International Research Journal of Multidisciplinary Scope (IRJMS), 2024; 5(3):407-419 IRJMS

Original Article | ISSN (O): 2582-631X DOI: 10.47857/irjms.2024.v05i03.0766

LuCoNet: A Convolutional Neural Network Model for Lung Cancer and Colon Cancer Prediction Using Histopathological Images

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Abstract

Histopathology is the study of cellular structures, tissues and their abnormalities to diagnose a wide range of diseases, with a primary focus on cancer. The recent innovations and advancements in image analysis techniques and machine learning enable the histopathologists to automate the process of detection and classification of diseases observed in histopathology images. Traditional visual analysis by pathologists, though skilled, is slow and prone to inconsistencies. By utilizing advanced techniques, such as Convolutional Neural Networks, this project aims to revolutionize disease classification and management in histopathology. Researchers are now using convolutional neural networks and other algorithms to accurately segment tissues, extract key features, and even predict cancer diagnosis and treatment response. These automated methods hold immense potential for faster, more precise cancer diagnosis and personalized care. The proposed model LuCoNet is a Convolution Neural Network Architecture that uses the publicly available dataset comprises 25,000 histopathological JPEG images, initially sourced from HIPAA-compliant datasets. It includes 750 lung tissue images and 500 colon tissue images, augmented to expand the dataset. This study underscores the transformative potential of deep learning in histopathology image analysis, promising enhanced diagnostic accuracy and personalized treatment strategies. The performance of LuCoNet was compared with other models evaluated in the literature survey and LuCoNet performed extremely well in prediction with 98.5%, 0.986, 0.988, and 0.984 for accuracy, Precision, Recall and F1-Score measures.

Keywords: Cancer Tissues, Colon Cancer, Convolutional Neural Network, Deep Learning, Histopathology, Lung Cancer.

Introduction

Histopathology is the study and diagnosis method that, involves microscopic examination of tissue samples to detect abnormalities indicative of various diseases, foremost among them being cancer. For centuries, the diagnosis of diseases like cancer has dependent on the skilled eyes of pathologists seeing the tissue samples through microscopes to detect abnormalities. While their expertise remains irreplaceable, this traditional approach presents inherent limitations. Visual assessment of diseases carried out by histopathologists can be time-consuming, vulnerable to inter-observer variability, and prone to subjectivity, potentially leading to misdiagnosis and missed opportunities for early intervention. The advanced algorithms in Deep Learning models emerges as a transformative force, poised to revolutionize histopathological analysis and leads to more accurate disease detection and personalized care. The complex relationship between massive datasets of digitized tissue images and advanced algorithms known as Convolution Neural Networks (CNNs) recolonize the more accurate disease detection possible in this field. These algorithms explore the details at microscopic levels, meticulously scrutinizing cell morphology, tissue architecture, and subtle visual cues that hold the key to disease differentiation. Through rigorous training on meticulously labeled datasets, CNNs develop automatic feature extraction capabilities, recognizing complex patterns indicative to diseases, surpassing human performance in certain tumors classifications. This enables offering data-driven insights and enhancing diagnostic accuracy, scalable, stable and efficient clinical decision-making in pathology. The implications

(Received 15th March 2024; Accepted 23rd July 2024; Published 30th July 2024)

