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A CRITICAL ANALYSIS OF DEEP LEARNING TECHNIQUES FOR MEDICAL IMAGE CLASSIFICATION AND DIAGNOSIS

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Abstract— Lung and Colon (L&C) cancers are fatal diseases that can develop in several organs simultaneously and, in certain situations, endanger human life. While the concurrent development of these two forms of cancer is very unlikely, delayed diagnosis greatly increases the likelihood of metastasis between the affected organs. To effectively treat certain types of cancer, histological diagnosis is essential. Traditionally, doctors had to go through a lengthy and laborious process to review histological images and diagnose cancer cases; however, with the new technology options, this process may now be completed much faster. In this study, a hybrid Deep Learning (DL) model combining an attention mechanism and a multipath network was employed to classify histological images of L&C tumors. To focus on the most important characteristics and disregard the less important ones, an attention mechanism was employed. Data is sent over numerous channels in a multipath network, which then converts each channel and combines the output from all of the branches. Simplified, the multipath network is just like grouped convolution. The LC25000 dataset was utilized, which included five categories of histopathological images. Among these categories were two for colon cancer and three for lung cancer. Several popular DL models, including ResNet-50, VGG-16, and AlexNet, were used to compare the effectiveness of the proposed model. The proposed approach showed the best performance in terms of accuracy (99.2%), specificity (99.12%), sensitivity (99.28%), precision (99.12%), and F1 score (99.2%), according to the experimental findings.
Keywords— Medical Image, Deep Learning, Accuracy, Histopathology, Cancer, Pre-process

Introduction

Cancer begins when abnormal cells in the body's organs or tissues multiply uncontrollably. Cancerous cells can be found in various organs and tissues throughout the human body [1]. The World Health Organization (WHO) reports that in 112 countries in 2019, cancer was the

primary or secondary cause of death for individuals under the age of 70 [2]. In addition, a study conducted in 2020 by the International Agency for Research on Cancer (IARC) found that cancer is the leading cause of mortality in 134 nations. There are more than 200 varieties of cancer. According to a statistical study done in the United States, L&C cancers are predicted to be the top three most prevalent cancer types by 2020. By 2020, L&C malignancies would account for the majority of cancer-related deaths in the US, per the report. According to GLOBOCAN 2020 statistics, L&C cancer rates are 11.4% and 18.0%, respectively [3]. In addition, the WHO estimates that 4 million people will be diagnosed with L&C cancer in 2020. Cancers like these have claimed the lives of over 2.7 million people. According to these statistics, L&C cancers have been the most frequent and deadly tumors worldwide.

Lung cancer may develop concurrently with colon cancer since around 17% of instances of both types of cancer occur concurrently [4]. Furthermore, without quick diagnosis, cancer cells have a high likelihood of spreading between the two organs. While cigarette smoking has been linked to an increased risk of lung cancer, it is believed that poor dietary habits raise the risk of colon cancer. To summarize, colon cancer can arise as a result of lung cancer's detrimental effects on the digestive tract. As a result, it is appropriate to consider lung cancer as a subsequent malignancy in those who have colon cancer. In other words, a patient may develop colon cancer as well as lung cancer. This is why early detection and detailed research into both cancer types in patients are critical.

There are no evident signs of cancer, but symptoms can help with early diagnosis [5]. Fatigue, coughing, muscle ache, and other symptoms are common in many disorders. Cancer detection is the most effective medical imaging instrument. Ultrasound, computed tomography (CT), mammography, histopathological imaging, and a variety of radiographic imaging modalities are frequently used in cancer detection [6]. Clinicians use histopathology images with phenotypic information to diagnose and evaluate cancer. Expert manual evaluation of these medical pictures is a difficult and delicate procedure. As a result, it requires concentrated attention and a significant amount of time. Furthermore, because the symptoms at the outset of the disease are ambiguous, early identification makes case detection even more difficult. The window of opportunity for early intervention closes once symptoms appear. Artificial intelligence (AI) has advanced significantly, and AI-powered medical image analysis systems can now assist physicians with early diagnosis and decision assistance [7].

