

# Multi Paths Technique on Convolutional Neural Network for Lung Cancer Detection Based on Histopathological Images

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## ABSTRACT

Lung cancer is the leading cancer cause of death and it's survival rate is very small. An early diagnosis is a good solution to increase the survival rate for lung cancer. To diagnose lung cancer using deep learning we present a convolutional neural network to diagnose three types of lung cancer (Adenocarcinoma, Benign and Squamous) based on histopathological images. The proposed model consists of a main path and three sub-paths. The main path works to extract the small features and creates feature maps at low-level. As for the sub-paths is responsible for transferring the medium and high levels feature maps to fully connected layers to complete the classification process, also the VGG16 was prepared to compare it with the performance of the proposed. After training the models and testing them on 1500 images, we obtained an overall accuracy of 98.53% for the proposed model and 96.67% for the VGG16 model. The proposed model achieved a sensitivity of 97.4%, 99.6% and 98.6% for Adenocarcinoma, Benign and Squamous respectively. We can say that it is not always necessary for the used to be very deep to diagnose histopathological images, and the most important thing is to create a sufficient number of feature maps at different levels.

**Keywords - Deep Learning, Convolutional Neural Networks, Lung Cancer Detection, Transfer Learning.**

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## I. INTRODUCTION

Cancer is a global health concern that eventually kills millions of people every year [1,16]. Cancer contributes an abnormal and uncontrollable division of cells. According to the World Health Organization (WHO), ~ 9.6 million people died in 2018 due to cancer [2]. What is threatening, cancer death accounts for ~ 16% of the total death globally [2]. Besides, statistics made by WHO in 2018 recorded more than 18 million new cases of cancer worldwide. Among them, lung cancer contributes for 11.69% of total recorded cancer cases [2].

Lung cancer is one of the most dangerous types of cancer that shows a little survival rate of ~ 18.6%, as compared to 64.5% of colon cancer, 89.6% of breast cancer, and 98.2% of prostate cancer [3]. Not only that, lung cancer owing to its hazardous effect has received attention of researchers and agencies. It has been split into several types, and scientists have classified it into two main groups; Small Cell Lung Cancer (SCLC) and Non-Small Cell Lung

Cancer (NSCLC). The NSCLC group constitutes three types: (1) Squamous Cell Cancer (SCC), (2) Lung Adenocarcinoma, and (3) large cell cancer [4]. Of course, each type has its own characteristics and different methods of treatment.

To this, it is crucial to increase the rate of survival for lung cancer and to impede its spreading and worldwide statistics. As a result, monitoring of lung cancer using an early diagnosis technologies is essential for controlling this deadly disease. There are many approaches to diagnose lung cancer using several techniques. Efforts to diagnose lung cancer using the low dose CT scan are succeeding [26]. This validated method could investigate the abnormal areas in the lung that may be cancerous. For sure, it has saved the life of many cancerous cases [26]. However, this approach consumes long time until the cancerous case are confirmed and requires a group of specialists who are highly skilled and experienced to review the images, which in turn doubles the costs and delay in treatment. Furthermore, the investigation of

histopathological images requires an expert and pathologist to precisely distinguish normal and abnormal tissue through the shape and size of the cell, the shape and size of the cell nucleus, and places of cells in the tissue [5]. In the recent past, the revolutionary technologies of artificial intelligence and image processing make the diagnosis of lung cancer easier and concise using artificial intelligence algorithms to analyze the histopathological images.

In recent years, numerous research groups are progressing in the field of lung cancer diagnosis using machine learning based on hisopathological images [6-14]. In this regards, Zhu Y. et al. in [6] Method to select texture feature of solitary pulmonary nodules and used a genetic algorithm to select best features and classify them using Support Vector Machine. J. Dcruz et al., 2015 [7] provided a genetic algorithm and neural networks to extract features of X-Ray and CT scan images and to classify them into cancerous and non-cancerous categories. Atsushi Teramoto et al. in [8] used a CNN to classify three types of lung cancer SCLC, SCC and LA on dataset consisting of 298 images, they also used a cross validation and data augmentation to increase the classification accuracy. After training the network, they obtained an accuracy of 71.1%. QingZeng Song et al. used a CNN, Deep Neural Networks and Stacked Auto-encoder in [9] to classify CT images of two classes benign and malignant. After training the networks, the CNN achieved the best results, as accuracy was 84.15%, sensitivity 83.96% and specificity 84.32%. Lakshmanaprabu and his team [10] used an Optimal Deep Neural Network to analyze CT images and used deep learning to extract features from the images and then classify them as whether a malignant or benign. They obtained an accuracy of 92.2%. Amazingly, S. Wang and his coworkers (2020) [11] implemented the transfer learning technique to train a Convolution Neural Networks (CNN) on 2054 CT images for four classes of lung cancer Invasive Adenocarcinoma(IA), Adenocarcinoma in Situ(ISA), SCC, and SCLC.