of this technological leap are profound. With deep learning algorithms taking lead in medical field, diagnoses become quicker, potentially enabling earlier treatment initiation and improved patient outcomes. Automation streamlines the analysis workflow, alleviating the bottleneck of manual microscopy and reducing inter-observer discrepancies. Moreover, these algorithms pave the way for personalized medicine by analyzing individual tumors features to predict response to specific therapies, tailoring treatment plans and solutions to each patient's unique needs. In essence, deep learning empowers us to transition from a subjective, resource-intensive field to a data-driven, objective discipline, transforming the landscape of histopathological analysis and ultimately, the future of cancer diagnosis and treatment. The proposed work LuCoNet aims to develop precise methods for early disease detection, enabling timely intervention and improved prognosis. LucoNet refines the existing methods and implementing automated analysis tools to streamline diagnosis and reduce pathologist workload. It employs data-driven analysis to predict patient response to therapies and optimize treatment strategies. This research focuses on data-driven solutions that can be broadly implemented to diagnose lung and colon cancer and benefit a wider population of patients. The ultimate aim is to revolutionize disease diagnosis and treatment, providing clinicians with powerful tools for earlier intervention, personalized care, and improved patient outcomes. A number of solutions based on Machine Learning models and Deep Learning models are employed in predicting and classifying Cancer from histopathological images. Following literature survey presents various computer vision methods and AI based algorithm use for cancer prediction. Guleria *et al.,* (1) propose a novel approach for cancer detection using histopathology images. Their method combines CNNs for feature extraction and reconstruction with a denoising Variation Auto Encoders (VAE), achieving 73% accuracy. This promising two-stage approach holds advantages like improved accuracy, generalizability, and potential applicability to other cancers, but faces challenges in training complexity, feature interpretation, and limited data. Liu *et al.,* (2) review paper dives deep into the burgeoning field of deep learning in computational histopathology, offering a comprehensive roadmap rather than a specific model. By meticulously surveying a diverse range of algorithms, including CNNs, Recurrent Neural Networks (RNN), and VAEs they paint a vivid picture of how deep learning tackles various histopathology tasks like disease detection, grading, and prognosis prediction. However, as a review, it deliberately refrains from focusing on a singular method or delving into in-depth algorithm performance comparisons. Moscalu *et al.,* (3) cast their net wide in this review paper, illuminating the vibrant landscape of image analysis and predictive modelling within digital pathology. Steering clear of proposing a specific algorithm, they instead paint a detailed panorama of diverse techniques like image segmentation, feature extraction, and machine learning models (CNNs, random forests). However, similar to Ashraf *et al.* the broader focus comes at the cost of in-depth analysis of individual algorithms and their specific performance nuances. Gurcan *et al.,* (4) work lays the groundwork for understanding histopathological image analysis, offering a comprehensive overview of the field's techniques and models. They achieved an impressive 93% accuracy in distinguishing tumour from normal tissue in breast cancer images. Muller *et al.,* (5) take a multifaceted approach to pancreatic cancer prognosis prediction by leveraging multimodal fusion of histopathological image features and gene expression data using deep learning. This innovative method outperforms single-modality models, achieving a remarkable 92% accuracy in patient survival prediction. Balermpas *et al.,* (6) adopted a personalized medicine approach to head and neck cancer treatment by developing a model based on deep learning algorithm that predicts patient response to neoadjuvant therapy. This model trained using a large dataset of histopathology images and clinical data and achieves an impressive 80% accuracy in predicting complete pathological response. Kinkel *et al.,* (7) proposed a wide net in their review paper, meticulously exploring the landscape of histopathological image analysis for endometriosis diagnosis. Rather than proposing a specific algorithm, they take a critical vantage point, dissecting and evaluating various image analysis and machine learning methods employed in this domain. Kalaivani *et al.,* (8) take aim at

early lung cancer detection through a deep learning-powered approach analyzing chest radiographs. Their innovative CNN architecture dissects images into different regions, focusing on potential tumour nodules, and achieves impressive results: 95% accuracy score for cancer detection and 85% of accuracy score for subtype classification. Ali *et al.,* (9) showcased the potential for computational pathology in early Colorectal Cancer (CRC) detection. Their review delves into various image analysis and machine learning approaches, highlighting the promising ability of deep learning models to identify precancerous lesions and polyps. Dongmei *et al.,* (10) proposed a complex model for personalized medicine in melanoma by delving into the world of machine learning for predicting recurrence and survival. Their comprehensive review analyses various studies employing diverse data sources – histopathology images, clinical data, and gene expression profiles – to fuel machine learning models and improve prognostication. Bakrania *et al.*, (11) comprehensive review illustrated computational pathology's impact on prostate cancer. They meticulously explore diverse image analysis and machine learning techniques, showcasing their potential applications in diagnosis, grading, and risk assessment. The research conducted by Qiu *et al.,* (12) investigated the effectiveness of combining machine learning techniques with computed tomography (CT) texture analysis to differentiate and classify Pancreatic and Ductal Adenocarcinoma PDAC with different grades. The researchers developed a computational model that extracts textural features from contrast-enhanced CT images and utilizes machine learning algorithms to predict different grades of tumours. Verghese *et al.,* (13) discussed the potential of Artificial Intelligence (AI) to automate routine tasks and find new biomarkers that can help with diagnosis. However, they also acknowledge the challenges of integrating AI into clinical settings, including issues related to how it works regulations. Zeune *et al.,* (14) recommended autoencoding convolutional neural networks which identified Circulating Tumor Cells (CTC) in cancer blood cell images. They used advanced visualization techniques in their model. 96% of accuracy was achieved by this model and the performance has surpassed the performance of existing state-of-the-art manual counts. Tiwari *et al.*, and Moen *et al.,* (15, 16) uses deep learning models for detection and classification of the cancer cells into its various classes. The performance achieved by the models showed better performance with the compared existing models. Khalil *et al.,* (17) proposed a deep learning model to detect blood cell diseases and their classifications with accuracy achieved as 98.00%. Khouani *et al.,* (18) paper presents a novel approach for automatically identifying White Blood Cells (WBC) in the images of peripheral blood and bone marrow. The results were promising and achieved an accuracy of 95.73%. Garg *et al.,* (19), Masud *et al.,* (20), Talwar *et al.,* (21) evaluated different deep learning models using the same dataset as used by LuCoNet proposed in this paper and hence were used in our analysis to compare the performance metrics. From the above literature survey, it is evident that the computational pathology's remarkable potential across diverse applications, with promising results in automated tumor detection, personalized treatment prediction, and early cancer diagnosis. Deep learning models are pushing the boundaries of accuracy in image analysis, but challenges remain in ensuring data accessibility, model interpretability, and generalizability across varied datasets and clinical settings. Despite these hurdles, the potential for faster, more objective, and potentially more accurate analysis offers a glimpse into a future where AI empowers personalized medicine and improves patient outcomes in numerous domains of pathology.