The automated diagnostic processes are built on AI technologies such as Machine Learning (ML) and DL. Thus, diagnostic systems that are completely automated and require no human intervention arose from data analysis activities that relied on expert knowledge. The medical industry, as well as other health-related applications, has used classic ML approaches to address a variety of difficulties and concerns. The main disadvantages of these methods are feature selection and extraction, which can result in wasteful resource utilization and data loss if the incorrect method is applied. DL's capacity to overcome these disadvantages, combined with its superior discrimination power, has made it a popular choice for medical diagnostic applications [8].

The paper makes the following contributions:

The research describes a unique L&C cancer detection network that combines a multipath network with an attention block.

By integrating an attention block, our model can prioritize crucial information over less important information.

The multipath network distributes the input to numerous channels, thus increasing the pathways and effectively boosting accuracy.

Compare the suggested model's results to those obtained by transfer learning (TL) and recent research methodologies.

The remainder of this paper is organized as follows: Section 2 reviews recent methods used to diagnose L&C cancer. Section 3 describes our proposed DL model for evaluating histology images. Section 4 discusses system performance and compares algorithms to the state-of-the-art. Section 5 concludes the research.

Literature Survey

This section highlights some successful detection and classification approaches developed utilizing ML, DL, and TL. The study [9] proposed an ensemble classifier based on three different ML methods. The ensemble classifier is created by integrating the predictions of all the classifiers using the majority voting algorithm. Two methods, VGG16 and local binary pattern (LBP), were employed for extracting deep features from images. The ensemble classifier's appropriate characteristics are obtained by combining the LBP and VGG16 features. The proposed approach is validated using the LC25000 datasets. According to the outcomes of the investigation, the proposed approach outperforms current models. This strategy can improve prediction performance and applies to a wide range of classification issues, as opposed to employing a single classifier alone. The study [10] aims to develop an automated diagnosis system capable of correctly identifying five types of L&C tissues from LC25000 histopathological images. ML, feature engineering, and other image-processing approaches are used to classify these images. ML models, with their base in feature engineering, considerably increase the interpretability of classification models; DL models, on the other hand, are similar to black box networks, with their elaborate design making their operation extremely opaque. In terms of reliably categorizing subtypes of L&C cancer, the experimental data show that ML models yield acceptable results. By far, the most effective model was XGBoost.

The article [11] aims to develop an effective automated diagnosis system for identifying L&C cancer by integrating digital histopathology images with DL and ML algorithms. This is accomplished by designing a framework that optimally integrates DL with ML. This structure consists of two components. The primary phase involves extracting features from images of the L&C using a principal component analysis network. Then, five distinct categories of L&C cancer are identified using an extreme learning machine (ELM) and the rider optimization method. The empirical analysis discovered that outcomes on the standard LC25000 dataset have significantly improved. In this study [12], three lightweight DL networks were employed to categorize images of L&C cancer. Pre-trained models SqueezeNet, AlexNet, and ShuffleNet were employed to demonstrate the effectiveness of the TL concept. The first scenario involved

using CNNs to categorize L&C cancer images. Each model's categorization performance was shown as an individual SoftMax performance. In the second scenario, the SVM classifier received just features created from the images by the pre-trained model. Finally, the number of features was reduced by doing a principal component analysis (PCA) on the recovered network features. To boost classification accuracy, SVM was also given smaller feature sets after feature selection. The third scenario produced the greatest images of L&C cancer.

