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ColoNet: A CNN-Based System for Early Diagnosis and Classification of Colon Adenocarcinoma in Digital Histopathology

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Abstract: Colon cancer remains a significant global health challenge, contributing to high morbidity and mortality rates. Accurate diagnosis through histological analysis is critical for effective treatment and improved patient outcomes. In this study, we present ColoNet, a convolutional neural network (CNN)-based system designed to enhance the early detection and classification of colon adenocarcinoma using LC25000 dataset comprising 10,000 digital histopathology images. Unlike conventional CNN-based models, ColoNet integrates an optimized feature extraction strategy with deeper convolutional layers, and dropout regularization, leading to improved generalization and reduced overfitting. Additionally, the proposed model achieves faster convergence and superior classification performance compared to existing methods. The system addresses the unique challenges in distinguishing benign from malignant conditions, automating the diagnostic process and streamlining colon cancer assessments for pathologists. ColoNet was rigorously evaluated across key performance metrics, including recall, accuracy, precision, and F1-score, achieving a maximum accuracy of 96.66%. This surpasses several state-of-the-art CNN models in colon cancer classification, demonstrating its effectiveness. Its high accuracy and robust classification capabilities make it a reliable tool for identifying different colon cancer stages. By providing an efficient and automated solution for pathologists, ColoNet is expected to significantly enhance colon cancer diagnosis, supporting early detection and staging, ultimately leading to better treatment outcomes and reduced cancer-related mortality. This research underscores the importance of AI-driven systems in transforming the landscape of digital pathology and improving clinical decision-making for colon cancer.

Index Terms: Colon Adenocarcinomas, Colon Cancer, Cancer Detection, Convolutional Neural Networks

1. Introduction

Cancer stands as a significant contributor to the global decline in health standards. Specifically, colon cancer, often originating in the large intestine, presents a formidable challenge to public health. Defined by the uncontrolled growth of abnormal cells triggered by genetic mutations, cancer poses a grave threat to individuals worldwide, with WHO statistics indicating it as the second leading cause of mortality, accounting for nearly 10 million deaths annually [1].

While colon and rectal cancers are less prevalent in developing nations, they rank as the second most common form of cancer in affluent societies, with over 940,000 cases reported globally each year and a staggering 500,000 lives lost to the disease [2]. With global population expansion intensifying the incidence of malignant tumors, the impact of

colon cancer is most acutely felt among individuals in their 50s and 60s [3] with projections suggesting a concerning rise in the cancer death rate to 60% by 2035 [4].

Colon cancers often originate from benign polyps, evolving over time into malignant tumors characterized by the unchecked proliferation of healthy cells within the colon or rectum's epithelial lining. These tumors, notably mucinous adenocarcinomas and signet ring cell adenocarcinomas, pose unique challenges in diagnosis and treatment, influenced by factors such as age, gender, ethnicity, smoking status, and genetic predisposition.

Despite advances in diagnostic methods, distinguishing colon adenocarcinoma from benign conditions remains a critical challenge. Histopathological examination, the gold standard for diagnosis, requires expert pathologists to analyze high-resolution tissue images manually, which is time-consuming and prone to inter-observer variability. Furthermore, differentiating between mucinous adenocarcinoma, signet ring cell adenocarcinoma, and non-cancerous tissues based on microscopic features remains difficult due to overlapping morphological characteristics. This necessitates an automated and highly accurate computational model to assist pathologists in making precise diagnoses.

In addressing this complex healthcare challenge, advancements in computer science and technology offer promising solutions. Machine learning (ML) applications, leveraging vast datasets and computational power, are revolutionizing cancer diagnosis through automated, computer-aided diagnostics. By harnessing ML's ability to learn from data and refine predictive capabilities autonomously, researchers aim to enhance diagnostic precision and expedite the identification of cancerous lesions.

Deep learning algorithms, a subset of ML techniques, have demonstrated exceptional efficacy in image recognition tasks, often surpassing human performance. By training deep learning models on labeled images, researchers can develop adaptive software networks capable of accurately identifying and classifying cancerous lesions. These advancements led to a transformative shift in cancer diagnosis, promising more efficient and precise detection methods that can significantly improve patient outcomes [5].

