Lung and Colon Cancer Histopathological Image Classification Using 1D Convolutional Channel-based Attention Networks

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Abstract

Lung and Colon cancer are the leading diseases of death and disability in humans caused by a combination of genetic diseases and biochemical abnormalities. If these are diagnosed in their early stages, they can not be spread in organs and negatively impact human life. Many deep-learning networks have recently been proposed to detect and classify these malignancies. However, incorrect detection or misclassification of these fatal diseases can significantly affect an individual's health and well-being. This paper introduces a novel, cost-effective, and mobile-embedded architecture to diagnose and classify Lung squamous cell carcinomas and adenocarcinomas of the lung and colon from digital pathology images. Extensive experiment shows that our proposed modifications achieve 100% testing results for lung, colon, and lung-and-colon cancer detection. Our novel architecture takes around 0.65 million trainable parameters and around 6.4 million flops to achieve the best lung and colon cancer detection performance. Compared with the other results, our proposed architecture shows state-of-the-art performance.

Introduction

World Health Organization (WHO) reveals that cancer is the second leading cause of death globally in 2020. It predicts a 60% increase in cancer mortality by 2035 (Araghi et al. 2019). This cancer cell grows autonomously with significant metastatic power, which affects organs. Among these, colon and lung cancers are the leading causes of cancer-related deaths worldwide. In the US in 2020, 18.4% and 9.2% of lung and colon cancer-related deaths were recorded (Mangal, Chaurasia, and Khajanchi 2020). Early detection of life-threatening diseases can reduce mortality rates, but incorrect cancer detection can be harmful in two ways:

- If a patient is misdiagnosed with cancer, they may undergo harmful treatments like chemotherapy, radiation, and/or surgery and suffer psychological distress.
- Undetected cancer leads to delayed or no treatment, which worsens prognosis. If cancer is present but not detected, it misses a chance for effective intervention.

Several medical histopathological imaging techniques, such as X-rays, tomography, and magnetic resonance imaging (MRI) have been extensively investigated for lung and colon malignancy detection. This research proposes a novel but efficient mobile-embedded network architecture to detect lung and colon cancers by analyzing histopathological images.

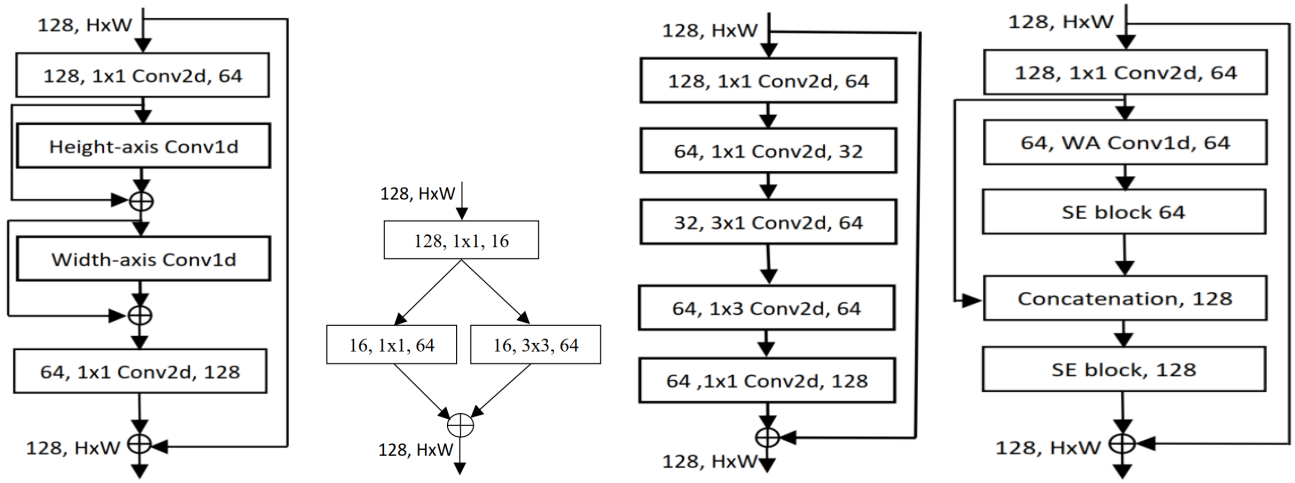
Lung cancer is a malignant tumor, develops from abnormal cells. It impairs lung function and can spread to other body parts. The most common types are Adeno and squamous cell carcinoma. And, Colon cancer affects the colon or rectum, parts of the large intestine. People over 50 are more susceptible. Early detection leads to successful treatment.