As an alternative to existing cancer detection approaches, the study [13] proposes a computationally efficient model that is both highly accurate and useful for the speedy and exact diagnosis of L&C cancer. This study's training and validation used a large dataset of L&C histopathology images. Four layers of an AlexNet were fine-tuned before being trained on a dataset. Initially, the categorization results appeared good for all but one group of images. A simple and effective contrast enhancement approach was used to improve the images of the underperforming class. Rather than employing image enhancement algorithms to update the entire dataset, this kept the model computationally efficient while increasing overall accuracy. Implementing the recommended procedures improved overall accuracy as well as processing efficiency. The study [14] proposes a new ML technique for identifying L&C cancers. The goal is to increase diagnosis accuracy by employing a hybrid ML/CV classification model. The LC25000 dataset, which includes 25,000 color histopathology images of cell tissues from the L&C, is used to detect adenocarcinomas. To extract features from images, the VGG-16 is employed. Three ML classification algorithms are used to detect cancer types. The model was evaluated using a 10-fold cross-validation technique, and CNN-SGD outperformed the other models. CNN-RF, a model that performs similarly to CNN-SGD, has training times that are 58.3 seconds faster than CNN-SGD's.

Researchers aimed to find promising results in identifying L&C cancer. Improving accuracy remains the objective of all researchers due to the similar characteristics exhibited by different types of cancer during their initial phases. As a result, this study focused on creating a more reliable DL model for detecting L&C cancer.

Deep Learning

In this study, we provide a novel DL architecture for L&C cancer prediction, as illustrated in Figure 1. The network's structure includes numerous levels of dual-attention blocks. It was built by integrating the multipath block, the Squeeze-and-Excitation (SE) block [15], and the Gated Channel Transformation [16].

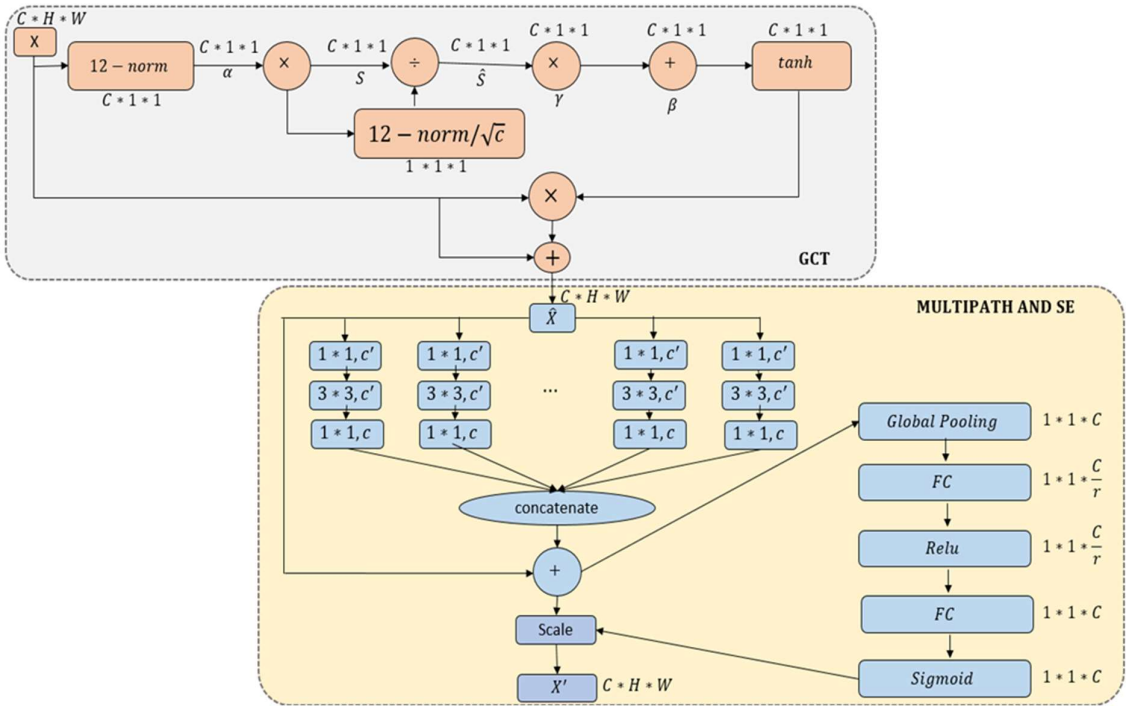

Fig. 1. LC25000 dataset

Gated Channel Transformation

A channel normalization layer effectively reduces both computational costs and parameter count. Due to the uncomplicated l2 normalization of this lightweight layer, the transformation unit can affect the operator directly without the need for extra parameters. GCT uses a normalization approach to determine if channel interactions are cooperative or competitive [17]. Using the normalized outcome of a global context embedding technique, GCT employs adaptive thresholding. Additionally, a model of the interconnections among the channels is generated by the GCT unit.