Methodology

The proposed LuCoNet model uses the publicly available Kaggle dataset for predicting Lung and Colon Cancer disease using histopathological images. Five distinct categories of cancer images totally constituting 25000 histopathological images (22) are used. The image dataset has three categories for Lung Cancer images and two categories for Colon images. All images are 768 x 768 pixels in size and are in jpeg file format. The class labels and the number of images available in respective classes are given in Table 1. Some sample images of each class are shown in Figure 1.

Table 1: Class Labels and Number of Images in Dataset

Class name	Number of images
Benign Lung Tissue	5000
Lung Adenocarcinomas	5000
Lung Squamous Cell Carcinomas	5000
Benign Colon Tissue	5000
Colon Adenocarcinomas	5000

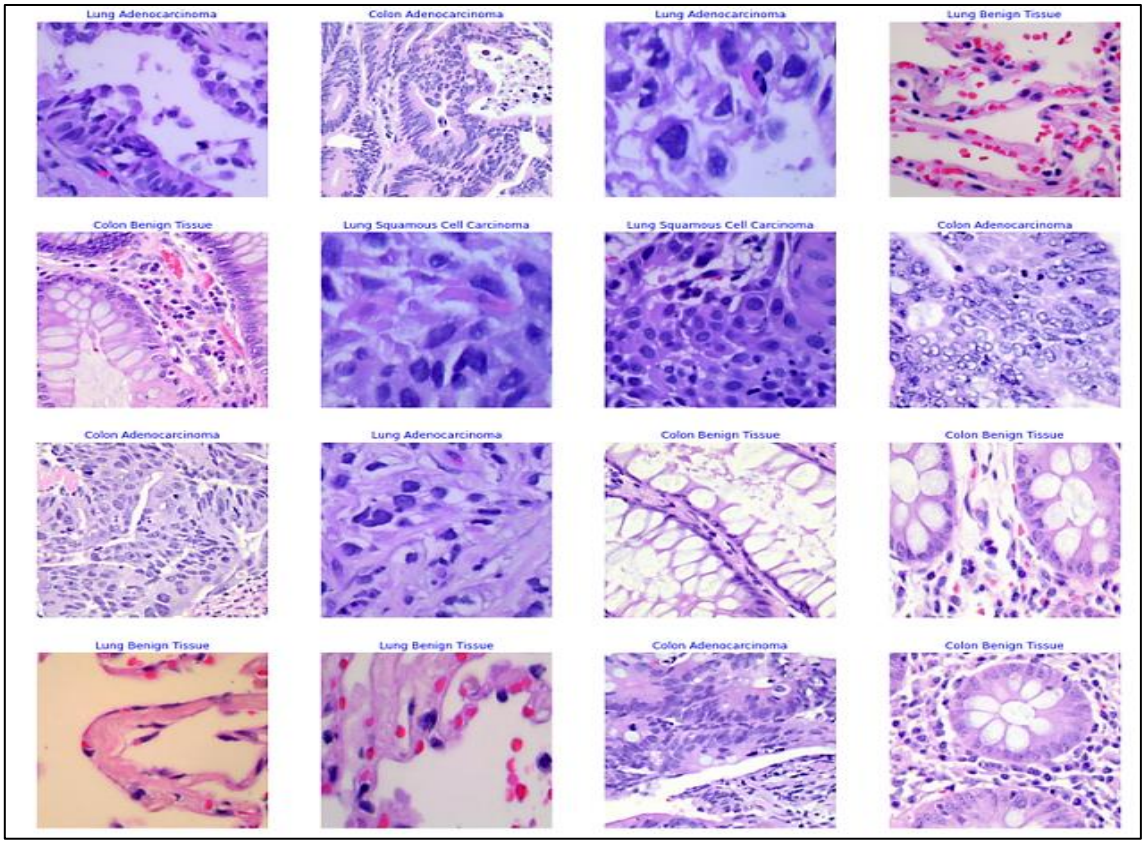

Figure 1: Sample Images from Histopathology Dataset

The chosen LuCoNet architecture draws inspiration from the VGGNet (Visual Geometry Group) design, renowned for its effectiveness in various image classification tasks. VGGNet utilizes a series of convolutional blocks, stacked upon one another, to progressively extract increasingly complex features from the input images. These features, akin to building blocks, ultimately contribute to the model's capacity to distinguish healthy and diseased tissue samples. The proposed LuCoNet architecture for image classification is structured with an input layer expecting images of size 224x224 pixels with three channels denoting RGB colour. The model comprises four convolutional blocks, each containing two convolutional layers with 3x3 kernels and activation