Confirming the presence of cancerous cells involves a series of imaging studies and biopsies. This study proposes a cost-effective deep learning architecture for mobile devices, aimed at accurately detecting early-stage lung and colon cancer. Our goal is to achieve 100% accuracy. The detection of false positives is crucial as they can result in severe consequences for human life. This architecture will help to set up an automated medical diagnosis by classifying cancer sub-types in digital histopathological images. We used two lightweight deep-learning architectures to create our proposed architecture: a 1D spatial convolution neural network (Conv1D) and Squeeze-and-Excitation (SE) blocks, to accurately classifies lung and colon cancer sub-types without misclassifications and achieve state-of-the-art results. The key novelties and contributions of this proposed architecture are: (1) Introducing a more cost-effective network using channel concatenation instead of pointwise (1×1) CNN layer; (2) Using a SE block to imply channel-wise feature re-calibration in the network; (3) Finally, Construct our proposed block using the lightweight Conv1D, pointwise CNN, and SE block to detect lung and colon cancer.

We have demonstrated the effectiveness of our proposed model in detecting lung and colon cancer. Our novel architecture has been compared to existing models, where our proposed model outperforms its predecessors. This assessment was based on trainable parameters, FLOPS (number of multiply-add operations), and Top-1 testing accuracy.

Related Works

This study presents a new method for analyzing histopathological images of lung and colon cancer from LC25000 dataset. Many researchers have implemented deep learning on this dataset. Some of these applications are discussed below.



(a) Residual 1D CNNs block. (b) Fire block in SqueezeNet. (c) SqueezeNext block. (d) Proposed block.

Figure 1: Illustration of (a) RCN block (Shahadat and Maida 2023), (b) SqueezeNet block (Hu, Shen, and Sun 2018), (c) SqueezeNext block (Gholami et al. 2018), and (d) Proposed block constructed with Residual 1D CNN and SE layers.

Mengash et al. utilized a marine predator algorithm integrated with deep learning to detect lung and colon cancer malignancies in histopathological images and achieved a testing accuracy of 99.27% (Mengash et al. 2023). Hadiyoso et al., presented an automatic classification of lung and colon cancer using CNN with VGG16 architecture and CLAHE and reported 98.96% testing accuracy (Hadiyoso, Aulia, and Irawati 2023). The DarkNet-19 model was one of the deep learning model extracted features using Equilibrium and Manta Ray Foraging optimization and achieved 99.69% accuracy for lung and colon cancer sub-types (Toğaçar 2021).

After analyzing the studies, we discovered that deep features are extracted through various CNN models, transfer learning, and machine learning techniques. Our analysis is not restricted to these papers. The analysis indicates that each proposed method has been subject to misclassifications, which could be more harmful than the cancer diagnosis itself. Unlike the previous studies, this paper uses 1D CNN models with feature recalibration layers.

Lightweight Deep Learning Models

Residual 1D Convolutional Networks

Spatial 2D CNNs have demonstrated great effectiveness in extracting features for various computer vision tasks. The 2D CNN-based residual bottleneck block architecture is depicted in (Shahadat 2023) (Figure 1 right). These 2D CNNs are computationally very expensive. Shahadat and Maida proposed a residual network architecture that uses 1D CNN with residual connection (RCN) in the spatial domain illustrated in Figure 1a, as opposed to 2D CNN (Shahadat and Maida 2023). They used two RCN layers instead of a 2D CNN layer as their RCN layer reduces the computational costs with a factor of $(w \cdot d_{in} \cdot k)$, where w, d_{in}, and k are the input width, number of input channels, and kernel size, than the original standard 2D CNNs. Our proposed block uses this cost-effective RCN layer.