In this study, we introduce ColoNet, a CNN-based model specifically designed to tackle the unique challenges in colon adenocarcinoma detection. Unlike conventional models, ColoNet incorporates advanced preprocessing techniques to enhance contrast and clarity in histopathology slides, making feature extraction more effective. The model integrates deep convolutional layers with dropout regularization to mitigate overfitting and improve generalization across diverse tissue samples. Additionally, the architecture is optimized to accurately distinguish adenocarcinoma subtypes from non-cancerous tissues, addressing the major bottleneck in histopathological diagnosis.

The primary aim of the present study is to assess the efficacy of deep learning in the context of histological analysis of colon cancer by examining the influence of the suggested CNN model and assessing digital pathology images. ColoNet demonstrates the ability to extract hierarchical features that surpass traditional handcrafted filters, enabling more precise and automated adenocarcinoma classification. The developed model can differentiate among input images assigned weights (comprising learnable weights and biases) corresponding to various attributes. The dataset comprises histopathology slides, chosen due to the comprehensive insight into the pathology and its impact on tissues while upholding the fundamental tissue structure. This study developed a highly sophisticated deep learning model adept at recognizing organs and cancers within medical data. Furthermore, it has proven effective in categorizing image samples and identifying disorders, thereby bringing about a transformative impact on the healthcare sector.

The primary contributions of this research work are as follows:

1. Development of ColoNet, an efficient system tailored for identifying and categorizing colon adenocarcinomas through digital histopathology images, addressing the need for precise and dependable methods in colon cancer diagnosis.
2. ColoNet employs a tailored feature extraction and categorization method, specifically engineered to overcome the unique challenges associated with identifying colon cancer, ensuring accurate classification of tumors.
3. ColoNet's architecture integrates multiple convolutional and max pooling layers for robust feature extraction, followed by densely connected layers for accurate classification. This optimized configuration enhances ColoNet's ability to detect colon anomalies in digital histopathology images.
4. A critical enhancement in ColoNet's design is the inclusion of dropout layers, effectively combating overfitting and enhancing the model's versatility and effectiveness in classifying previously unseen colon cancer images, thus increasing its clinical applicability.
5. ColoNet undergoes extensive evaluation across key performance metrics such as recall, accuracy, precision, and F1-score, demonstrating its efficacy in diagnosing various stages of colon cancer. This comprehensive assessment validates ColoNet's potential to improve the classification and diagnosis of colon cancer stages.
6. Implementation of ColoNet is expected to significantly improve colon cancer diagnosis, leading to better patient outcomes by enabling early detection, staging, and treatment, thereby reducing cancer-related morbidity and mortality rates.

The paper is structured as follows. Section 2 presents literature review and methodology is presented in section 3. Section 4 discusses the results obtained by the model and section 5 concludes.

2. Literature Review

This section presents a brief review of the literature in this field. A. Karthikeyan *et al*. [6] proposed a model to detect colon cancer using the Convolutional Neural Networks and Ranking Algorithm, and reported an accuracy of 91% and a precision of 93%. In a review study conducted by Muthu Subash Kavitha *et al.* [7] summarized the recent advancements in deep learning models for the prediction of colorectal cancer and they have concluded the result with the accuracy of 94.5%.

In 2022, Mai Tharwat *et al.* [8] have presented an article with a comprehensive survey on the diagnosis of colon cancer, and they have covered various aspects related to colon cancer, such as symptoms, grades, available imaging modalities, common diagnosis systems and diagnosis using deep learning. Dabiah Alboaneen *et al.* [9] have reviewed 42 research papers and concluded that although the objectives of prior research varied, 83.3% of it sought to forecast the patient's medical condition, while 15.9% sought to predict the tumor stage and survival time. From a technical standpoint, fifty percent of the researchers utilized Machine Learning algorithms and fifty percent utilized Deep Learning algorithms. With respect to the colorectal cancer dataset, 57.2% of the researchers utilized publicly accessible datasets found on the internet, while 42.8% of the researchers relied on their own datasets.

