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Lung and Colon Cancer Histopathological Image Classification Using Deep Learning Approaches

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***Abstract*—This paper investigates the application of deep learning for multi-class classification of lung and colon cancer histopathological images using the LC25000 dataset. The dataset contains 25,000 images equally distributed across five classes: benign and adenocarcinoma for both lung and colon tissues, and squamous cell carcinoma for lung tissue. Preprocessing involved converting labels to one-hot encoding and removing 1280 identified duplicate images to prevent data leakage. Three models were trained and evaluated: a baseline CNN, an enhanced CNN with architectural modifications and regularization, and a transfer learning model utilizing ResNet50. The baseline model, using Adam optimizer and categorical cross-entropy loss, achieved a test accuracy of 62.6% and validation accuracy of 63.7%. The enhanced model, incorporating increased depth, adjusted kernel size, L2 regularization, dropout, and the Adamax optimizer with early stopping, reached a test accuracy of 97.9% and validation accuracy of 98.1%. Finally, the transfer learning model with ResNet50, fine-tuned with additional dense layers, dropout, and early stopping, achieved near-perfect performance with 98.9% test accuracy and 99.3% validation accuracy. This study demonstrates the significant performance improvement achieved through architectural enhancements and transfer learning, highlighting the potential of deep learning for automated diagnosis of cancer from histopathological images. The removal of duplicate images proved essential for accurate performance evaluation and preventing artificially inflated results due to data leakage.**

***Index Terms*—Histopathological Image Classification,Lung and Colon Cancer,Convolutional Neural Network (CNN),Transfer Learning,ResNet50.**

I. Introduction

Lung and colon cancers are among the leading causes of cancer-related mortality worldwide, underscoring the critical need for early detection to improve patient outcomes. Histopathological imaging plays a pivotal role in the diagnosis of these cancers, as it allows for the detailed examination of tissue samples to identify malignant cells. However, the high variability in tissue structures and staining techniques presents significant challenges in accurately interpreting these images. Studies have highlighted the importance of histopathological examination in colorectal cancer, emphasizing that early detection can significantly expand treatment options and reduce mortality rates [1]. Similarly, the manual analysis of histopathology images for lung cancer detection is labor-intensive and highly dependent on the pathologist's expertise, which can lead to variability in diagnostic accuracy [2]. These challenges necessitate the development of automated, reliable methods to enhance the precision and efficiency of cancer diagnosis. Deep learning, particularly convolutional neural networks (CNNs), offers promising solutions to these challenges by improving the accuracy of histopathological image analysis. CNNs have demonstrated impressive capabilities in image processing tasks, including medical imaging, by learning complex patterns and features from large datasets [2]. Transfer learning, using architectures like ResNet, has been particularly effective in leveraging pre-trained models to enhance classification performance, even with limited labeled data [1], [2]. This approach allows for the adaptation of models trained on large, diverse datasets to specific tasks, such as cancer detection, thereby improving generalization and reducing the need for extensive annotated datasets [3]. Despite these advancements, challenges remain, such as the need for models to generalize across different centers and staining protocols, which can lead to overfitting if not properly addressed [4]. Nonetheless, the integration of deep learning techniques in histopathological image analysis holds significant potential for advancing cancer diagnostics and improving patient care.

II. Related Work

Convolutional Neural Networks (CNNs) have revolutionized medical imaging, offering significant advancements in classification, segmentation, and detection tasks. Seminal architectures like AlexNet, VGG, and ResNet have laid the groundwork for these applications, demonstrating their efficacy in various medical domains. For instance, CNNs have been pivotal in enhancing diagnostic accuracy and efficiency in radiology and pathology, where they have been used to automate the analysis of complex medical images, thus reducing the reliance on manual interpretation and improving early disease detection [5]. In the context of cancer histopathology, CNNs have been employed to classify lung and colon cancer images, leveraging their ability to learn intricate patterns from large datasets.

Recent studies have focused on applying deep learning, particularly CNNs, to classify cancer from histopathological images, with a strong emphasis on lung and colon cancer.

For example, the BIC-SGODL method utilizes DenseNet and convolutional LSTM to capture complex features and spatiotemporal information, achieving high performance in cancer diagnosis [6]. Another study compared various pre-trained models, including VGG-16 and ResNet, on the LC25000 dataset, achieving accuracies up to 100% for certain categories, highlighting the effectiveness of transfer learning in this domain [2]. Additionally, novel architectures like the 1D Convolutional Channel-based Attention Networks have been proposed, achieving state-of-the-art performance with minimal computational resources [7]. These studies underscore the potential of deep learning models to significantly improve the accuracy and efficiency of cancer diagnosis.