SqueezeNet Architecture

The Squeeze-and-Excitation (SE) block is the key building block of SqueezeNet (Hu, Shen, and Sun 2018), illustrated in Figure 1b. CNNs utilize the SE network for channel-wise attention mechanism within feature maps. The attention mechanisms adjust each channel's significance in the final representation, improving the feature's representational capabilities using channel-wise feature recalibration throughout the network. The "squeeze" operation in computer vision tasks involves the global average pooling of feature maps, resulting in a single value per channel. A dense layer is then applied to capture inter-channel dependencies and generate scaling factors for each channel to highlight important ones. The SE block is integrated with other blocks to improve performance by incorporating channel-wise attention, reducing overfitting, and improving generalization. We use this SE block to apply channel-wise attention and improve feature maps in our proposed block.

SqueezeNext Architecture

SqueezeNext is an architecture optimized for efficient model deployment, aiming to decrease the number of parameters while maintaining competitive performance. This architecture belongs to the SqueezeNet family, which aims to achieve high accuracy using a few parameters. Like SqueezeNet, SqueezeNext uses the "Fire" module as a fundamental building block. This Fire module consists of a mixture of 1×1 pointwise convolutions (squeeze layer) and a mix of 1×1 and 3×3 convolutions (expand layer) described in Figure 1c (Gholami et al. 2018). We have applied our proposed block to the SqueezeNext network architecture to construct our proposed network.

Proposed Parameter Efficient Architecture

The aim behind the development of the proposed network block is to introduce a lightweight, mobile-embedded, and

Table 1: Distributions of Lung and Colon cancer LC25000 histopathological images dataset.

Data Samples	Lung Dataset			Colon Dataset		Total
	Adenocarcinomas	Cell Carcinomas	Benign	Adenocarcinomas	Benign	
Training Data Samples	4000	4000	4000	4000	4000	20000
testing Data Samples	1000	1000	1000	1000	1000	5000

parameter-efficient network architecture and improve the accuracy of detecting lung and colon cancer. We used the RCN and SE blocks to construct our proposed block, depicted in Figure 1d. Like SqueezeNet (Hu, Shen, and Sun 2018) and SqueezeNext (Gholami et al. 2018), we construct the fire module using the pointwise down-sampled CNN layer and spatial 1D CNN layer along the width axis.

Our proposed architecture is computationally cost-effective compared to the lightweight SqueezeNext block (Gholami et al. 2018). We used one pointwise squeeze layer than the two in the SqueezeNext block. It helps to save at least $h \times w \times d_{in} \times d_{out}$ costs. We replace the two separable CNN layers (3×1 and 1×3) using the RCN and SE layers. The cost comparisons of these modifications are defined as,

$$\begin{aligned} Cost_R &= \frac{Cost\ of\ 3 \times 1\ CNN}{Cost\ of\ RCN} + \frac{Cost\ of\ 1 \times 3\ CNN}{Cost\ of\ SE - Block} \\ &= \frac{h \cdot w \cdot d_{in} \cdot d_{out} \cdot k}{w \cdot d_{out} \cdot k} + \frac{h \cdot w \cdot d_{in} \cdot d_{out} \cdot k}{d_{in} \cdot d_{out}} \\ &= h \cdot d_i + h \cdot w \cdot k \end{aligned} \tag{1}$$

where h, w, d_{in}, and d_{out} are the input height, width, and number of input and output channels, respectively. Also, k is the kernel size. Equation 1 shows that our proposed block is $h \cdot d_{in} + h \cdot w \cdot k$ times more cost-effective than the separable CNN layers in the SqueezeNext block.