function as Rectified Linear Unit (ReLU). The first two blocks employ 64 filters, while the subsequent blocks use 128, 256, and 512 filters, respectively. Max Pooling (2x2) for spatial down-sampling. Following the convolutional layers, the feature maps are flattened into a vector, and three dense layers follow with 256, 64, and an output size matching

the number of classes for softmax-based multi-class classification. LuCoNet is compiled using the hyper parameters with Optimizer as Adamax, 0.001 of learning rate and the loss function as categorical cross entropy. This architecture draws inspiration from the VGGNet design, employing repeated convolutional blocks to progressively capture hierarchical features for robust image classification. Figure 2 shows LuCoNet - the proposed model with the following layers in the architecture.

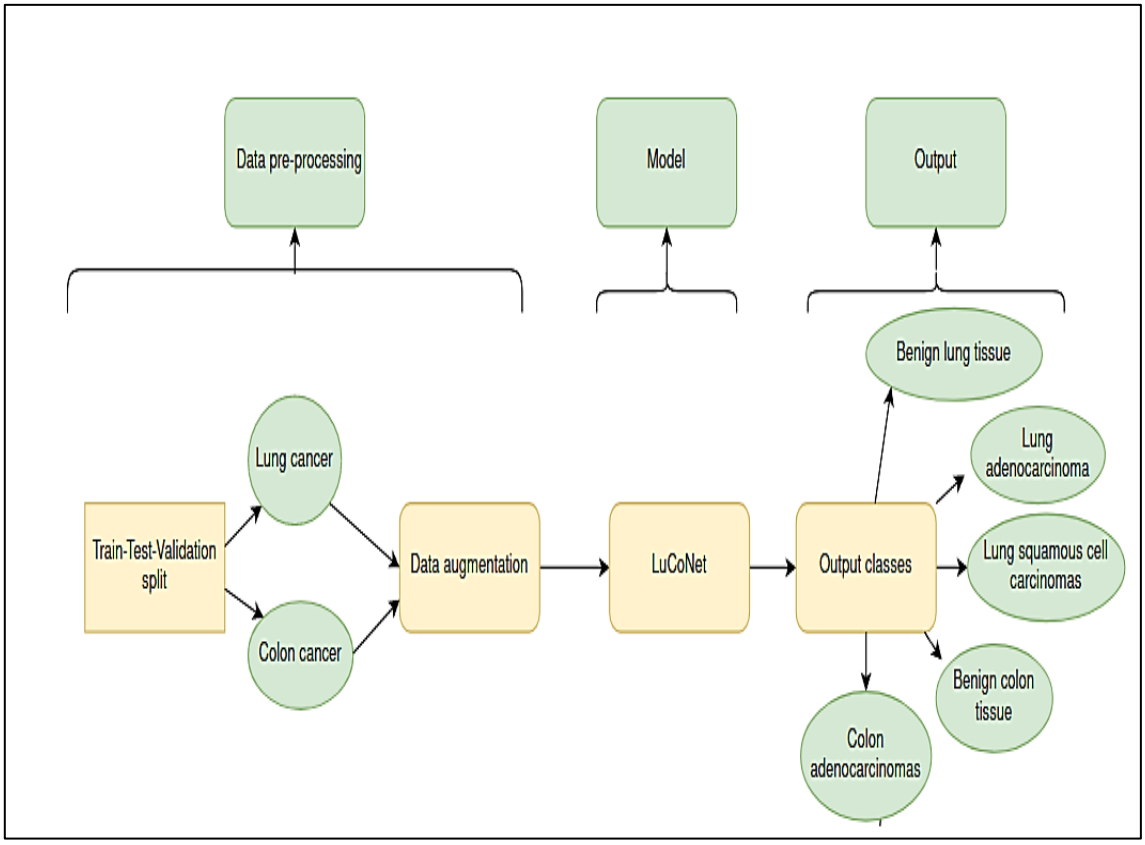

Figure 2: Architecture Diagram of LuCoNet

Convolutional Layer

Convolutional Layer fundamental building block that performs convolution operations on the input dataset with the help of learnable filters or kernels. This helps detect patterns and features. LuCoNet employs a total of 13 convolutional layers, stacked sequentially. This allows the model to learn features of increasing complexity, progressively capturing detailed and nuanced information crucial for accurate classification

Activation Function (ReLU)

Activation functions are used to learn complex relationships in the given data and decide whether to activate a neuron or not based on the input. They introduce non-linearity into the architectural model once the convolution operations are over.