Their amazing results summarized in achieving ~85.71% accuracy after training and testing the network on 168 images only. Fahdi Kanavati et al. [12] design a CNN model based on Efficient Net architecture [13], and the model was trained via transfer learning and weakly-supervised learning on a dataset of 3554 Whole Slide Images(WSI) and they got Area Under Curve(AUC) and Receiver Operating Characteristics(ROC) for lung carcinoma and non-neoplastic of 0.975, 0.974, 0.988 and 0.981 respectively.

Asuntha A. [14] they used great ways to extract features like Histogram of Oriented Gradients, Wavelet Transform-based Features, Local Binary Pattern, Scale Invariant Feature Transform and Zernike Moment, they also used Fuzzy Particle Swarm Optimization to select the best features and classify them using deep learning.

The main objective of this paper is to design a Convolutional Neural Networks (CNN) capable to extracting and generating low-level and high-level features

map in large number with a suitable depth, and to diagnose three types of lung cancer (Adenocarcinoma, Benign and Squamous) based on the histopathological images with high accuracy to contribute to the development of Computer Aided Diagnose field.

## II. METHOD AND DATASET

### 1. DATASET

In this paper we used a dataset of 15000 lung tissue images from LC25000 dataset [15]. The lung cancer dataset contains three subset. Subset1 contains 5000 digital images of histopathological slides for benign lung tissue. Subset2 contains 5000 digital images of histopathological slides for lung squamous cell carcinoma. Subset3 contains 5000 digital images of histopathological slides for lung adenocarcinoma. We split dataset into 9000 images for training (3000 images for each class), and 4500 for validation (1500 images for each class) and 1500 images for testing (500 images for each class).

### 2. CONVOLUTIONAL NEURAL NETWORKS

Convolutional Neural Network (CNN) is a type of neural networks that are widely used in the field of Computer Vision. Such as image recognition, image classification, object detection and facial recognition. It had a great success in robots vision and self-driving cars. In order to form CNN, four basic building blocks are required.

#### 2.1 CONVOLUTION LAYER

The goal of using convolution layer in CNN is to extract features from images or videos by applying difference filters on the image array pixels. When applying the filter or so-called kernel, which is a single array that be 3x3, 5x5 or 7x7 on the image array pixels, the dot product process occurs and the result of the process is combined to create one pixel in a new matrix[22], which is called a convolved feature or Feature Map(FM). To find out the dimensions of FM we can calculate it using the following equations.

$$H_o = \frac{H_i - F_h + 2P}{S} + 1 \quad (1)$$

$$W_o = \frac{W_i - F_w + 2P}{S} + 1 \quad (2)$$

In these equations  $H_o$  and  $W_o$  are the length and width of FM emerging from the Convolution layer.  $H_i$ ,  $W_i$  are the length and width of FM entering to the Convolution layer.  $F_h$ ,  $F_w$  are kernel size,  $P$  indicates the padding added around the array of the input image.  $S$  is the amount of step the filter moves on the input array. Each Convolution layer has a number of parameters or so-called weights. Weights are calculated by using the following equation.

$$\omega = F \times ((i \times h \times w) + 1) \quad (3)$$

Whereas  $F$  is output FM,  $i$  input FM,  $h$  and  $w$  are kernel size and 1 is bias for each FM.

## 2.2 RECTIFIED LINEAR UNIT (RELU)

ReLU function[23] is used to convert all pixels whose value is less than zero into zero, which facilitates the computation process and reduce the time and cost of training.

## 2.3 POOLING

Pooling or down-sampling layer is used to reduce the dimension of FM while keeping the important information. The most popular type of pooling is the max pooling which takes the height values from the FM array by applying pooling array on it. And the average pooling which takes the average values from the FM array when applied on it.

