architecture, the determination of hyperparameters includes specifying the number of epochs. The number of epochs determines how many times the learning algorithm iterates through the complete training dataset. The batch size, representing the number of samples processed before updating the model, is also defined. In this case, the chosen values are 50 epochs and a batch size 32.

7. Model Evaluation

The next stage is the model evaluation stage, which functions to see the performance of the model that has been built, which can be seen from the accuracy value obtained, predictions for testing image samples based on the model, viewing graphs generated from iterations of model training, and confusion matrix tables.

$$Accuracy \quad = \frac{TP+TN}{TP+FP+TN+FN} \; x \; 100\% \qquad (1)$$

Formula (1) is used to calculate the accuracy rate of a Convolutional Neural Network model in classifying histopathological images of the colon for cancer detection.

$$Recall \quad = \frac{TP}{TP+FN} \; x \; 100\% \qquad (2)$$

The formula (2) calculates the recall rate or accuracy in identifying the positive class (colon cancer) by the model. Recall measures the proportion of true positives correctly identified by the model out of all actual positive cases.

$$Precision \quad = \frac{TP}{TP+FP} \; x \; 100\% \qquad (3)$$

This formula (3) is used to calculate the precision rate of the classification model. Precision measures the proportion of true positives identified correctly by the model out of all instances identified as positive. Precision measures how well the model avoids assigning a positive label to examples that are negative.

8. System Implementation

The last stage is the implementation stage of the architectural model that has been built into a prediction system, where this system will be made using Flask web development using the Python programming language. As a Python microframework, Flask provides flexibility in organizing web behavior. It allows extensions to add unavailable features and components by default, thereby increasing the ease of developing structured web applications (Mulyo & Sucipto, 2023).

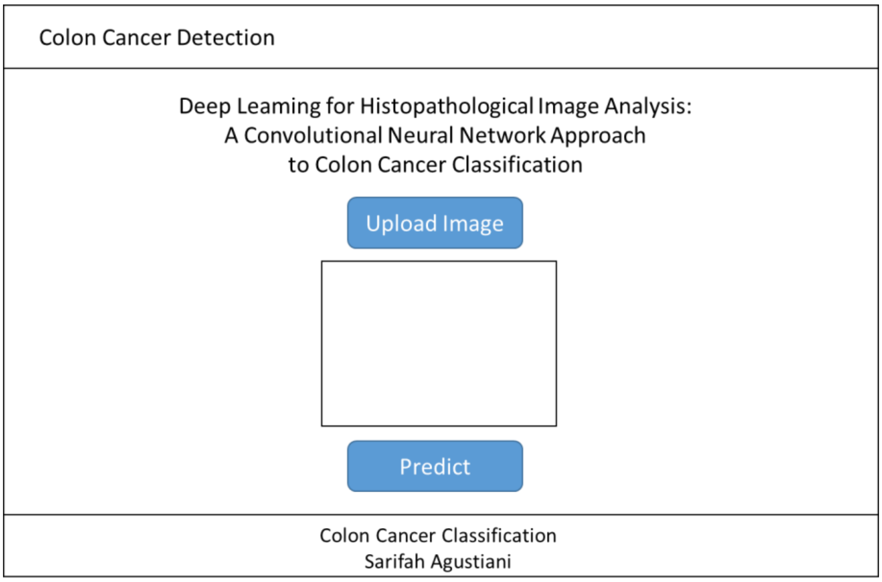


Figure 3. System Interface Design

RESULTS AND DISCUSSION

This study uses the CNN method with a modified architecture to classify colon cancer based on histopathological images into two classes, namely Colon Adenocarcinoma and Colon Benign. In this study, several pilot scenarios were conducted to measure the success rate of the proposed method. This test is carried out by testing the number of convolution layers, optimization types, data sharing, and transfer learning methods: MobileNet, DensNet, VGG16, and ResNet50. The following are the results of the tests that have been carried out in this study:

1. Convolution Layer Number Test Results

In this evaluation, the testing involves varying the number of convolution layers in the model. The purpose is to compare the accuracy values sequentially, considering configurations with 1, 2, 3, 4, and 5 layers for the proposed CNN architecture. The outcomes of this examination are detailed in Tables 3, 4, 5, and 6.

Table 3. Convolution Layer Number Test Results

No	*Number of Convolution Layers*	*Accuracy*
1	1	0.4964999854564667
2	2	0.9670000076293945
3	3	0.9890000224113464
4	**4**	**0.9955000281333923**
5	5	0.4964999854564667

Table 3 shows that the highest accuracy value resulted from the use of 4 convolution layers with an accuracy value of 99.55%. From the table, it can also be seen that the use of too few or too many layers affects the accuracy value produced, especially in the tests applied to the case of this study. This can be seen from the accuracy results obtained by testing using 1 convolution layer and 5 convolution layers, which produced the same accuracy value of 49.64%. The accuracy values generated from the two tests have a range of values that are quite far from those produced by tests using 2, 3, or 4 convolution layers, which are quite stable in the 90% and above range.