In 2022, Cowan Ho *et al.* [10] proposed an AI model and they have trained the model over 105 resections WSIs and then validated their model over 150 biopsies WSIs, they have achieved an accuracy of 91.7%. S. U. K. Bukhari *et al*. [11] presented a method the peri-tumoral stroma (PTS) score was shown to have a 0.038 predictive value for LNM. This study classified digital images of colonic tissue using three CNN architectural variations: ResNet-18, ResNet-50, & ResNet-30. They reported that the ResNet-50 achieved the highest accuracy at 93.91%, while ResNet-30 & ResNet-18 both achieved 93.04% accuracy. Gang Yu. *et al.* [12] proposed a semi-supervised deep learning model to utilize pathological images and predict the presence of colon cancer.

Zheng Cao *et al.* [13] proposed a deep learning approach to predict colorectal cancer using Raman Spectra and their experimental results show that the introduced deep learning method achieves 98.5% accuracy in the detection of colorectal cancer and outperforms traditional methods. And they have concluded that overall, Raman spectra are a novel modality for clinical detection of colorectal cancer. Zarrim Tasnim *et al.* [14] proposed a deep learning model which utilizes CNN and MobileNetV2 and they have achieved an accuracy of 97.49% using max pooling layers and an accuracy of 95.48% using average pooling layers.

3. Methodology

This section presents description of the data set, the model architecture of ColonNet and the performance evaluation metrics to assess the efficacy of the developed model.

3.1 Dataset

This study utilizes LC25000 dataset comprising 10,000 digital images of histopathology slides subdivided into two classes as shown in Table 1.

Table 1. Dataset Description

Cancer type	Class name	Number of samples
Colon adenocarcinoma	colon_aca	5000
Colon benign tissue	colon_n	5000

The dataset maintains an equal distribution of samples between malignant and benign tissues, which helps mitigate class imbalance issues during model training. However, beyond numerical balance, ensuring diversity in image characteristics such as variations in staining intensity, resolution, and dataset source is equally crucial. The LC25000 dataset consists of images collected from multiple histopathology slides, potentially covering different staining protocols and sample preparations, ensuring a degree of variability. Despite this, demographic diversity (such as age, gender, or ethnicity of patients) is not explicitly provided in the dataset, which remains a limitation. Future studies can benefit from datasets that include broader demographic details to assess model generalizability across different patient populations.

To ensure high-quality input for model training, several preprocessing techniques were applied to the histopathology images. Normalization was performed by scaling pixel values to [0,1] for consistency. Data augmentation, including random rotation, flipping and brightness adjustments were employed to enhance model generalization. Noise reduction was achieved using Gaussian blurring and median filtering, and contrast enhancement through adaptive histogram equalization improved visibility of histopathological structures. These preprocessing steps helped mitigate staining variations, imaging artifacts, and overfitting, leading to improved feature extraction and model performance.

Data Splitting is a crucial phase in the development of machine learning models, as it involves partitioning the dataset into individual subsets designated for training, testing and validation purposes. In this study, the dataset with initially 10,000 images has been divided as 7000 images for training, 1000 images for testing and 2000 images for validation. The primary reasons for data splitting are as follows:

Training set: The training set serves the purpose of instructing the model to recognizing patterns and features corresponding to the different classes within the dataset. A larger training set allows the ColoNet to acquire a vast array of features and variations, enhancing its ability to generalize new, unseen data.

Validation set: For refining the model's hyperparameters, the validation set plays a pivotal role. It aids in mitigating overfitting by evaluating the model's performance on data not seen during training. Adjustments can be made based on the validation set performance to optimize the model's generalization capability.

Test set: The test set serves as a completely independent dataset not used during training or validation. Offering an impartial evaluation of the model's generalizability to novel, unseen data, the validation set simulates real-life scenarios.

3.2 Model Architecture

The architecture of ColoNet is presented in Fig. 1. It is designed to optimize hierarchical feature extraction while maintaining computational efficiency. The choice of multiple convolutional layers with increasing filter sizes (from 32 to 128) allows for capturing both low- and high-level spatial features, essential for distinguishing subtle histopathological patterns. Max-pooling layers are incorporated to reduce spatial dimensions, preventing excessive parameter growth, and enhancing model generalization. The use of ReLU activation ensures non-linearity, aiding in better learning of complex tissue structures. Dropout layers (0.3 and 0.4) were strategically placed after fully connected layers to reduce overfitting, a common issue in medical image classification. These dropout rates were chosen based on empirical validation, where a balance between reducing overfitting and retaining sufficient model complexity was observed. Alternative dropout rates were tested (e.g., 0.2 and 0.5), but the selected values provided better generalization on validation data. The selection of filter sizes (3x3) is based on its effectiveness in deep CNN architectures, allowing efficient feature extraction while keeping computational complexity manageable. Alternative larger filter sizes (e.g., 5x5) were tested but did not provide significant performance improvements while increasing training time.