## 2.4 FULLY CONNECTED LAYER (FCL)

FCL is the last part of CNN architecture and has been called that name because all neurons are connected to each other. FCL is the part responsible for classification task where it receives FM that was extracted in the previous layers and converted to a vector and then do the classification process. So we can have divided CNN into two part, the first part (Convolution, ReLU [23] and Pooling) is responsible for extraction feature and the second part (FCL) is responsible for classification task. To calculate weights for FCL we use the following equation.

$$\omega = (n + 1) \times m \quad (4)$$

Whereas m is output nodes, n is inputs FM to layer and 1 is bias for each node. Figure 1 demonstrates the basic architecture of a CNN.

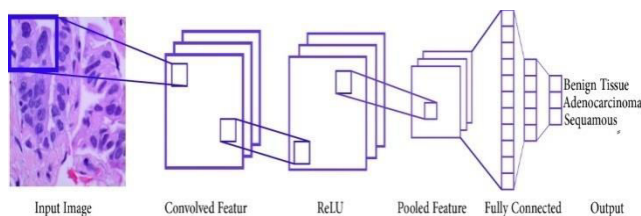


Fig.1. Basic CNN Architecture.

## III. PROPOSED MODEL

The number of Feature Maps (FM) plays an important role in improving the performance of the CNN model, and it is known to increase the FM numbers, the depth of the model must be increased by increasing the number of filters in the Convolution layers which gives us greater accuracy for classification [22]. But several studies have shown that increasing the depth of CNN model on biological images does not always improve the performance of the model [25]. For this reason, the proposed model which was constructed in affective manner, was presented to generate the maximum amount of FM at various level. The bottom convolution layers are responsible for learning and extracting high-level features, while the top convolution layers are responsible for extracting the low-level features [18], so the proposed model is built of one main path and three sub-paths. From the main path 768 FM at low-level

will be generated, and this important for identifying the tiny details. While sub-paths will transfer FM with different levels from the convolution layers to fully connected layers, and then number of FM that will be transferred is 672 with high and medium levels, which is necessary for the large and medium details in the images. The traditional way in which CNN models are built is that number of FM coming out of the Convolution layer is greater than the number of FM entering into the same layer and in this case the convolution layer may produce an number of weak and bad FM which is useless and consume additional energy in computational process. But in the proposed model, the number of FM entering the convolution layer is greater than the number of FM coming out of the same layer. In this way we ensure that a large number of weak and bad FM are not produced and that is no benefit from them. Each Block consists of three layers Convolution, Max pooling and Dropout [17]. In the main path, the number of filters in the convolution layers starts with 32, then 64, 128 and filly 256 filters.

We have used Global Average Pooling to improve model performance and help to prevent overfitting and create one feature map for each category in the last layers [21].Figure 2 show the architecture of the proposed model.

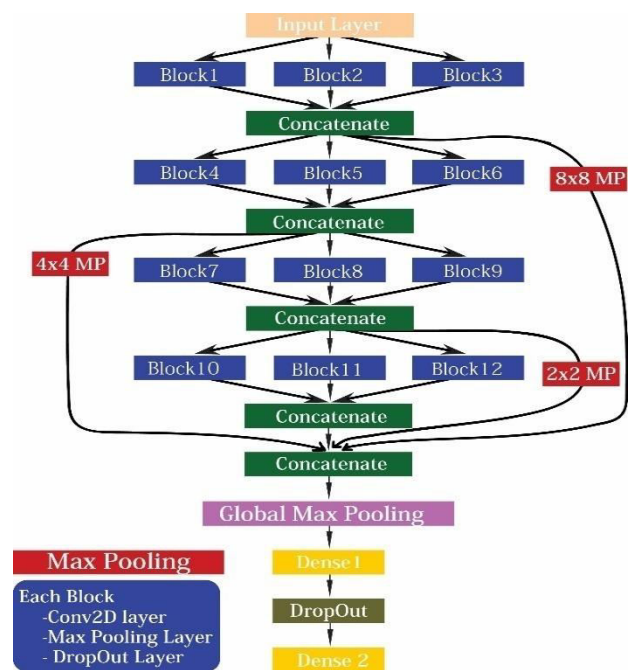


Fig. 2. Architecture of Proposed Model.

## 1. IMPLEMENTATION

Proposed model is implemented using keras[19], and we used dropout[17] with 0.05 in features extraction part and 0.1 in fully connected part. Adam optimizer[20] is used with learning rate of  $1e^{-4}$ . The model has 4.278M parameters and trained for 50 epochs with a batch size of 32. The training process of the model takes 13 hours on computer with I5-3317U CPU at 1.7 GHz and 4 GB memory.