2. Optimization Type Test Results

This scenario is done by testing the type of optimization used in the test model that produces the best accuracy value in the previous test scenario, namely a model with 4 convolution layers according to the proposed model. This is done to compare the accuracy values when using adam, nadam, adadelta, adagrad, adamax, RMSprop , and SGD optimizations sequentially for the proposed CNN architecture. In this test, the only difference is the use of the optimization type. It aims to see the effect of the use of optimization. The following are the results of testing on models with different types of optimization.

Table 4. Optimization Type Test Results

No	*Optimization Type*	*Accuracy*
1	**Adam**	**0.9955000281333923**
2	RMSProp	0.9940000176429749
3	Nadam	0.9940000176429749
4	Adamax	0.9919999837875366
5	SGD	0.9769999980926514
6	Adagrad	0.7070000171661377
7	Adadelta	0.5034999847412109

Table 4 shows that Adam's optimization produces the highest accuracy value compared to other optimizations. However, other optimizations also have no less high accuracy, namely in the 97-99% range, except for Adagrad optimization, which has an accuracy of 70.70%, and Adadelta, which produces the lowest accuracy. That is 50.34%.

3. Test Results Percentage of Data Sharing

In this particular scenario, the testing continues using the proposed model, with alterations introduced in training and test data distribution. This adjustment is repeated three times, each with different data ratios: 9:1, 8:2, and 7:3. The objective is to assess the performance of the proposed model and identify which data ratio yields the highest accuracy value. The subsequent results outline the outcomes of the model testing under various data distribution scenarios.

Table 5. Test Results of the Percentage of Data Sharing

No	*Data Percentage*	*Accuracy*
1	9:1	0.9909999966621399
2	**8:2**	**0.9955000281333923**
3	7:3	0.9950000047683716

Table 5 shows that the difference in the percentage of data sharing can produce different accuracy values. In this scenario, the use of 8:2 produces the highest accuracy value of 99.55%, with further accuracy obtained from a comparison of 7:3 with an accuracy value of 99.50%, and a comparison of 9:1 produces an accuracy value of 99.09%.

4. Transfer Learning Method Test Results

At this stage, a trial using the transfer learning method was conducted to determine the best accuracy between the proposed method and the transfer learning method. Transfer learning architecture methods include Resnet50, VGG16, Densnet121, and Mobilenet. The results of the experiments carried out in Table 6.

Table 6. Test Results of Transfer Learning Method

No	*Transfer Learning Method*	*Accuracy*
1	VGG16	0.9725000262260437
2	DensNet	0.9559999704360962
3	MobileNet	0.926999986171722
4	Resnet	0.925000011920929
5	**Proposed Method**	**0.9955000281333923**

Table 6 shows that the architecture of the proposed method has a higher accuracy value of 99.55% compared to the transfer learning method. In this test, the highest accuracy produced by the transfer learning method was obtained by the VGG16 method with an accuracy of 97.25%, and the lowest accuracy was obtained from the ResNet method with an accuracy of 92.50%.

5. Model Evaluation

The research outcomes encompass multiple test scenarios, including comparisons of accuracy values based on the number of convolution layers employed, the optimization type, and the percentage of data allocation. Additionally, the study explores comparisons between the proposed CNN non-transfer learning method and the transfer learning approach. The findings reveal that the most favorable results are achieved with the proposed method, attaining an accuracy value of 99.55%.

To assess the effectiveness of the constructed model, its performance can be evaluated through several metrics. These include examining the accuracy values, predicting outcomes for testing image samples using the model, observing graphs generated from iterations of model training, and reviewing confusion matrix tables.

a. Model Evaluation with Predicted Results

Besides being able to be evaluated based on the accuracy value, the performance of the proposed CNN method can also be seen from the results of image prediction. In this case, the proposed method can predict the image well, as shown in Figure 4.