Model: "sequential_3"

Layer (type)	Output Shape	Param #
conv2d_18 (Conv2D)	(None, 510, 510, 32)	896
max_pooling2d_12 (MaxPooling2D)	(None, 255, 255, 32)	0
conv2d_19 (Conv2D)	(None, 253, 253, 32)	9,248
conv2d_20 (Conv2D)	(None, 251, 251, 64)	18,496
max_pooling2d_13 (MaxPooling2D)	(None, 125, 125, 64)	0
conv2d_21 (Conv2D)	(None, 123, 123, 32)	18,464
conv2d_22 (Conv2D)	(None, 121, 121, 64)	18,496
max_pooling2d_14 (MaxPooling2D)	(None, 60, 60, 64)	0
conv2d_23 (Conv2D)	(None, 58, 58, 128)	73,856
max_pooling2d_15 (MaxPooling2D)	(None, 29, 29, 128)	0
flatten_3 (Flatten)	(None, 107648)	0
dense_18 (Dense)	(None, 256)	27,558,144
dropout_6 (Dropout)	(None, 256)	0
dense_19 (Dense)	(None, 128)	32,896
dense_20 (Dense)	(None, 64)	8,256
dropout_7 (Dropout)	(None, 64)	0
dense_21 (Dense)	(None, 32)	2,080
dense_22 (Dense)	(None, 16)	528
dense_23 (Dense)	(None, 1)	17

Fig. 1. Proposed CNN Architecture of ColoNet

In the initial convolutional layer, the input images undergo filtering with 32 filters of size 3x3, resulting in an output tensor of dimensions (510, 510, 32). Subsequently, a max-pooling layer is applied with a 2x2 frame, reducing the spatial dimensions to (255, 255, 32). Following this, another convolution layer employs 32 filters of size 3x3, and a subsequent max-pooling layer further reduces the dimensions to (253, 253, 32). Continuing, another convolutional operation is conducted with 64 filters of size 3x3, maintaining the output shape as (251, 251, 64). This is succeeded by a max-pooling layer with a 2x2 window, resulting in spatial dimension reduction to (125, 125, 64). Further, a convolution

layer with 32 filters of size 3x3 is applied, followed by max-pooling, reducing the dimensions to (123, 123, 32). Another convolution layer follows suit, this time with 64 filters of size 3x3, maintaining the output shape as (121, 121, 64). Subsequently, utilizing a 2x2 window, the max-pooling layer reduces spatial dimensions to (60, 60, 64). Further, a convolution layer applies 128 filters of size 3x3, followed by max-pooling, reducing the dimensions to (58, 58, 128), and then further down-sampling to (29, 29, 128).

Next, a Flatten layer is added to transform the convolution layer's output into a one-dimensional tensor, followed by a fully connected layer with 256 neurons. Dropout of 0.3 is then introduced for regularization, leading to another fully connected layer with 128 neurons, and subsequently, a layer with 64 neurons. Another dropout layer of 0.4 is added for further regularization, followed by a fully connected layer with 32 neurons, and then 16 neurons. Finally, the output layer classifies the various colon cancer images. The model comprises a total of 27,741,377 parameters, representing the weights and biases learned during training. This architecture exemplifies a typical combination of convolutional, pooling, and dense layers in a CNN for image classification tasks, supplemented by dropout layers to mitigate overfitting.

3.3 Hyper Parameters

The tunable hyper parameters in the model are shown in Table 2.