GCT units provide more efficient processing of contextual information. Despite being a parameter-free operation, the normalization technique seeks to establish cooperative or competitive connections between channels. This work proposes a method for embedding a global context that normalizes the channel, embeds context information, and controls parameters to make GCT learnable. Furthermore, the normalized output is used to change the channel parameters via an adaptive threshold operation. Because there are only a few training parameters, GCT is simple to implement. The intuitive GCT parameters can provide a visual representation of GCT's behavioral value. The following transformation is performed using GCT, assuming that x∈R^(C*H*W) represents the CNN activation feature:

$$\hat{X} = F(x|\alpha, \beta, \gamma), \alpha, \beta, \gamma \in R^c \quad [1]$$

In this case, α increases the embedding output flexibility, whereas β and γ govern activation thresholds. They determine how GCT operates in each channel. The complexity of the GCT is O(C), while the SE module is O(C^2).

Multipath Network Architecture

Our network follows ResNet's lead and utilizes a multipath architecture. In a multipath network, cardinality refers to the total number of paths that a given block can traverse. The other two dimensions, width and depth, do not encompass this specific dimension. Instead of emphasizing network depth or expansion, investigations have demonstrated that increasing cardinality enhances accuracy. Cardinality can also aid in improving the precision of multipath networks. A multipath network augments the number of potential paths. The multipath network module comprises parallel paths, each incorporating a GCT module, 1×1 and 3×3 convolution layers. The module's output can be obtained by summing the input and output from each path in the multipath network, along with utilizing a residual connection.

Dual Attention Block

To minimize processing in a standard CNN, image data is compressed using maximum or average pooling; nevertheless, this can result in the loss of essential information [18]. Successfully extracting features from a classic CNN requires a deep network. However, dealing with a large number of parameters with limited resources is not an easy process. By efficiently eliminating unnecessary data, our dual-attention block effectively handles the constraints of limited computational resources. To utilize deep features, each tensor X∈R^(W^'*H^'*C^') generates a new tensor U∈R^(w*H*C) after the convolution operation F_tr. This is accomplished by including the attention module in each multipath network block. Following the adjustment of u's channel dimension, each feature network is processed immediately. The channel's descriptor is 1*1*C, a map-characterizing scalar. As illustrated in Equation (2), Global Average Pooling is applied to each channel's feature map u_c (i,j).

$$Z_c = F_{sq}(u_c) = \frac{1}{W*H}\sum_{i=1}^{W}/\ \sum_{j=1}^{H} u_c(i,j) \quad [2]$$

The average value, Z_c, is calculated by summing all of the values in the feature map matrix. As shown in Equation (3), the channel weight for each map is calculated using the past-acquired channel descriptor 1*1*C.

$$s = F_{ex}(z,W) = \sigma\big(g(z,W)\big) = \sigma\big(W_2\delta(W_1 z)\big) \quad [3]$$

As demonstrated in Equation (4), x̃ is rebuilt using U.

$$\tilde{X}_c = F_{scale}(u_c, s_c) = s_c.u_c \quad [4]$$

Here, W_1 and W_2 are components of the sets R^(c/γ*C)and R^(C*c/γ) respectively, and σ represents the ReLU function. With these two features, we can minimize the model's complexity while increasing its generalizability; the construction of a "bottleneck" consisting of two Fully Connected layers around a nonlinear mapping ensues. To achieve better results by controlling the data flow of all feature maps and hierarchically exploiting the depth information of the gathered data, multiply the gate of each channel s_c by the matching feature map u_c after acquiring the gate-like architecture. The next step is to train the backbone network using GCT so that visual recognition tasks can extract features more effectively. We have eight blocks in our network that are stacked with dual attention. C=32 signifies the image's

cardinality of 32, while the following integer indicates the amount of repeated stacks in the block.