Transfer learning has emerged as a powerful technique in histopathology, allowing models to leverage pre-trained weights from large datasets to improve performance on specific tasks. For instance, the Inception-ResNetV2 model, combined with local binary pattern features, achieved 99.98% accuracy in lung and colon cancer detection, demonstrating the utility of integrating texture-based features with deep learning [8]. Similarly, EfficientNet variants, when applied with transfer learning, achieved notable accuracy improvements, with EfficientNetB2 reaching 97% accuracy on the LC25000 dataset [9]. These approaches highlight the advantages of transfer learning in overcoming challenges such as limited labeled data and enhancing model generalizability.

Future research directions include developing more robust models that can handle diverse data sources and improving the interpretability of deep learning models to facilitate their integration into clinical workflows [5]. Additionally, exploring novel architectures and training strategies could further enhance the performance and applicability of these models in real-world settings.

III. Data Collection and Preprocessing

This section details the dataset used, preprocessing steps performed, and exploratory data analysis conducted.

A. Dataset Description

This study leverages the LC25000 Lung and Colon Cancer Histopathological Image Dataset introduced by [10], a publicly accessible resource containing 25,000 RGB histopathological images across five balanced classes: Colon Benign Tissue, Colon Adenocarcinoma, Lung Benign Tissue, Lung Adenocarcinoma, and Lung Squamous Cell Carcinoma, with each class comprising 5,000 images. Figure 1 showcases representative images from eachclass, visually highlighting the diversity of histopathological features within thedataset.

B. Data Preprocessing

Data cleaning and preprocessing were essential steps in preparing the histopathological images for effective model training. The following methods were applied to ensure data quality, standardize input, and optimize the dataset for Convolutional Neural Networks (CNNs):

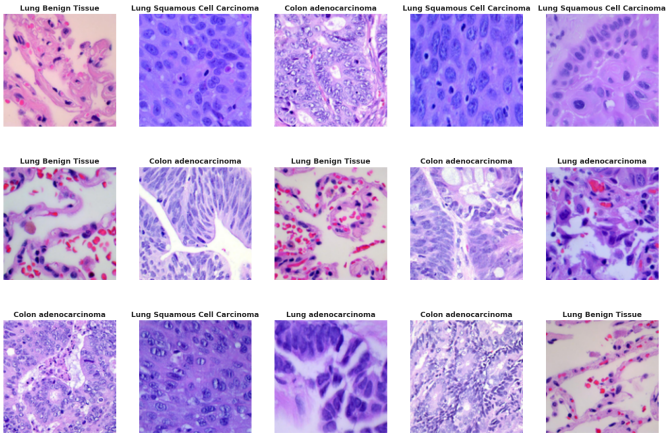

Fig. 1: Visual examples of histopathology slides from the LC25000 dataset.

- **Data Cleaning and Duplicate Removal**: An initial exploratory data analysis (EDA) assessed class distribution and identified duplicate images. This process removed 1,280 duplicates, resulting in a final dataset of 23,720 images (See Figure 2).
- **Image Resizing**: All images were resized to 120x120 pixels using LANCZOS resampling, balancing computational efficiency with preservation of critical histopathological details for feature extraction.
- **Normalization**: Although not explicitly applied in the code, normalization is recommended to scale pixel values between 0 and 1 (or -1 and 1). This practice stabilizes model training and prevents dominant features from skewing the learning process.
- **One-Hot Encoding of Target Classes**: To support multi-class classification, categorical target variables were transformed into binary vectors using one-hot encoding, preventing unintended ordinal relationships among diagnostic categories.
- **Train-Validation-Test Split**: The dataset was divided into training, validation, and test sets in a 60%-20%-20% ratio, ensuring balanced class representation across all phases (Figure 3).

IV. Methodology

This section details the methodologies employed for developing and evaluating the deep learning models for lung and colon cancer histopathological image classification. Figure 4 provides an overview of the proposed system, illustrating the workflow from dataset acquisition and preprocessing through model training, evaluation, and final classification.