Table 2. Hyper-Parameters

Hyperparameter	Value
Optimizer	Adam
Learning Rate	Default (Adam optimizer's default)
Loss Function	Binary Cross-entropy
Batch Size	64
Epochs	50
Dropout Rate (Layer 1)	0.3 (30%)
Dropout Rate (Layer 2)	0.4 (40%)

The selection of hyperparameters, including the learning rate, number of epochs, batch size, and dropout rates, was based on a combination of empirical experimentation and validation performance analysis. The Adam optimizer's default learning rate was chosen due to its adaptive properties, which allow for efficient convergence across deep learning models. The number of epochs (50) was determined through iterative experimentation, where training beyond this point showed minimal improvements while increasing computational costs. To fine-tune key hyperparameters, an initial grid search was conducted over a range of values for dropout rates (0.2–0.5), batch sizes (32–128), and number of neurons in fully connected layers. The final configuration was selected based on validation accuracy and generalization performance.

3.4 Evaluation Metrics

Performance metrics are quantitative measurements used to evaluate how well machine learning models predict or classify data based on a dataset. These metrics provide insight into how accurately models work in real-life scenarios by providing insights into several performance metrics such as:

3.4.1 Accuracy

Accuracy as described in equation 1 defines how often the model's prediction comes true out of the total predictions it makes.

$$Accuracy = \frac{\text{True Positive+True Negative}}{\text{True Positive+False Positive +True Negative+False Negative}} \quad (1)$$

3.4.2 Precision

Precision of the model focuses on the positive predictions that the model makes. It shows how often the model predict positive instances without mislabeling negative as positive as defined in equation 2.

$$Precision = \frac{\text{True Positive}}{\text{True Positive + False Positive}} \quad (2)$$

3.4.3 Recall

Recall measures as shown in equation 3 defines how well the model is at finding every positive instance present in the dataset. It indicates whether the model can catch all the positives without missing any.

$$Recall = \frac{\text{True Positive}}{\text{True Positive + False Negative}} \quad (3)$$

3.4.4 F1-score

It is a harmonic mean of precision and recall which provides a balance between precision and recall when the classes in the dataset are imbalanced as depicted in equation 4. It ranges between 0 to 1. A higher F1 – score indicates that model performed well in terms of both precision and recall.

$$F1\ Score = 2 * \frac{\text{Recall} * \text{Precision}}{\text{Recall} + \text{Precision}} \quad (4)$$

4. Results and Discussion

This section analyzes the results obtained by ColoNet for the detection of colon cancer.

4.1 Confusion Matrix

The confusion matrix in Fig. 2 provides an overview of ColoNet's performance in classifying colon cancer images into benign and malignant categories. The rows represent the actual class, while the columns denote the predicted classifications. The diagonal elements indicate correctly classified instances, whereas the off-diagonal values correspond to misclassifications.

In this study:

True Positives (TP): 463 cases of colon adenocarcinoma (colon_aca) were correctly identified.

True Negatives (TN): 499 cases of benign tissue (colon_n) were correctly classified.

False Positives (FP): 1 benign sample was misclassified as adenocarcinoma.

False Negatives (FN): 37 adenocarcinoma cases were misclassified as benign.

The false negative (FN) count of 37 is particularly critical, as missing malignant cases could lead to delayed diagnosis and treatment. However, the false positive (FP) count is very low (only 1 case), which means the model rarely misclassifies benign tissues as cancerous, reducing unnecessary follow-up tests and anxiety.

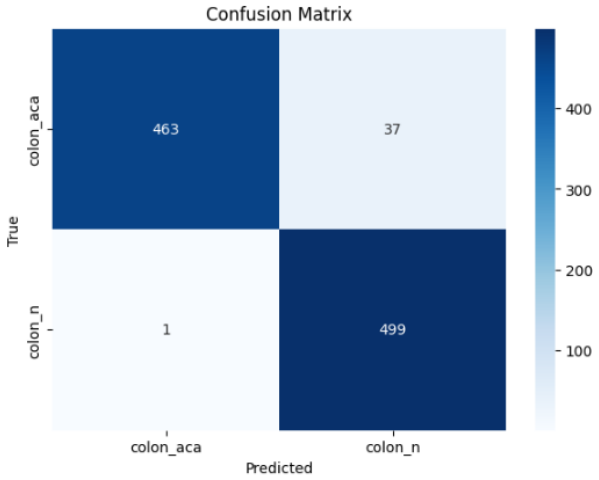

Fig. 2. Confusion Matrix obtained by ColoNet

4.2 Classification Report

The classification report shown below in Table 3 demonstrates the model's performance for each class.