Network Optimization Algorithm

During training, a range of optimization strategies are used to improve classification accuracy and accelerate convergence. In this study, we optimize using Rectified Adam (RAdam) and smooth our weights using stochastic weight averaging (SWA) [19].

Finding an optimal trade-off between convergence speed and accuracy is difficult. Training deep neural networks often involves using optimization techniques like Adam and stochastic gradient descent (SGD). RAdam is an improved method that builds upon Adam, an algorithm for adaptive stochastic optimization. The adaptive learning rate is activated or deactivated depending on the variation. To improve the network's accuracy, RAdam combines Adam's convergence speed with SGD's gradient updating behavior. To achieve a happy medium between the algorithm's accuracy and convergence speed, the RAdam optimization approach is helpful.

Using SWA, whether training on stable instances or random fluctuations, can enhance the model's generalizability during convergence and yield a big local maximum. The following is the formula for the method, which is typically applied in the final stage of convergence:

$$W_a = \sum_{i=n*range}^{n} w_i p_i \quad [5]$$

Here, n is the total training rounds, range is the range of rounds without weight smoothing, w_i is the model weight derived after each training round, and p_i represents the proportion to every round's weight. The initial round of weight smoothing is governed by n and range. Our testing has shown that SWA can yield weights that roughly approximate the model's ideal performance.

Experimental Outcome

Experimental Data

The primary purpose of this proposed study is to create an AI-powered tool to aid in the detection of L&C cancer by utilizing the LC25000 dataset [20]. The data contains five classes of histopathological images. The colon region generates two classes (Adenocarcinoma, and benign), while the lung region generates the remaining three (Benign, Adenocarcinoma, Squamous Cell Carcinoma). Each class in the collection has 5,000 images from a total of 25,000 images. The original dataset on which the LC25000 dataset is based contains 500 and 750 images of the colon and the lungs. Before presenting the images from the LC25000 dataset, the authors enhanced them further. Figure 2 depicts the LC25000 dataset by class, with three sample images per class. Table 1 provides a detailed breakdown of the data utilized for training, validation, and testing purposes.

Table 1. Distribution of the LC25000 dataset

Organ	Cancer	Actual Data	Train Data	Validate Data	Test Data

Lung	Benign	5000	3500	1000	500
	Adenocarcinoma	5000	3500	1000	500
	Squamous Cell Carcinoma	5000	3500	1000	500
Colon	Adenocarcinoma	5000	3500	1000	500
	Benign	5000	3500	1000	500
Total		25000	17500	5000	2500

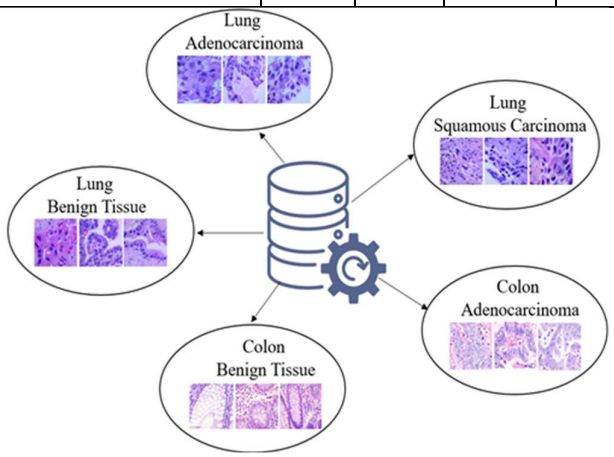

Fig. 2. Sample images from LC25000 dataset.

An initial examination of the histopathological images in the collection indicated that every single image was colored. Additionally, each of the dataset's classes contained 5,000 images. The size of the image dataset was estimated after a comprehensive examination. The images had a size of (768, 768, 3). We couldn't proceed further with the modeling phase without first preparing the images. The initial step in preparing histopathological images was to remove any noise. Denoising was achieved with Gaussian Blur [21]. Throughout the investigation, the Gaussian Blur's kernel size, SigmaX, and SigmaY parameters were calibrated to 3, 3, and 90, respectively. This method removed noise from all histopathological images in the collection. The images were resized to (64, 64, 3). They were saved after the denoising procedure. The images could then be further processed.