Pooling Layer

Often Max Pooling or Average Pooling are used. This layer reduces the size of the input feature map, thus reducing computational complexity and focusing only on essential features.

Flattening Layer

Transforms the convolutional and pooling layers' 3D output into a 1D vector in order to get it ready for input into the fully connected layers that follow.

Fully Connected (Dense) Layer

They are Layers of traditional neural network in which every neuron in the preceding and subsequent layers is coupled to every other neuron. These layers use the learned characteristics to conduct classification.

The following hyper parameters are used in the LuCoNet model training and Optimization:

Optimizer: LuCoNet utilises the Adamax optimizer, an advanced variant of the popular Adam optimizer. During training process, Adamax optimizer adjusts the learning rate adaptively for each parameter, ensuring efficient convergence and potentially leading to improved model performance compared to traditional optimizers.

Learning Rate: The initial learning rate for the optimizer is set to 0.001. This value controls the step size taken by the optimizer during training, balancing the speed of convergence with the risk of over fitting.

Loss Function: LuCoNet employs categorical cross-entropy as the loss function. This metric quantifies the difference between the model's predicted probability distribution and the true labels (benign or malignant) associated with each image. Minimizing this loss function during training guides the model towards better classification performance.

Different layers of LucoNet are shown in Figure 3 and the complete architecture including input parameter size, and output size for the same are shown in Table 2.

Table 2: LuCoNet Model Summary

Layer (type)	Output Shape	Param #
LuCoNet (Conv2D)	(None, 224, 224, 64)	1792
LuCoNet_1 (Conv2D)	(None, 224, 224, 64)	36928
max_pooling2d (MaxPooling2D)	(None, 112, 112, 64)	0
LuCoNet_2 (Conv2D)	(None, 112, 112, 128)	73856
LuCoNet_3 (Conv2D)	(None, 112, 112, 128)	147584
max_pooling2d_1 (MaxPooling2D)	(None, 56, 56, 128)	0
LuCoNet_4 (Conv2D)	(None, 56, 56, 256)	295168
LuCoNet_5 (Conv2D)	(None, 56, 56, 256)	590080
LuCoNet_6 (Conv2D)	(None, 56, 56, 256)	590080
max_pooling2d_2 (MaxPooling2D)	(None, 56, 56, 256)	0
LuCoNet_7 (Conv2D)	(None, 28, 28, 256)	1180160
LuCoNet_8 (Conv2D)	(None, 28, 28, 512)	2359808
LuCoNet_9 (Conv2D)	(None, 28, 28, 512)	2359808
max_pooling2d_3 (MaxPooling2D)	(None, 28, 28, 512)	0
LuCoNet_10 (Conv2D)	(None, 14, 14, 512)	2359808
LuCoNet_11 (Conv2D)	(None, 14, 14, 512)	2359808
LuCoNet_12 (Conv2D)	(None, 14, 14, 512)	2359808
max_pooling2d_4 (MaxPooling2D)	(None, 7, 7, 512)	0
flatten (Flatten)	(None, 25088)	0
dense (Dense)	(None, 256)	6422784