Table 3. Classification Report obtained by ColoNet

	Precision	Recall	F1-Score	Support
COLON_ACA	1.00	0.93	0.96	500
COLON_N	0.93	1.00	0.96	500
Accuracy			0.96	1000
MACRO AVERAGE	0.96	0.96	0.96	1000
WEIGHTED AVERAGE	0.96	0.96	0.96	1000

4.2.1 Precision

The precision metric assesses the model's accuracy in making positive predictions. In the case of COLON_ACA, the precision value is 1.00, indicating perfect classification of all instances predicted as COLON_ACA. Conversely, for COLON_N, the precision stands at 0.93, suggesting that 93% of instances predicted as COLON_N were accurately classified.

4.2.2 Recall (Sensitivity)

Recall, also referred to as sensitivity, gauges the percentage of actual positive instances correctly predicted by the model. For COLON_ACA, the recall rate is 0.93, demonstrating the correct classification of 93% of actual COLON_ACA instances. On the other hand, for COLON_N, the recall value is 1.00, implying the accurate prediction of all actual COLON_N instances by the model.

4.2.3 Specificity

Specificity reflects how well the model identifies benign cases (COLON_N). With 99.8% specificity, only 0.2% of benign cases were misclassified as cancerous, reducing unnecessary follow-ups or treatments.

4.2.4 F1-Score

The F1-Score serves as the harmonic mean of precision and recall, offering a balanced evaluation of the model's performance. Both COLON_ACA and COLON_N exhibit an F1-Score of 0.96, highlighting a high level of performance concerning both precision and recall.

4.2.5 Support

Support pertains to the frequency of actual occurrences of each class within the dataset. In this scenario, there exist 500 instances of both COLON_ACA and COLON_N.

4.2.6 Accuracy

The model's overall accuracy is 0.96, indicating that 96% of all instances in the dataset were correctly classified.

4.2.7 Macro Average

The macro average computes the average precision, recall, and F1-Score for each class independently before averaging these values. In this instance, the macro average precision, recall, and F1-Score all amount to 0.96, indicating a balanced performance across the classes.

4.2.8 Weighted Average

The weighted average determines the average metrics by considering the support of each class. Given that both classes have equal support with 500 instances each, the weighted average aligns with the macro average.

The findings suggest that the model is efficient in classifying both COLON_ACA and COLON_N, showcasing high precision, recall, and F1-Score, alongside an elevated overall accuracy level.

4.3 Model Accuracy

The accuracies obtained by ColoNet are shown in Table 4. The accuracy metrics indicate the performance of the model on different datasets.

Table 4. Accuracy of ColoNet

Training Accuracy	97.36%
Validation Accuracy	96.60%
Testing Accuracy	96.66%

4.3.1 Training Accuracy

This metric measures the accuracy of the model on the training dataset, which is the data used to train the model. A training accuracy of 97.36% means that the model correctly classified 97.36% of the instances in the training dataset.

4.3.2 Validation Accuracy

Validation accuracy is the accuracy of the model on a separate validation dataset that is not used during training but is used to tune hyperparameters and monitor the model's performance. A validation accuracy of 96.60% indicates that the model correctly classified 96.60% of the instances in the validation dataset.

4.3.3 Testing Accuracy

Testing accuracy measures the performance of the model on a completely new and unseen dataset, which is used to evaluate the model's generalization ability. A testing accuracy of 96.66% means that the model correctly classified 96.66% of the instances in the testing dataset.

4.4 Training Accuracy versus Validation Accuracy

The training accuracy curve and validation accuracy curve are essential tools for evaluating the performance of a machine learning model during training. The training vs validation accuracy curve for the Model architecture obtained

over 50 epochs is shown below in Fig. 3. It is apparent from the plot that initially, both curves show an upward trend, indicating that the model is learning from the training data, as reflected by increasing accuracy. As training progresses, the curves stabilize, converging to similar values. The training accuracy reaches around 97.3%, while the validation accuracy stabilizes at approximately 96.6%. The close alignment and stabilization of both curves suggest that the model is not overfitting and has successfully generalized to unseen data. This convergence indicates that the model has been effectively trained and exhibits reliable performance on both the training and validation datasets.