## 2. TRANSFER LEARNING

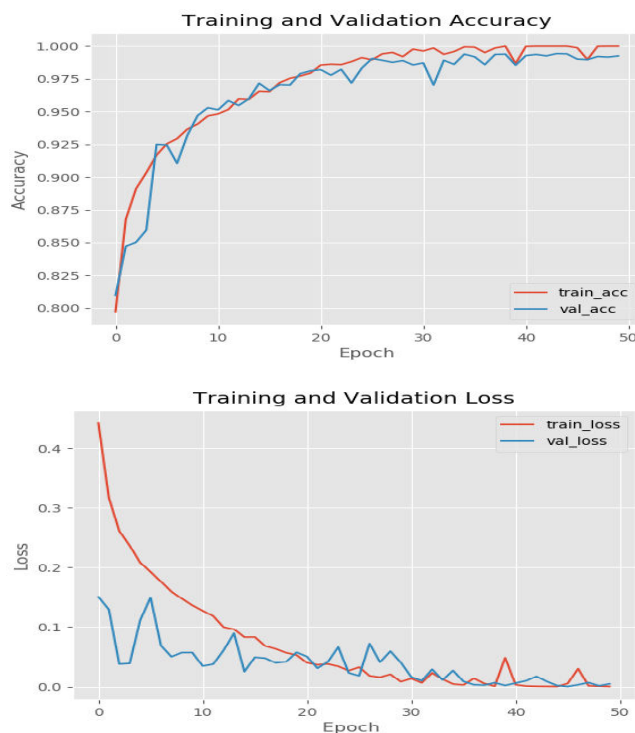
Transfer learning is technique for reusing the weights of pre-trained network on a task similar to the current task as classification, and in this study we has prepare a Visual Geometry Group (VGG16) [24] model and train this model on the same dataset that we used in our model, for making a comparison between the two models performance.

## 3. RESULTS

After training and testing the model in 1500 images, we obtained the accuracy and loss which are shown in Table 1. The accuracy and the loss curves that shown in Figure 3, where the accuracy curves are on the left and loss curves are on the right.

**Table.1.** Accuracy and loss values for proposed and Vgg16 models.

Metrics	Models	
	VGG16	Proposed
Training Loss	0.000170	0.0000036
Validation Loss	0.003479	0.004649
Testing Loss	0.328927	0.006328
Training Accuracy	99.92 %	100 %
Validation Accuracy	97.80 %	99.24 %
Testing Accuracy	96.67 %	98.53 %



**Fig. 3.** Accuracy and loss curves of proposed model.

In the field of Machine Learning, many methods are used to evaluate model performance. One of these method is a Confusion Matrix, which is a table that shows the performance of the classification model, and by using it we can calculate different metrics to measure model performance such as accuracy, sensitivity, specificity, and precision based on four different values calculated from confusion matrix which are True Positive (TP) which

represent the cases that belong to the class Adenocarcinoma and were classified within the class Adenocarcinoma. False Negative (FN) which represent the cases that belong to the class Adenocarcinoma and were classified under other classes. True Negative (TN) which represent the cases that belong to other classes and were classified within them. False Positive (FP) which represent the cases that do not belong to the class Adenocarcinoma and were classified within the class Adenocarcinoma. From the previous values, we will calculate the evaluation metrics to measure the performance of the model which are overall accuracy, accuracy for each class, sensitivity which is the percentage of cases with Adenocarcinoma were correctly identified. Specificity which is the percentage of cases of other classes were correctly classified. Precision which is the percentage of the correctly predictions from the total predictions that were classified as Adenocarcinoma.

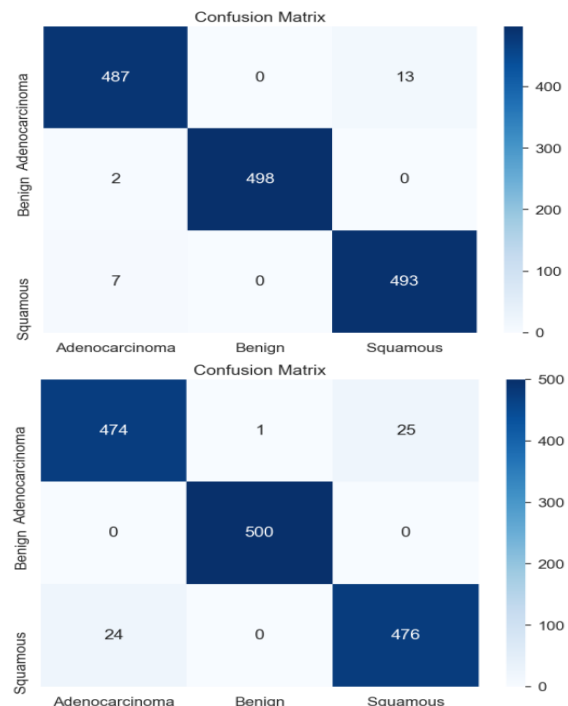
Overall Accuracy = Correct classified / total classified