Training Outcome

The proposed hybrid DL model successfully detected L&C cancer in the experiment conducted using MATLAB R2024a.

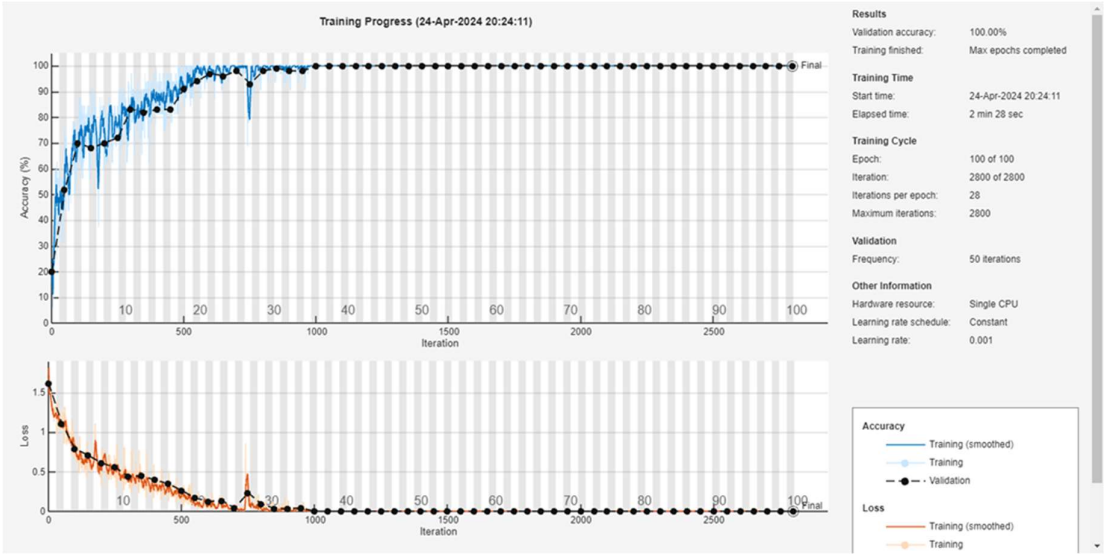

Fig. 3. Accuracy and loss plot of the proposed model for L&C cancer prediction

The outcome of the proposed model, including accuracy and loss values in both the training and validation phases, is illustrated in Figure 3. The model took 2 minutes and 28 seconds to train. Initially, the accuracy value of the proposed model started from 10% and gradually increased, reaching 100% accuracy in both the training and validation phases after 35 epochs. The validation results are represented by the black plot, while the accuracy and loss plots in the training phase are denoted by blue and orange colors, respectively.

Testing Outcome

Upon evaluation with testing data, the proposed model's performance was compared with several pre-trained models such as VGG-16, AlexNet, and ResNet-50. The proposed model achieved the highest metrics scores, including an accuracy of 99.2%, specificity of 99.12%, sensitivity of 99.28%, precision of 99.12%, and F1 score of 99.2%. The second-highest metrics were attained by the AlexNet model. And the metrics values are 98.16%, 97.52%, 98.8%, 97.55%, and 98.17%. Figure 4 provides a comparison of DL models for L&C cancer prediction, along with details of the acquired performance measures of all DL models