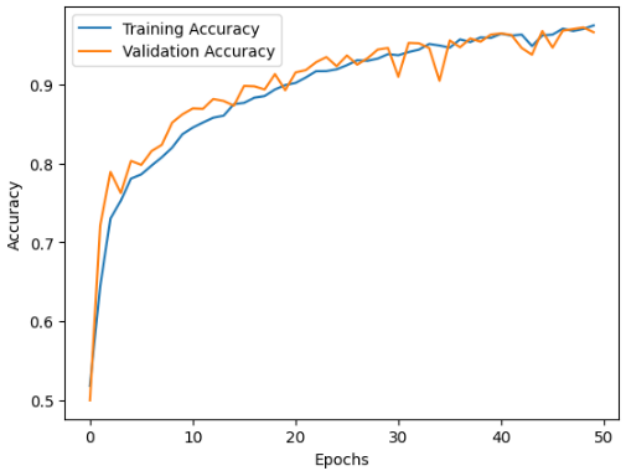

Fig. 3. Training vs Validation Accuracy Plot

4.5 Training Loss versus Validation Loss

The training versus validation loss curve over 50 epochs is shown in Fig. 4. The plot depicting training versus validation loss curves provides insights into the model's performance throughout the training process. Initially, both training and validation loss values start relatively high at 0.7 and gradually decrease with each epoch. This decrease indicates that the model is effectively minimizing its loss function and improving its predictive capabilities. As training progresses, both curves continue to decrease, converging to lower values. By the end of 50 epochs, the loss values have significantly decreased to around 0.1, indicating that the model has learned meaningful representations from the data and can make accurate predictions. The close alignment and convergence of both training and validation loss curves suggest that the model is not overfitting and has successfully generalized to unseen data, demonstrating robust performance across epochs.

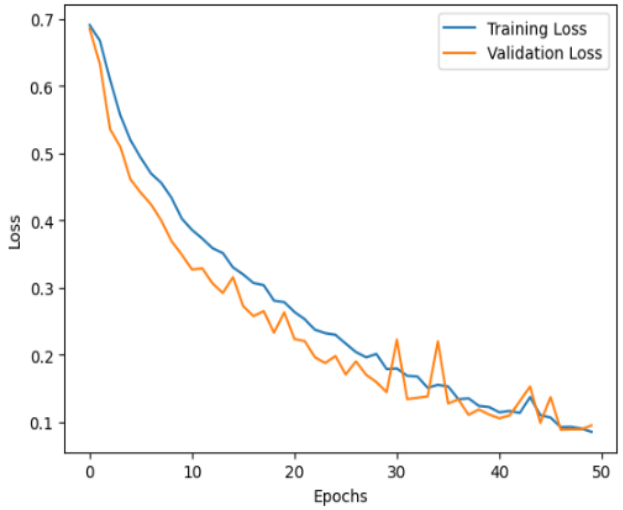

Fig. 4. Training vs Validation Loss Plot

5. Conclusion

In this research, we presented ColoNet, a CNN-based system designed for the early diagnosis and classification of colon adenocarcinoma using digital histopathology images. The model achieved 96.66% accuracy by integrating advanced preprocessing techniques, convolutional layers, and dropout layers to optimize feature extraction and reduce overfitting. ColoNet's strong performance across key metrics—recall, precision, accuracy, and F1-score—demonstrates

its potential in automating the diagnostic process, assisting pathologists in identifying and classifying colon tumors.

While ColoNet has shown excellent classification performance, further explorations could enhance its applicability in broader clinical settings. Expanding its validation to more diverse datasets and real-world histopathological slides would help in assessing its robustness across different imaging conditions. Additionally, integrating interpretability techniques, such as heatmaps, could provide visual insights into the model's predictions, improving its usability for pathologists. Future work may also explore benchmarking against other state-of-the-art models with statistical comparisons to further solidify its advantages.

In addition to diagnostic accuracy, efficiency and adaptability to clinical workflows are important considerations for real-world deployment. Optimizing computational performance and exploring avenues for seamless integration with digital pathology systems will be valuable next steps. In summary, ColoNet presents a promising AI-driven solution for colon cancer diagnosis, leveraging deep learning to enhance early detection and classification. By incorporating additional refinements in generalizability, interpretability, and clinical integration, ColoNet can serve as a reliable tool in digital pathology, supporting early intervention and improved patient outcomes.

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