$$Accuracy \text{ for each class} = \frac{TP+TN}{TP+TN+FP+FN} \quad (5)$$

$$Precision = \frac{TP}{TP+FP} \quad (6)$$

$$Sensitivity = \frac{TP}{TP+FN} \quad (7)$$

$$Specificity = \frac{TN}{TN+FP} \quad (8)$$



**Fig. 4.** Confusion matrixes for proposed model (left) and VGG16 model (right)

**Table.2.** Four values of proposed model.

Class	TP	FN	TN	FP
Adenocarcinoma	487	13	991	9
Benign	498	2	1000	0
Squamous	493	7	987	13

**Table. 3.** Four values of VGG16 model.

Class	TP	FN	TN	FP
Adenocarcinoma	474	24	976	26
Benign	500	1	999	0
Squamous	476	25	975	24

From previous values, we calculated overall accuracy and specificity, precision accuracy and sensitivity for each class and write down in the Table.4.

**Table. 4.** Evaluation Metrics of proposed and VGG16 models.

Metrics	Models	
	VGG16	Proposed
Overall Accuracy	96.67	98.53
Adenocarcinoma Accuracy	96.67	98.53
Benign Accuracy	99.93	99.87
Squamous Accuracy	96.7	98.67
Adenocarcinoma Sensitivity	94.8	97.4
Benign Sensitivity	100	99.6
Squamous Sensitivity	95.2	98.6
Adenocarcinoma Specificity	97.6	99.1
Benign Specificity	99.9	100
Squamous Specificity	97.5	98.7
Adenocarcinoma Precision	95.18	98.18
Benign Precision	99.8	100
Squamous Precision	95	97.43

#### 4. DISCUSSION

The proposed and the VGG16 models were tested on 1500 images at a rate of 500 images per class. The models were evaluated by calculating the confusion matrix shown in Figure4. and through it we calculate the overall accuracy and accuracy, sensitivity, precision and precision for each class as shown in Table4. Through the results shown in Table4., we note that the proposed model has achieved an overall accuracy of 98.53%, while the VGG16 model has achieved an overall accuracy of 96.67%. From the same Table we note that the proposed model accuracy for Adenocarcinoma and Squamous classes has outperformed the accuracy of the VGG16 model for the same classes, but the VGG16 model has outperformed the proposed model through the accuracy of class Benign. We note also the superiority of the proposed model over the VGG16 model with all the remaining values except for the sensitivity of the Benign class only that the VGG16 model was superior to it. For the proposed model the sensitivity is 97.4%, 99.6% and 98.6% for classes Adenocarcinoma, Benign and Squamous respectively. These values indicate the ability of the model to classify these classes with every small error of 1.47%. From the same Table , we note the sensitivity are precision values of three classes are very high, and this indicates the effectiveness of the proposed model for classifying these classes correctly. There is some deficiency in the proposed model, which is the superiority of the class Benign results over the other classes.

#### IV. CONCLUSION AND FUTURE WORK

In this study we presented a CNN model for lung cancer diagnosis that was trained on three types of lung cancer. From the results we obtained, we can say that it is not always necessary for the used to be very deep to diagnose histopathological images of lung tissue, but more importantly to generate the largest possible number of feature maps necessary to complete the diagnostic process. The model that was presented and built in this a way and shown in Figure2. is very effective for diagnosing lung cancer as the model generates a large number of feature maps at different levels to make the diagnosis more accurate and with every small error rate. The proposed model outperformed the VGG16 model with the most results and this is indication of the model's effectiveness. In the future work we intend to develop the model to be able to diagnose the largest number of lung cancer, we also intend to test the model on different datasets, measure the effectiveness of the model with other types of cancer as well as address deficiencies in the model.

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