We have made modifications beyond these. We also remove the ConvUp (the 1×1 CNN layer is used to increase the output channel) layer and use the channel concatenation to reduce the network's complexity. While the pointwise CNN layer is a channel-based weight layer, our channel concatenation does not offer this, leading to a reduction in performance. To address this limitation, we use the SE layer, which helps to increase the performance using a channel-wise attention mechanism. This SE layer is also cost-effective compared to the 1×1 CNN layer, which can be defined as,

$$\begin{aligned} Cost_R &= \frac{Cost\ of\ 1 \times 1\ CNN}{Cost\ of\ SE - Block} \\ &= \frac{h \cdot w \cdot d_{in} \cdot d_{out}}{d_{in} \cdot d_{out}} = h \cdot w \end{aligned} \tag{2}$$

Our proposed block reduces the computational cost of the SqueezeNext block with a factor of $Cost_R = h \cdot w \cdot d_{in} \cdot d_{out} + h \cdot d_{in} + h \cdot w \cdot k + h \cdot w$. So, our proposed architecture is a parameter-efficient, and cost-effective architecture. In the case of boosting performance, the proposed block precisely uses two SE layers, producing better output feature maps using channel-wise feature recalibration. These channel-wise feature recalibrations are responsible for improving model performance, reducing overfitting, and focusing on important channels. We stack this proposed block to construct the proposed network.

Experimental Results

We experimented on lung and colon cancer datasets to enhance cancer sub-type analysis. We designed an efficient SqueezeNext-based architecture to analyze cancer datasets and compared its performance with other similar works.

Table 2: The performance on the LC25000 dataset to detect lung and colon cancer using our proposed networks.

Dataset	Epochs	Params	Batch size	Testing Accuracy
Colon Cancer	30	0.65M	8	100
			16	100
			32	100
			64	100
			128	100
Lung Cancer	40	0.65M	8	99.17
			16	100
			32	100
			64	100
			128	100
Lung and Colon Cancer	50	0.66M	8	99.6
			16	99.94
			32	99.98
			64	100
			128	99.98

Dataset

This research utilizes the histopathological lung and colon cancer images dataset (LC25000) (Borkowski et al. 2019). This comprehensive dataset has two main categories of cancer cells: lung and colon cancer. The dataset includes 25,000 images, with 10,000 dedicated to colon cancer and 15,000 to lung cancer. The lung cancer has three cell types: adenocarcinoma, squamous cell carcinoma, and benign tissue. The colon cancer has two cell types: adenocarcinoma and benign tissue. The original LC25000 dataset includes 750 lung and 500 colon tissue samples, which were augmented to generate $25,000$ images.

In our experiment, we divided the main dataset (LC25000) into two parts: 80% for training and 20% for testing samples. Image distribution of the lung-and-colon dataset is explained in Table 1. For convenience, we resized the images to 256×256 pixels, randomly cropped to 224×224 pixels, and normalized using the mean and standard deviation.

Table 3: Comparison between our proposed mobile-embedded model and other previous methods on histopathological images.

Dataset	Models/year	Method	Testing Accuracy
Colon Cancer	Sakr et al., 2022	Lightweight deep CNN networks	99.50
	Yildirim and Cinar, 2022	CNN based MA˙ColonNET	99.75
	Bhattacharya et al., 2023	Deep feature selection + AdBet-WOA	99.99
	Our Proposed Model	1D CNN with SE blocks	100
Lung Cancer	Shandilya and Nayak, 2022	ResNet 101	98.6
	Civit-Masot et al., 2022	Image preprocessing + CNN	99.8
	Bhattacharya et al., 2023	Deep feature selection + AdBet-WOA	99.97
	Our Proposed Model	1D CNN with SE blocks	100
Lung and Colon Cancer	Singh, Sharma, and Gupta, 2023	EfficientNet B3 Model	98
	Ijaz et al., 2023	Deep Neural Networks + Gray Wolf	98.73
	Stephen, Sain, and others, 2023	Bayesian–Gaussian CNN	97.92
	Mengash et al., 2023	Marine predator's algorithm	99.27
	Bhattacharya et al., 2023	Deep feature selection + AdBet-WOA	99.96
	Shourie, Anand, and Gupta, 2023	Efficientnetb7	98.49
	Singh and Singh, 2023	Feature extraction + Ensemble method	99
	Hadiyoso, Aulia, and Irawati, 2023	CNN-CLAHE-VGG16	98.96
	Our Proposed Model	1D CNN with SE blocks	100