A. Baseline Model

A baseline Convolutional Neural Network (CNN) model was established to serve as a benchmark for subsequent, more complex architectures. This model provides a foundation for evaluating the performance gains achieved through architectural modifications and transfer learning. The baseline

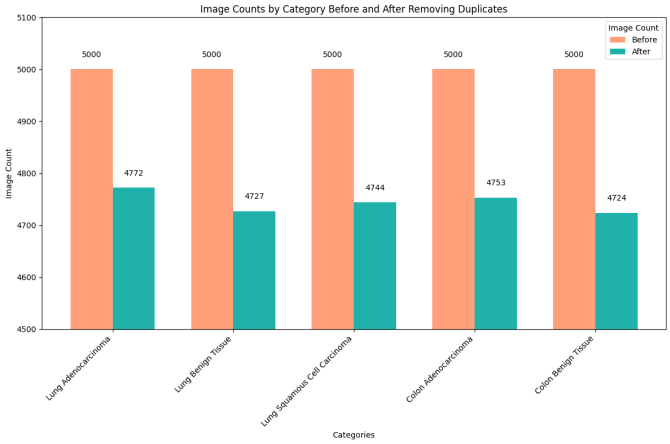

Fig. 2: Image Counts by Category Before and After Removing Duplicates.

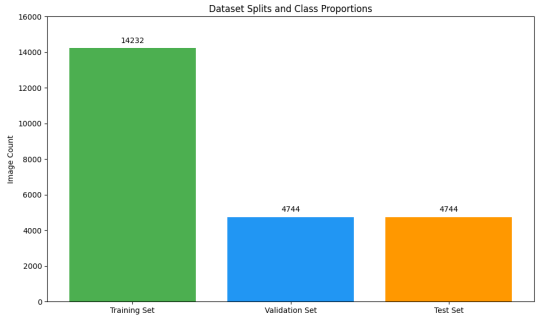

Fig. 3: Dataset Splits and Class Proportions.

model architecture, comprising convolutional, max pooling, and dense layers, is summarized in Figure 5.

B. Enhanced Model

To improve upon the baseline CNN, the enhanced model introduces additional convolutional layers, regularization techniques, and an optimized architecture to further capture the intricate patterns present in histopathological images. These modifications aim to reduce overfitting and enhance classification accuracy across the five cancer-related categories. The enhanced CNN architecture, incorporating increased depth, adjusted kernel size, and regularization, is detailed in Table I.

C. Transfer Learning Model (ResNet50)

we employed ResNet50 a deep residual network pre-trained on the ImageNet dataset, as the foundation for our transfer learning model. The architecture of the transfer learning model, utilizing a pre-trained ResNet50 base and custom classification layers, is depicted in Figure 6. This figure outlines the layer configurations and the distinction between trainable and non-trainable parameters.

D. Training Configuration

This section provides an overview of the key training configurations used across the baseline, enhanced, and transfer learning (ResNet50) models. The configurations include essential hyperparameters, optimizers, learning rates, batch sizes, and epochs, highlighting the specific settings employed to achieve optimal performance for each model (see Table II).

TABLE I: Enhanced Model Architecture

Layer (type)	Output Shape	Param #
conv2d_4 (Conv2D)	(None, 120, 120, 64)	1792
conv2d_5 (Conv2D)	(None, 120, 120, 64)	102464
max_pooling2d_4 (MaxPooling2D)	(None, 60, 60, 64)	0
conv2d_6 (Conv2D)	(None, 60, 60, 128)	73856
conv2d_7 (Conv2D)	(None, 60, 60, 128)	147584
max_pooling2d_5 (MaxPooling2D)	(None, 30, 30, 128)	0
conv2d_8 (Conv2D)	(None, 30, 30, 256)	295168
conv2d_9 (Conv2D)	(None, 30, 30, 256)	590080
max_pooling2d_6 (MaxPooling2D)	(None, 15, 15, 256)	0
conv2d_10 (Conv2D)	(None, 15, 15, 512)	1180160
conv2d_11 (Conv2D)	(None, 15, 15, 512)	2359808
max_pooling2d_7 (MaxPooling2D)	(None, 7, 7, 512)	0
flatten_2 (Flatten)	(None, 25088)	0
dense_6 (Dense)	(None, 256)	6422784
dropout (Dropout)	(None, 256)	0
dense_7 (Dense)	(None, 64)	16448
dense_8 (Dense)	(None, 5)	325
Total params:	11190469 (42.69 MB)	
Trainable params:	11190469 (42.69 MB)	
Non-trainable params:	0 (0.00 Byte)	

V. Result

The results of this study are based on the evaluation of three deep learning models—baseline CNN, enhanced CNN, and transfer learning with ResNet50—using a diverse set of performance metrics.