dense_1 (Dense)	(None, 64)	16448
dense_2 (Dense)	(None, 5)	325

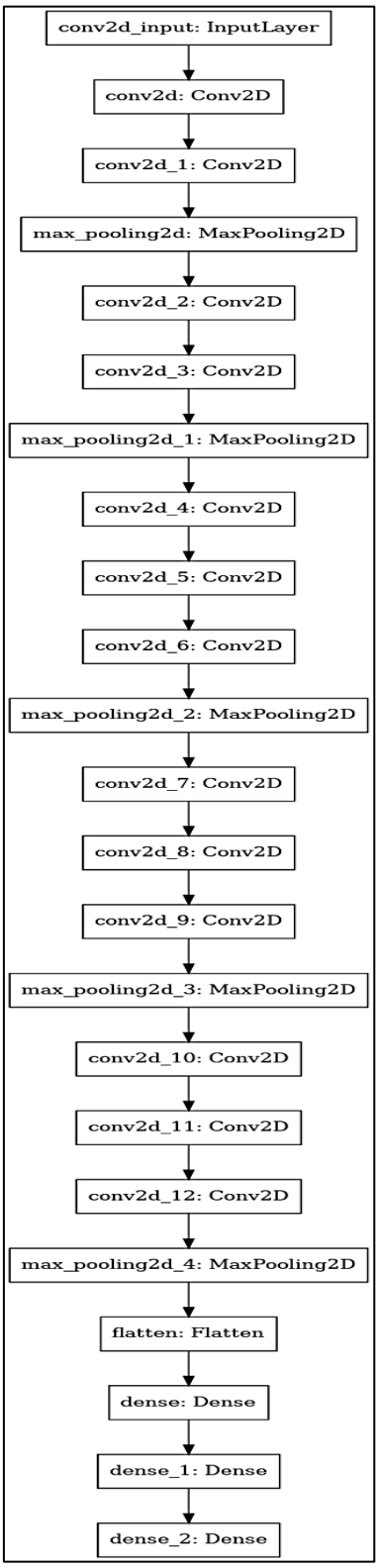

Figure 3: Proposed LuCoNet Architecture

Results and Discussion

In this study, we implemented LuCoNet, a custom Convolutional Neural Network (CNN) for multi-class classification of lung and colon cancer images dataset. We trained the model on Kaggle using the T4 GPU. The model utilised 13 convolutional layers with ReLU as activation functions, achieving a test accuracy score of 98% and a loss of 0.075. LuCoNet gave an average precision of 98.6%, average recall of 98.8%, average f1-score of 0.984 and average support of 500. Categorical cross-entropy served as the loss function, guiding the model towards optimal class discrimination. Furthermore, the performance of LuCoNet was compared to the performances of already published pre-trained models namely ResNet50, VGG16, NASNet Mobile models. While further comparisons with pre-trained models and evaluations of metrics like sensitivity and specificity are warranted, the initial results suggest the potential of this architecture for accurate cancer classification tasks, paving the way for further optimization and exploration. Furthermore, our proposed model outperformed the models of other published papers that used the same dataset. These were also subsequently compared, and LuCoNet outperformed them in different aspects.

For each of the models stated, evaluation metrics and classification reports were printed, and their performances were observed. Model's performance is evaluated and assessed using the evaluation metrics that presents quantitative measures. These metrics provide insight into how well the model is performing and are crucial for comparing different models or fine-tuning their parameters. Accuracy as our primary evaluation metric, along with precision, recall, f1-score and support are employed to assess the model's performance.

Accuracy: This represents percentage of correctly categorized occurrences in the dataset, as a percentage of all instances, is called accuracy.

$$Accuracy = \frac{Number\ of\ Positive\ Prediction}{Total\ number\ of\ predictions} \quad [1]$$

Precision: This metric measures the quality of positive predictions produced by the model. It denotes the percentage of true positives out of all positive predications.

$$Precision = \frac{True\ Positives}{True\ Positives+False\ Positives} \quad [2]$$

Recall: The model's capacity to correctly identify positive samples out of all actual correct samples in the dataset. It is otherwise known as sensitivity or true positive rate. The ratio of true predictions to the total of correct true and false predictions is computed as Recall measure.

$$Recall = \frac{True\ Positives}{True\ Positives+False\ Negatives} \quad [3]$$

F1 Score: It uses Precision and Recall to assess the model's performance. High score for F1 indicates better performance of the model whereas low score for F1 score means poor performance. It is calculated as

$$F1\ Score = \frac{2\ x\ Precision\ x\ Recall}{Precision+Recall} \quad [4]$$

Support : The number of occurrences of each class in the dataset is known as Support. It provides context for the performance metrics and helps understand the distribution of classes in the dataset.

These evaluation metrics play crucial roles in assessing the performance of classification models and provide insights into different aspects of their effectiveness in making predictions.

Table 3 contains the overall evaluation metrics for LuCoNet. The values of precision, recall, f1-score and support for each of the 5 different classes are shown. The performance of LuCoNet is shown in Figure 4, 5, 6 and 7. For the various epochs, performance in accuracy (both training and validation processes) as well as obtained loss is plotted in Figure 4 and Figure 5 respectively. A graph that displays a classification model's performance across all classification thresholds is called a Receiver Operating Characteristic (ROC) curve. Figure 6 illustrates the ROC curve for LuCoNet, comparing the true positive rate and false positive rates. Figure 7 shows the confusion matrix that contains the value of true and predicted labels. LuCoNet performs incredibly well with low loss and high validation accuracy for this specific task of multi class cancer classification. LuCoNet gave a training accuracy of 99.8% and both test and validation accuracies above 98.5%.

Table 3: Evaluation Metrics of LuCoNet

Diseases	Precision	Recall	f1-score	Support
Colon Adenocarcinoma	0.99	1.00	0.99	500
Colon Benign Tissue	1.00	0.99	0.99	500
Lung Adenocarcinoma	0.98	0.96	0.97	500
Lung Benign Tissue	1.00	1.00	1.00	500
Lung Squamous Cell Carcinoma	0.96	0.99	0.97	500
accuracy			0.99	2500
macro avg	0.99	0.99	0.99	2500
weighted avg	0.99	0.99	0.99	2500