Method

Our mobile-supported network was designed by incorporating our proposed block architecture, illustrated in Figure 1d, into SqueezeNext-based architectures (Gholami et al. 2018). To ensure a fair comparison, we employed similar training protocols and hyperparameters as (Gholami et al. 2018; Shahadat and Maida 2023) for our proposed SqueezeNext architectures. Our proposed block uses fewer CNN layers than the SqueezeNext block architecture. However, we analyze 23-layer architecture with the block multiplier "[6, 6, 8, 1]" and the channel widening factor 1.

We trained our network using batch sizes, like 8, 16, 32, 64, and 128. The SGD (stochastic gradient descent) optimizer and warmed-up linear learning for the initial ten epochs, followed by a switch to cosine learning scheduling from epoch 11 to epoch 120 have been employed to train our models. The experiments are run on a workstation with an Intel(R) i9-9820X CPU @ 3.30GHz, 128GB memory, and NVIDIA Titan RTX GPU.

Results and Discussion

The proposed method is tested on histopathological images obtained from the LC25000 dataset (Borkowski et al. 2019). The experimental analysis is divided into lung, colon, and lung-and-colon cancer. Table 2 shows the testing performance of cancer histopathological images for different batch sizes. Our proposed 1D CNN with SE layers architecture performed with 100% testing accuracy for all datasets. To achieve this 100% performance, the model takes 30, 40, and 50 epochs for colon, lung, and lung-and-colon cancer datasets. Our proposed 23-1 architecture shows state-of-the-art 100% testing accuracy for $0.66M$ trainable parameters and $6.4M$ FLOPS.

Comparison with the Literature

This section compares the results obtained from the proposed model and the existing models on the Lung, Colon, and Lung-and-Colon cancers. This analysis aims to comprehensively understand the proposed framework's performance and contribution to the current state of the art. The evaluation criteria and the experimental setup used in this comparison are described in detail to ensure the replicability of the findings. We demonstrate the effectiveness of our proposed model by comparing the results obtained from it.

Table 3 compares recent deep-learning approaches on lung, colon, and lung-and-colon cancer detection datasets. We partitioned our comparison based on lung, colon, and lung-and-colon cancer datasets. The performance of our proposed framework was better and attained 100% testing accuracy for all datasets. Compared with all of the lung and colon cancer dataset models, our novel architecture showed state-of-the-art lung and colon malignancy detection results using histopathological images. This system can assist pathologists in the early detection of lung and colon cancers without inaccurate detection.

Conclusions

Lung and colon cancer are among the most frequently diagnosed types of cancer globally. Early diagnosis is a highly effective measure in preventing fatalities, and accurate diagnosis is very crucial for this type of life-threatening disease. This paper studied to detect this life-threatening cancer disease without misclassification and conducted several experiments on the LC25000 dataset using our proposed lightweight, mobile-embedded, and parameter-efficient deep learning architecture. Our experimental results improved performance in detecting colon, lung, and lung-and-colon cancers with an accuracy rate of 100%. Our proposed model demonstrated state-of-the-art performance on the lung and colon cancer detection LC25000 dataset, outperforming other published works. The proposed concept is confined to this dataset only. Subsequent research endeavors may be oriented toward investigating other medical conditions.

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