A. Model Performance Comparison

Each model was assessed on accuracy, precision, recall, and F1-score, providing a comprehensive view of performance across categories.The bar graph in Figure 7 further highlights these performance improvements across models, illustrating the ResNet50 model's significant gains over the baseline and enhanced CNN models.

B. Confusion Matrix Analysis

The confusion matrices for each model illustrate the model's effectiveness in differentiating between benign and malignant tissues. Misclassifications were notably reduced in the enhanced and ResNet50 models compared to the baseline.

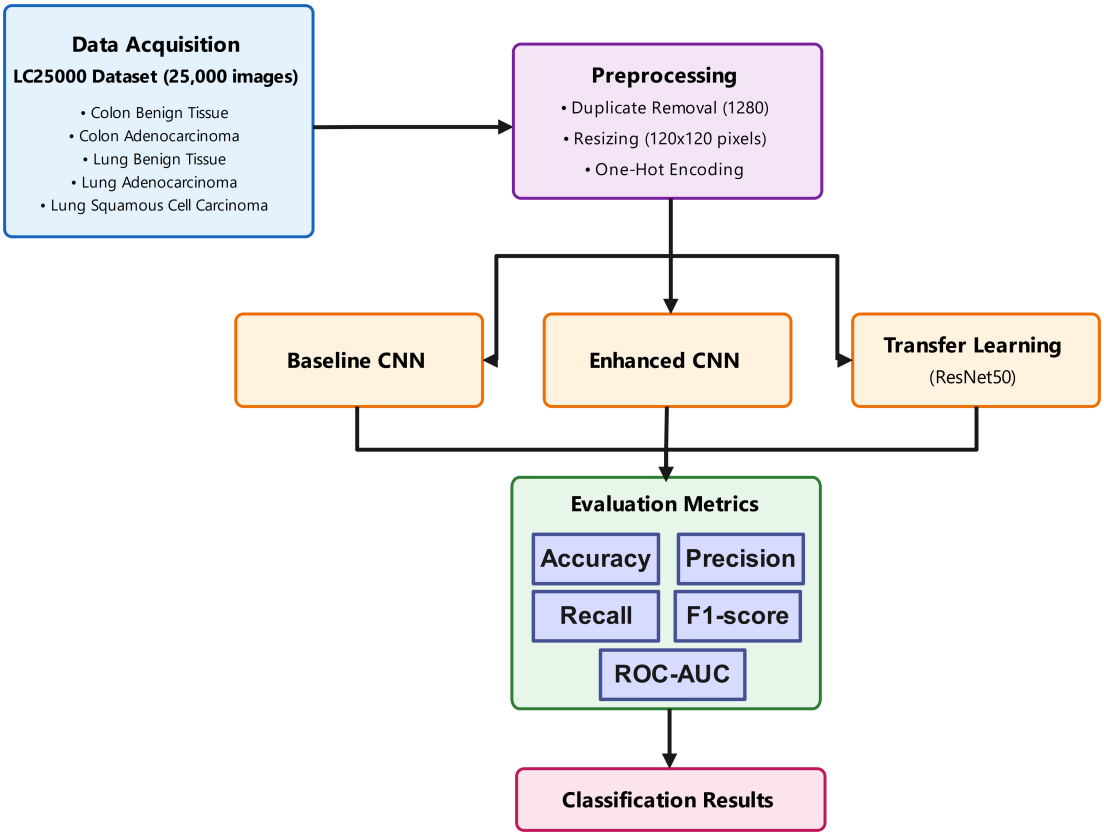

Fig. 4: Proposed System Diagram.

TABLE II: Training Configurations for Each Model

Model	Optimizer	Learning Rate	Batch Size	Epochs	Regularization	Early Stopping
Baseline Model	Adam	Default	32	10	None	No
Enhanced Model	Adamax	0.0005	32	30	L2 Regularization, Dropout (0.2)	Patience 2
Transfer Learning Model (ResNet50)	Adamax	0.0005	32	30	Dropout (0.2)	Patience 3

C. ROC-AUC Analysis

ROC-AUC curves were generated for each model to evaluate the models' abilities to distinguish between classes. The ResNet50 model achieved an AUC close to 1.0 across all categories, indicating strong discriminative power.