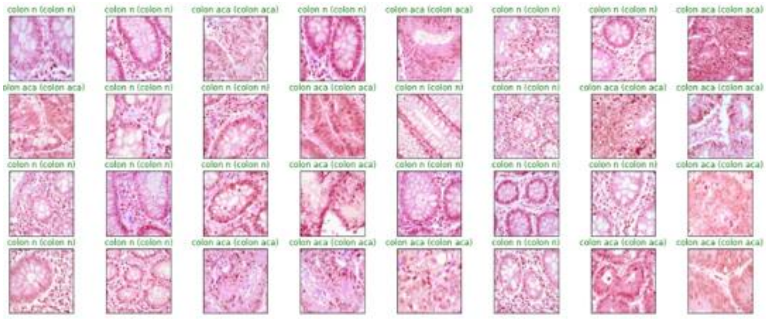


Figure 4. Prediction Results of Colon Cancer Image

Figure 4 illustrates several predictions from the CNN model introduced in this study. The image provides details regarding the classifications of colon cancer, specifically "colon aca" for the colon adenocarcinoma class and "colon n" for the benign colon class. In this representation, correct predictions aligning with actual values are indicated in green, while incorrect predictions are highlighted in red. Overall, the proposed model demonstrates accurate image predictions, as evidenced by the prevalence of correct predictions depicted in green.

b. Model Evaluation with Loss Graph and Accuracy

The following is a graph of accuracy, val accuracy, loss and val loss generated from the proposed method.

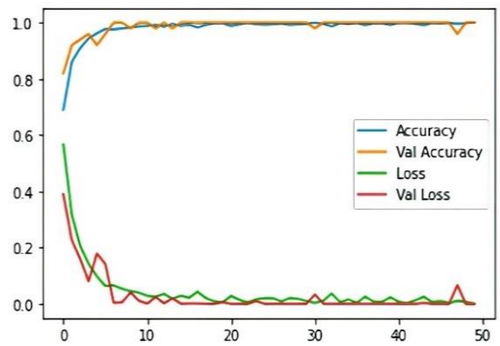


Figure 5. Graphics of the Proposed Method

Figure 5 presents a graph depicting the accuracy values across various epochs. From the graph, it can be deduced that the accuracy values for each epoch in the average training data exhibit a consistent and steady increase. Starting from the initial epoch with an accuracy value of 0.6907, the values progressively improve, reaching a high accuracy value of 0.9999 by the 50th epoch. This indicates an improvement in the proposed model, as higher accuracy values signify better performance. Similarly, the accuracy values for the validation data exhibit stability with some fluctuations observed.

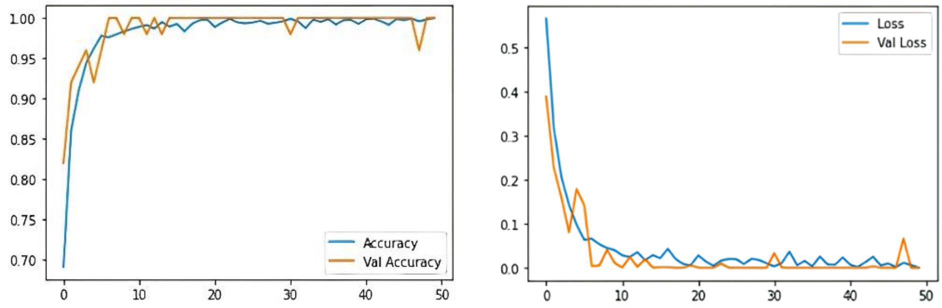


Figure 6. Accuracy Graph and Loss Graphs

The loss value in the test data produced in this study shows that it is decreasing where the first loss value is 0.5656 to 0.0058 towards the last epoch. The smaller loss value indicates a low error rate. In this case, the loss value in the validation data has increased or decreased. The decline at certain epochs is relatively stable.

c. Evaluate Model with Confusion Matrix

The evaluation results are further illustrated through the confusion matrix table. This table delineates the count of positive predictions that accurately correspond to true positive values, denoted as true positives (TP), and the count of negative predictions that align with true negative values, known as true negatives (TN). Additionally, it highlights the count of positive predictions that inaccurately match actual negative results, termed false positives (FP), and the count of negative predictions that inaccurately correspond to actual positive values, referred to as false negatives (FN). Below is the confusion matrix table generated in the course of this study.

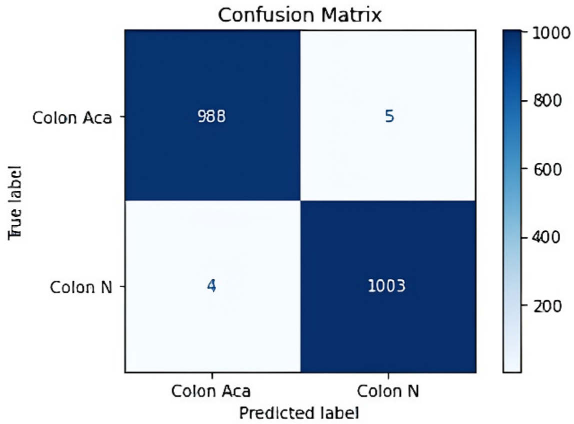


Figure 7. Confusion Matrix Value

Based on the results of the confusion matrix in Figure 7, it can be seen from the amount of test data used, which is as many as 2000 images. From 1007 images for the colon n class, 1003 images were correctly detected, and the aca colon detected 4 other images, while for the colon aca class, 988 images were correctly detected and detected colon n as many as 5 images. From this confusion matrix value, manual calculations can be carried out to determine the accuracy, recall, and precision values as follows:

$$
\begin{aligned}
Accuracy &= \frac{988 + 1003}{988 + 5 + 1003 + 4} \text{ x } 100\% \\
&= \frac{1991}{2000} \text{ x } 100\% \\
&= 99.55\%
\end{aligned}
$$

$$Recall \quad = \frac{988}{988+4} \text{ x } 100\%$$
$$= 99.59\%$$
$$Precision \quad = \frac{988}{988+5} \text{ x } 100\%$$
$$= 99{,}49\%$$

6. System Implementation

From the results of tests conducted on research with the proposed CNN architecture, we obtained a model that can be used to be implemented into a program system. Programs created using the Python programming language with the Flask Python Web Development framework. The test is carried out using one of the images in the colon adenocarcinoma class, then click Predict to see the prediction results generated from the system that has been created. Testing the system implementation is conducted to compare the outcomes of the available image types with the predictions generated from the implemented model. The results of the system implementation are as follows:

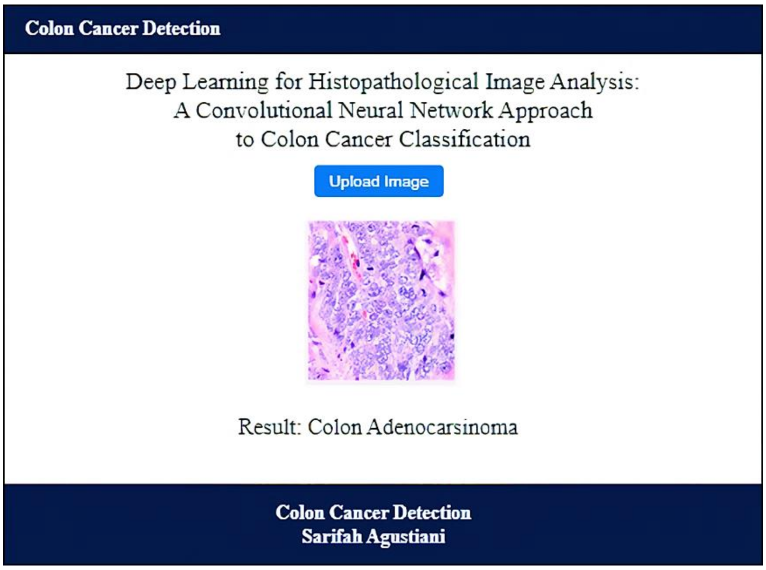


Figure 8. Test Results for Colon Adenocarcinoma Class

Figure 8, shows the results obtained from testing the system. Based on these tests, it can be seen that the predictions generated by the system are in accordance with the type of image from the class that is used as an example case. With the implementation of this system, it is hoped that it can help doctors or health analysts to diagnose colon cancer based on histopathological images with a faster and more accurate time.

CONCLUSIONS AND RECOMMENDATIONS

From the results of research into the classification of colon cancer based on histopathological images using the Convolutional Neural Network (CNN) method, several significant conclusions were found. First, the use of CNN methods in modeling requires a customized architecture, as seen in the integration of 4 convolution layers with filter sizes of 16, 32, 64, and 128 respectively. Setting the kernel at a standard size of 2x2 with the addition of two layers provides impressive performance with 99.55% accuracy. Second, the application of hyperparameters in the proposed CNN model plays an important role in producing good results. The use of Adam optimization with the binary cross entropy loss type is proven to be more effective than other variations such as Nadam, Adamax, RMSprop, SGD, Adadelta, and Adagrad. Third, experiments with an epoch configuration of 50, batch size 32, and image resolution size of 50x50 show a significant

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increase in performance, especially in increasing the accuracy value. Moreover, the proposed CNN method is not only effective in colon cancer classification but can also be successfully implemented in a web-based system to classify this type of cancer with high accuracy.

Several steps can be considered to develop this research further. First, exploring more complex CNN architectures or using pre-trained models such as ResNet or Inception can help improve model performance in better classifying colon cancer histopathology images. Optimization of other hyperparameters, such as learning rate or momentum, must also be considered to improve model convergence and obtain better results.

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