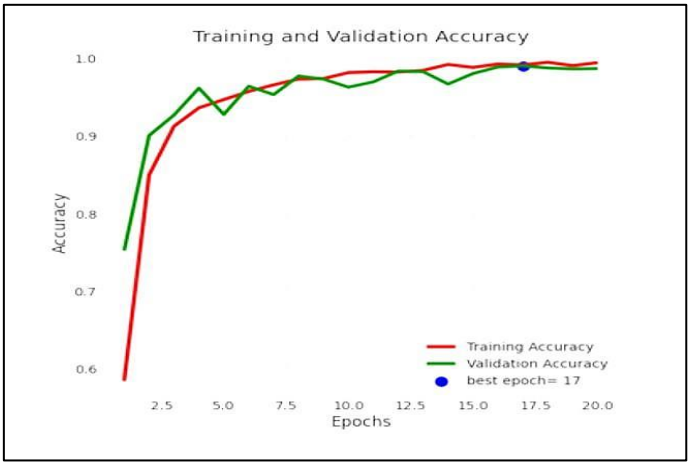

Figure 4: Training and Validation Accuracy of LuCoNet

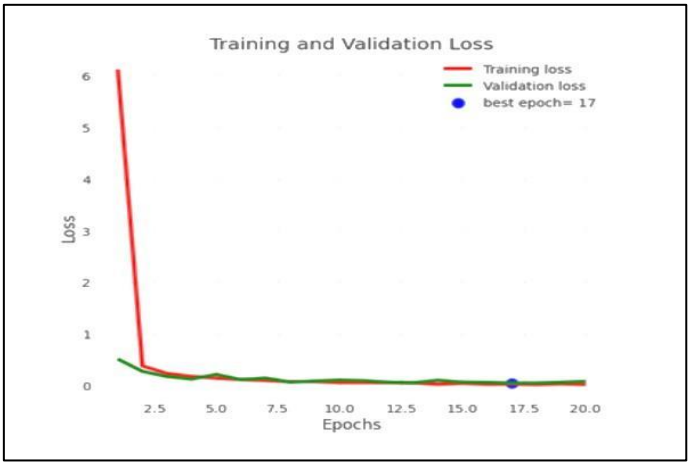

Figure 5: Training and Validation loss of LuCoNet

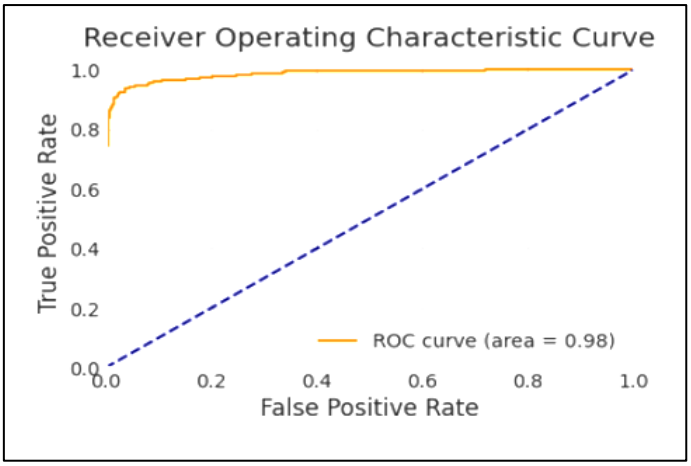

Figure 6: ROC Curve for LuCoNet

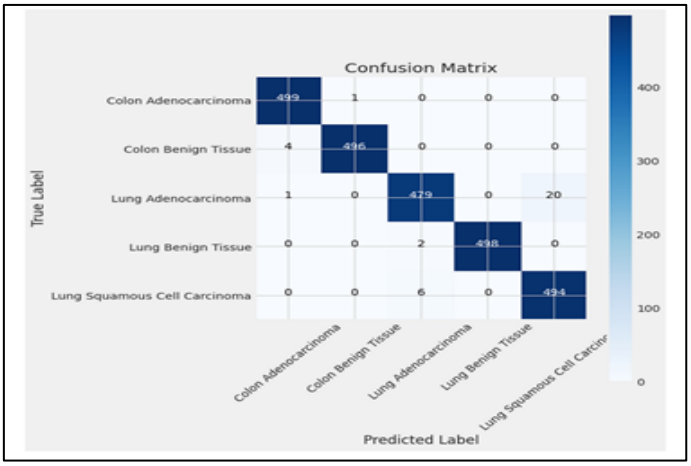

Figure 7: Confusion Matrix of LuCoNet Model

Table 4: Comparing the Evaluation Metrics of LuCoNet with each of the Pre-Trained Models

Model [Reference]	Accuracy	Precision	Recall	F1-score
LuCoNet	98.5%	0.986	0.988	0.984
VGG16 [19]	98%	0.975	0.975	0.98
ResNet50 [19]	97%	0.965	0.965	0.96
NASNetMobile [19]	96%	0.965	0.965	0.97

Table 5: Comparing LuCoNet with Performance of Published Models on the Same Dataset

