Deep Learning Framework for Colon and Lung Cancer detection using CNNs

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ABSTRACT

Cancer remains one of the leading causes of mortality worldwide. The World Health Organization (2025) reports approximately 10 million cancer deaths in 2020, with lung and colorectal cancers among the largest contributors, accounting for an estimated 20% and 9% of cancer deaths, respectively. This study presents a convolutional neural network (CNN)-based framework for classifying histopathological images into five classes: lung adenocarcinoma (lungaca), lung squamous cell carcinoma (lungscc), benign lung tissue (lungn), colon adenocarcinoma (colonaca), and benign colon tissue (colonn), with the goal of supporting diagnostic workflows across clinical contexts. The model was trained on the publicly available LC25000 dataset and evaluated using accuracy, precision, recall, F1-score, confusion matrices, receiver operating characteristic (ROC) curves, and area under the curve (AUC). The architecture consists of four convolutional blocks, global average pooling, dropout, and a 512-unit dense layer, achieving 98.53% accuracy, 98.57% precision, and 98.53% F1-score. These results suggest that the proposed framework could serve as a decision-support tool to assist pathologists in the earlier and more consistent detection of lung and colon cancer from histopathological images.

INTRODUCTION

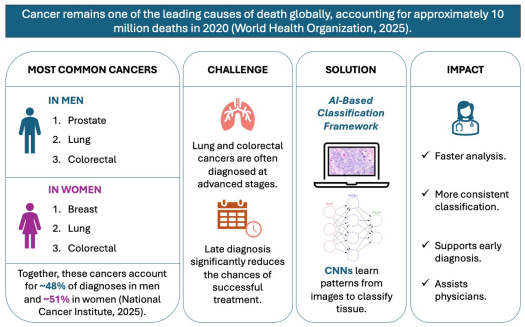


Figure 1. Introduction to the research program (Torres and Valera, 2026).

OBJECTIVES

The main objective of this research is to design a deep learning framework based on convolutional neural networks (CNNs) for the classification of histological images of colon and lung tissue, differentiating between cancerous and non-cancerous tissue.

METHODOLOGY

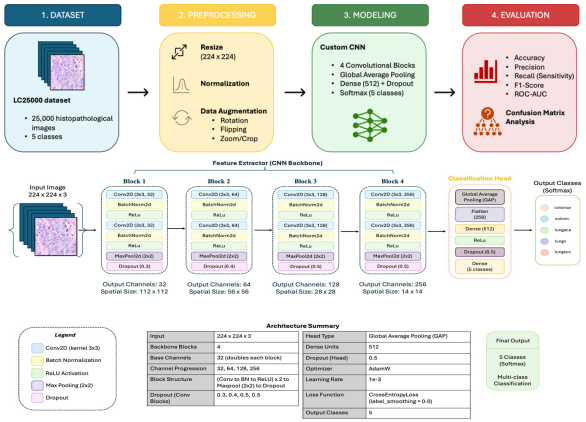


Figure 2. Proposed CNN architecture and methodology for multi-class classification of histopathological images (Torres and Valera, 2026).

DATA

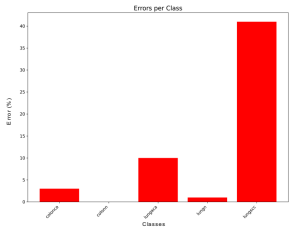


Figure 3. Error per Class (Torres and Valera, 2026).

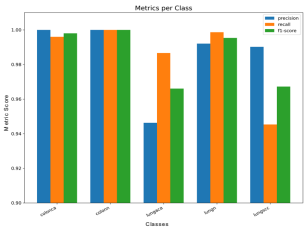


Figure 5. Metrics per Class (Torres and Valera, 2026).

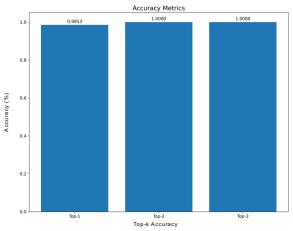


Figure 4. Accuracy metrics (Torres and Valera, 2026).

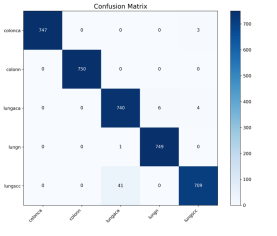


Figure 6. Confusion matrix after testing (Torres and Valera, 2026).

ANALYSIS AND RESULTS

The proposed framework demonstrated strong classification performance through a systematic model development process. Twelve pre-experiments were conducted to identify the optimal optimizer and classification head configuration, with AdamW and GAP producing the highest overall performance. The final model achieved a Top-1 accuracy of 98.53%, demonstrating strong performance on previously unseen histopathological images. The confusion matrix showed that most tissue classes were classified correctly, while the greatest classification difficulty occurred between lung adenocarcinoma and lung squamous cell carcinoma, likely due to their similar histopathological characteristics. Despite this limitation, precision, recall, and F1-score remained consistently high across all five classes, indicating that the framework learned robust discriminative features. Overall, these findings demonstrate that the proposed modular deep learning framework provides a reliable and reproducible approach for the classification of colon and lung histopathological images.

Overall Test Performance	
Metric	Value
Test Accuracy	0.9853
Top-2 Accuracy	1.0000
Top-3 Accuracy	1.0000
AUC (OVR Macro)	0.9997

Table 1. Overall model performance (Torres and Valera, 2026).

CONCLUSIONS

Overall, the proposed framework successfully achieved the objectives of this research by providing a structured methodology for the development, training, and evaluation of a convolutional neural network for histopathological image classification. Beyond its high classification performance, the framework demonstrates the importance of combining systematic preprocessing, model optimization, and comprehensive evaluation to develop reliable deep learning models for biomedical applications. Although opportunities for future improvements remain, the proposed framework provides a strong foundation that can be extended and adapted to other histopathological image classification tasks and broader biomedical imaging applications.

ACKNOWLEDGEMENTS AND REFERENCES

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