D. Discussion

The ResNet50 transfer learning model achieved the highest performance across metrics, followed by the enhanced CNN model. The baseline model, while effective as an initial benchmark, demonstrated limited accuracy and a higher rate of misclassification. The results underscore the impact of deep learning architectures and transfer learning in handling complex histopathological data, with the ResNet50 model emerging as the optimal approach for cancer classification in this study.

VI. Conclusion

This paper evaluated lung and colon cancer classification using three models: a baseline CNN, an enhanced CNN, and a ResNet50-based transfer learning model. The ResNet50 model achieved the highest performance, with 98.9% accuracy and strong precision, recall, and F1-scores, demonstrating its superior capability in feature extraction for complex histopathological images. These results confirm the value of transfer learning in medical image analysis and set a foundation for future advancements in automated cancer diagnosis.

Acknowledgment

The authors would like to extend their gratitude to the members of LASS Laboratory (University of M'sila, Algeria) for their valuable support and assistance in publishing this work.

Layer (type)	Output Shape	Param #
conv2d_2 (Conv2D)	(None, 120, 120, 128)	3584
max_pooling2d_2 (MaxPooling2D)	(None, 60, 60, 128)	0
conv2d_3 (Conv2D)	(None, 60, 60, 64)	73792
max_pooling2d_3 (MaxPooling2D)	(None, 30, 30, 64)	0
flatten_1 (Flatten)	(None, 57600)	0
dense_3 (Dense)	(None, 128)	7372928
dense_4 (Dense)	(None, 32)	4128
dense_5 (Dense)	(None, 5)	165

Total params: 7454597 (28.44 MB)
Trainable params: 7454597 (28.44 MB)
Non-trainable params: 0 (0.00 Byte)

Fig. 5: Summary of the baseline CNN architecture.

Model: "sequential_3"

Layer (type)	Output Shape	Param #
resnet50 (Functional)	(None, 4, 4, 2048)	23587712
global_average_pooling2d_1 (GlobalAveragePooling2D)	(None, 2048)	0
dense_9 (Dense)	(None, 256)	524544
dropout_1 (Dropout)	(None, 256)	0
dense_10 (Dense)	(None, 64)	16448
dense_11 (Dense)	(None, 5)	325

Total params: 24129029 (92.04 MB)
Trainable params: 541317 (2.06 MB)
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Fig. 6: Architecture of the transfer learning model using ResNet50.

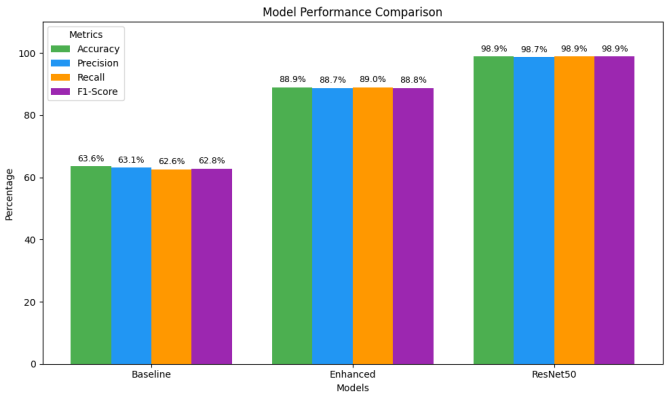
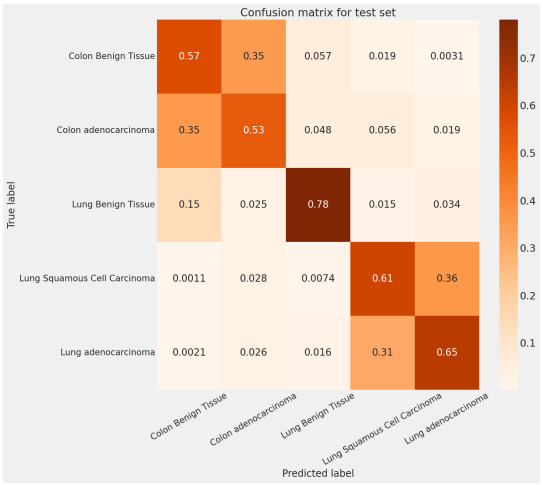
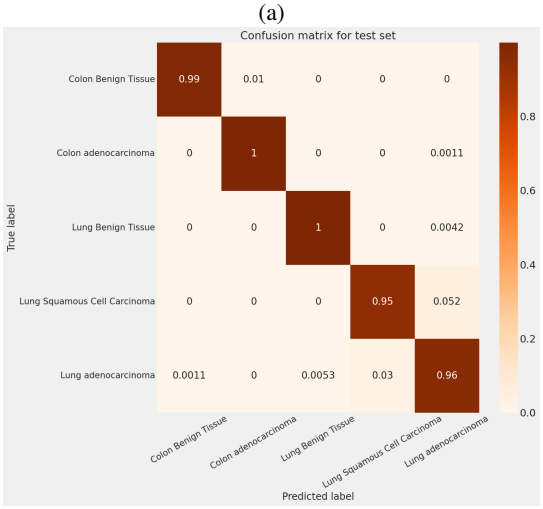