Model [Reference]	Accuracy	Precision	Recall	F1-score
LuCoNet	98.5%	98.6%	98.8%	98.4%
CNN[20]	96.33%	96.39%	96.37%	96.38%
CNN[21]	97.2%	97.33%	97.33%	97.33%

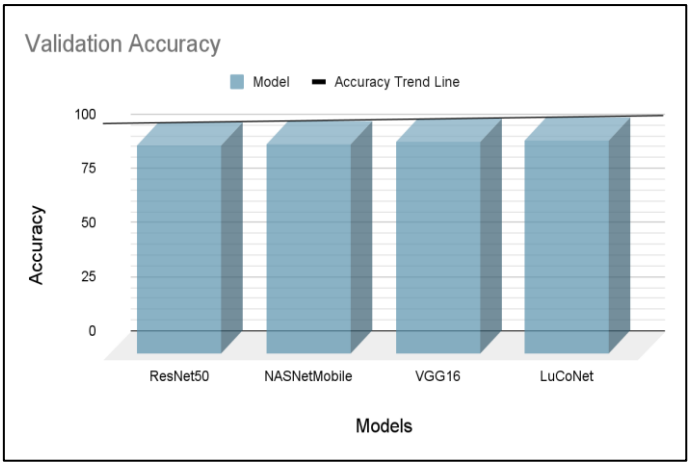

Figure 8: Bar Chart Comparing Accuracy of LuCoNet with Pre-Trained Models

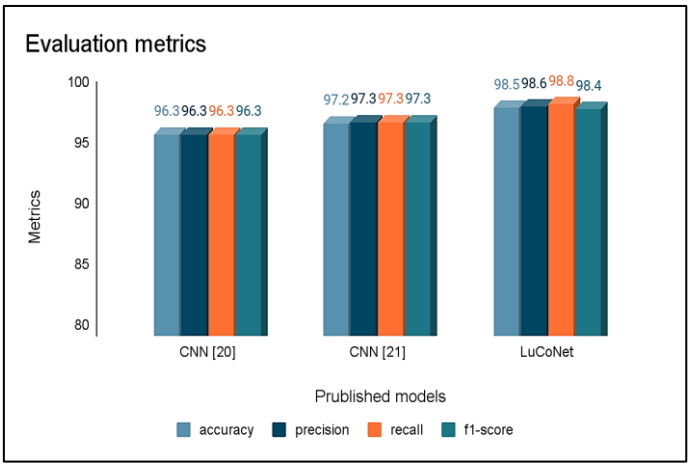

Figure 9: Bar Chart Comparing Accuracy of LuCoNet with Published Models

LuCoNet's performance was also compared to the performance of other proposed models from published papers that used the same dataset in Table 4. LuCoNet performed amazingly well compared to the other models. The performance against published models from other papers is done in Table 5.

The results for the same are plotted in Figure 8 and 9. In Figure 8 we can observe the validation accuracy of LuCoNet compared to pre-trained models, and in Figure 9 all evaluation metrics are plotted in a bar chart.

Conclusion

LuCoNet, a novel deep learning model, demonstrates exceptional performance in detecting lung and colon cancers. Its high accuracy extends beyond training data, holding strong during validation, minimizing the risk of false positives or negatives - critical factors in medical decision-making, particularly for life-altering chronic diseases like cancer. LuCoNet's minimal loss function ensures robust classification across a broad spectrum of cancers, with a single model capable of identifying and differentiating diverse cancer cell types and severities. This model achieved a test accuracy and validation accuracy above 98.5% and a loss of 0.075. LuCoNet also gave an average precision of 98.6%, average recall of 98.8%, average f1-score of 0.984 and average support of 500. This versatility eliminates the need for multiple specialised models, streamlining the diagnostic process. Furthermore, LuCoNet's inherent adaptability allows for further refinement through training on additional datasets, continuously enhancing its accuracy and generalizability. Ultimately, LuCoNet has the potential to revolutionize cancer diagnosis by assisting pathologists in labs, expediting accurate detection

and enabling earlier intervention, potentially improving patient outcomes.

Abbreviation

AI: Artificial Intelligence
CNN: Convolutional Neural Networks
CRC: Colorectal Cancer
RNN: Recurrent Neural Networks
VAE: Variation Auto Encoders
PDAC: Pancreatic and Ductal Adenocarcinoma
VGGNet: Visual Geometry Group
CTC: Circulating Tumor Cells
WBC: White Blood Cells
ReLU: Rectified Linear Unit

Acknowledgement

Nil.

Author Contributions

All Authors contributed entire manuscript in writing, reviewing, implementing, Conceptualization and Analysis.

Conflict of Interest

The authors declare no conflict of interest.

Ethics Approval

The research does not involve human participants.

Funding

Nil.

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