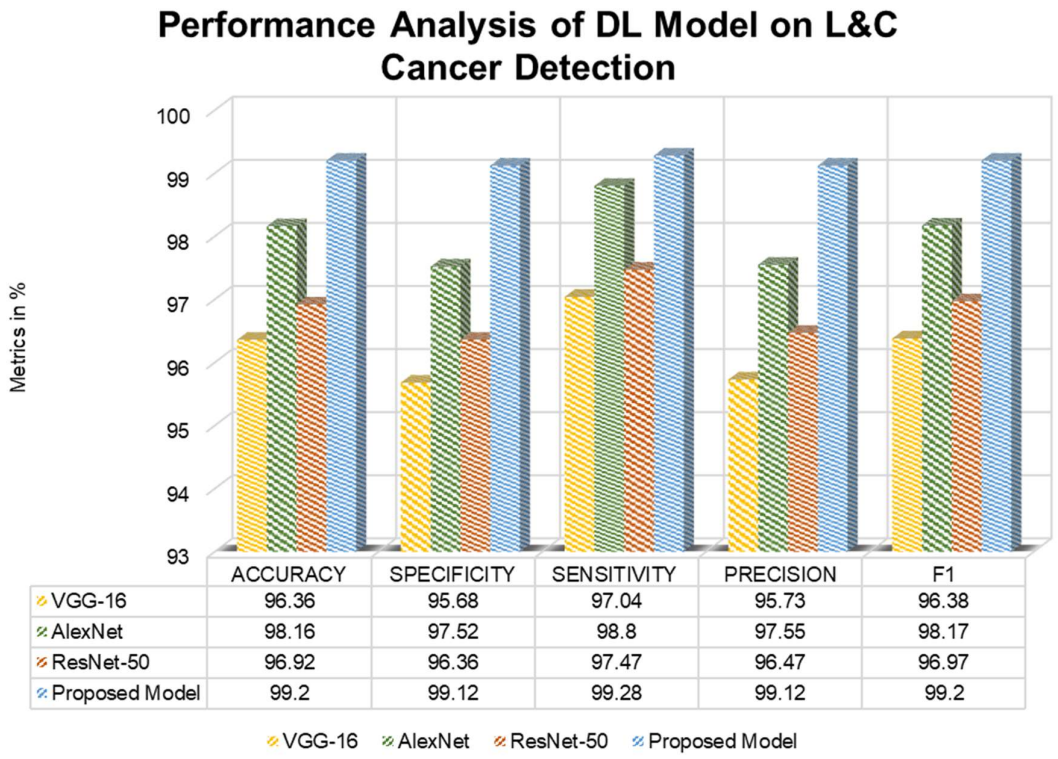

Fig. 4. Performance analysis of DL model on L&C cancer testing data

The proposed model's outcome was further compared with recent research works, as tabulated in Table 2. References [22] and [24] addressed both lung and colon cancer, achieving accuracies of 96% and 97%, respectively. References [23] and [25] focused solely on lung cancer and achieved an accuracy of 97%. By comparison, our proposed model gives a maximum accuracy of 99%.

Table 2. Comparison of the proposed model with recent research papers

Ref	Cancer	Accuracy	Sensitivity	Precision	F1-Score
[22]	Lung	97.89%	-	-	-
	Colon	96.61%	-	-	-
[23]	Lung	97.2%	97.33%	97.33%	97.33%
[24]	Lung & Colon	96.33%	96.39%	96.39%	96.38%
[25]	lung	97.11%	97.13%	97.15%	97.14%
Ours		99.2%	99.28%	99.12%	99.2%

Overall, the results demonstrate that the proposed hybrid DL model outperforms existing models, making it a promising tool for the detection of L&C cancer.

Conclusion

L&C cancer are among the most common and dangerous cancers. Worldwide, 4.19 million cases of lung and colon cancer were diagnosed in 2020, with over 2.7 million people losing their lives to the disease. These cancers are often diagnosed using techniques like biopsy and laboratory testing. However, the availability of healthcare resources and qualified medical professionals, particularly in underdeveloped countries, remains limited. Furthermore, manual diagnosis is time-consuming and might result in differing opinions among specialists. DL approaches provide alternatives to these problems. In this paper, we created a robust hybrid DL model for the earlier L&C cancer detection of histopathological images from the LC25000 dataset. Pre-processing techniques were used to enhance the histopathology images. The proposed model is evaluated by comparing it with TL techniques and recent research findings. The proposed model achieved the maximum accuracy of 99.2% compared to other methods. In the future, we hope to test the proposed model with histological images for various malignancies and eventually construct a universal model capable of recognizing all types of cancer from histopathological images.

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