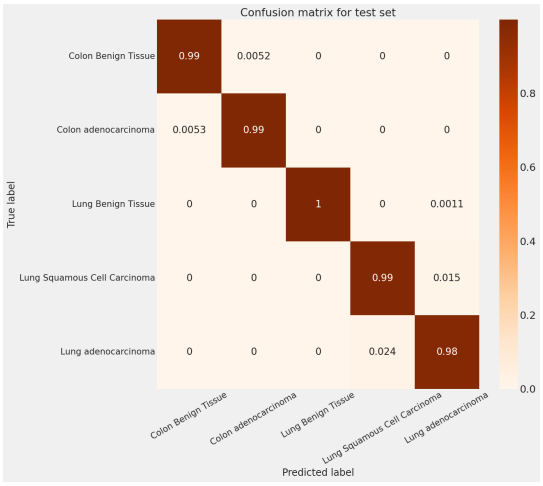
Fig. 7: Bar graph comparison of model performance metrics.



(a)

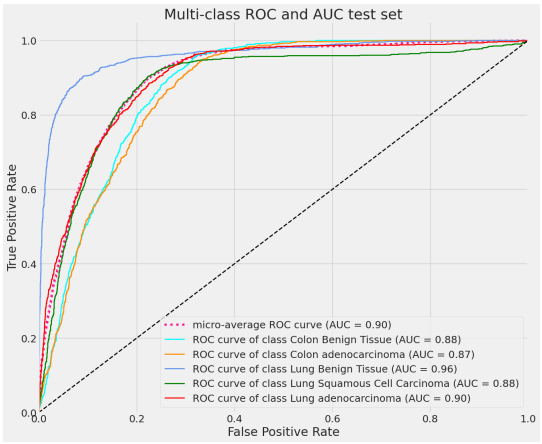


(b)

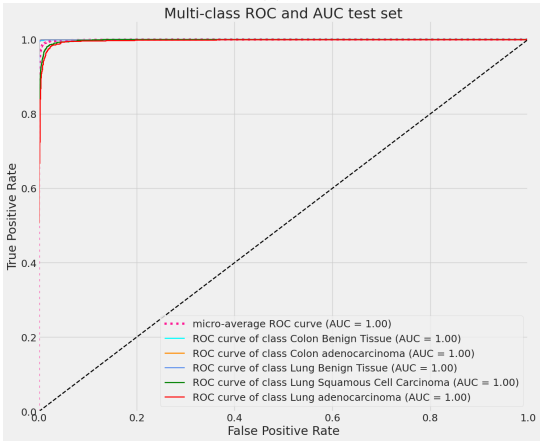


(c)

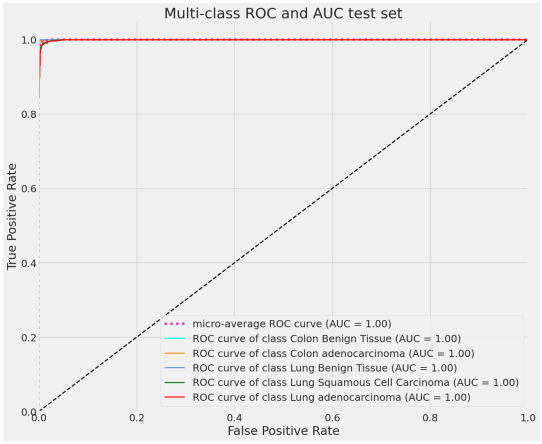
Fig. 8: Confusion matrix for (a:baseline model,b:enhanced model,c:ResNet50 model)



(a)



(b)



(c)

Fig. 9: ROC-AUC curves for (a:baseline model,b:enhanced model,c:ResNet50 model)

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