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Enhancing Diagnostic Precision in Oncology: A Machine Learning Approach for Tissue Sample Classification

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***Abstract*—Lung cancer significantly affects the respiratory system and is characterized by prodromes such as a prolonged cough, dyspnea, and angina. Smoking remains the leading risk factor for lung cancer. In contrast, colon cancer affects the digestive system. A Computed Tomography (CT) scan can provide valuable insights for diagnosing lung diseases. This study aims to utilize advanced ML and deep learning techniques to classify the histopathological images of tissue samples into various classes, determining whether the cells are cancerous based on distinct morphological patterns. These patterns may include irregular shapes, increased density, and inconsistent sizes compared to normal cells. The goal is to reduce the reliance on pathologists to make manual diagnoses, which can be both time-consuming and subjective. In the proposed approach, a comparative analysis is conducted on image classes that have been preprocessed and trained from scratch using various models namely Support Vector Machine (SVM), Convolutional Neural Networks (CNN), and XGBoost. A CNN based on the EfficientNetB0 architecture is employed, which is the most minor and most efficient version in the EfficientNet family. This model is pre-trained on the ImageNet dataset for feature extraction, omitting the top fully connected layer to enable transfer learning. As a result, this model achieves an overall accuracy of 99.54%, surpassing all other models tested.**

***Index Terms*—Histopathological images, SVM, CNN, XGBoost, EfficientNetB0**

I. Introduction

Cancer is a significant global health issue, with lung and colorectal cancers ranking among the most prevalent and fatal types. [1] Lung cancer accounts for 18.4% of worldwide cancer-related deaths, while colon cancer accounts for 9.2%. [2] The concurrent occurrence of these two cancers is rare; however, their high metastatic potential, particularly between the lungs and colon, emphasizes the vital need for early and precise diagnosis. Timely detection not only improves survival rates but also facilitates more effective management of these malignancies.

Traditional diagnostic approaches, such as imaging techniques and biopsy analysis, rely on expert pathologists to evaluate histopathological slides. Although these methods are effective, they are labor intensive, susceptible to human error and time consuming particularly when processing large volumes of data. The growing complexity and scale of medical data necessitate innovative solutions to complement and enhance traditional practices.

Machine learning models have demonstrated a remarkable ability to analyze complex patterns within histopathological images, delivering faster and more consistent results. Within this domain, deep learning (DL) [3], a subset of ML, has excelled in large-scale image analysis through architectures namely convolutional neural networks (CNNs) [4]. However, despite their high performance, deep learning models offers limited transparency in feature interpretation — an important factor in clinical decision-making. [5].

This study aims to address these challenges by developing a robust automated diagnostic support system for multi-class classification of histopathological images of lung and colon cancers. Our approach integrates traditional feature engineering methods, namely Support Vector Machines (SVM) [6] and XGBoost, with advanced deep learning models, including CNN and EfficientNetB0. [7] By combining these methodologies, the proposed system seeks to balance interpretability and accuracy while leveraging their strengths for cancer subtype classification. The ultimate goal is to enhance diagnostic precision and streamline the evaluation of histopathological

TABLE II: Comparison of Model Performance

Metric	CNN	XGBoost	SVM	EfficientNetB0
Overall Accuracy	95.60%	91.48%	73.56%	99.54%
Precision (Macro Avg)	0.96	0.92	0.74	1.00
Recall (Macro Avg)	0.96	0.91	0.74	1.00
F1-Score (Macro Avg)	0.96	0.91	0.74	1.00
Execution time	~9 sec/epoch	Faster than CNN	Fastest	Slower
Best Performing Class	High in all (especially "Lung N")	"Lung N"	"Lung N"	High in all
Worst Performing Class	Slight drop for "Lung ACA" (F1:0.91)	"Colon ACA" (F1:0.87)	"Lung ACA" (F1:0.64)	"Lung ACA" (F1:0.99)

$$\text{Precision} = \frac{TP}{TP + FP} \tag{2}$$

C. Recall (Sensitivity)

One important indicator for evaluating the model's capacity to identify good cases is recall. Recall is frequently given priority in the medical field, as it shows the ability to recognize all pertinent examples, such as the identification of all malignant tissues. The ratio of real positive instances to all actual positive instances is known as recall [24].

$$\text{Recall} = \frac{TP}{TP + FN} \tag{3}$$

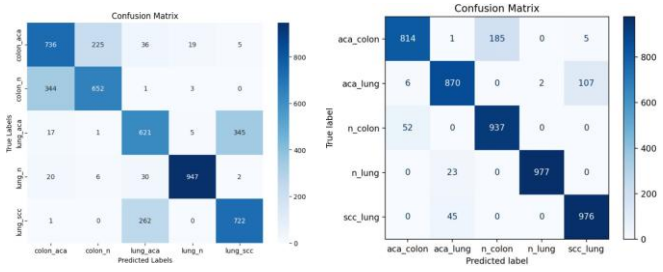
A higher recall indicates fewer false negatives, ensuring that most positive cases are correctly detected.

D. F1-Score

The F1-score provides a comprehensive evaluation of a model's effectiveness by calculating the harmonic mean of recall and accuracy. It is especially beneficial for imbalanced datasets [3], since it includes both false positives and false negatives in calculation. By balancing the trade-off between precision and recall, the F1-score offers a single, unified performance metric [24]:

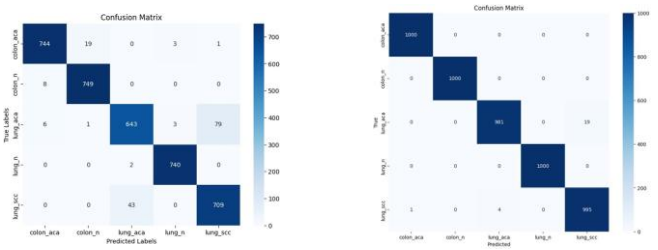
$$\text{F1 Score} = 2 \times \frac{\text{Precision} \times \text{Recall}}{\text{Precision} + \text{Recall}} \tag{4}$$

A higher F1 score indicates a better trade-off between precision and recall, which is essential for tasks involving both false positives and false negatives carry crucial weight [24].



(a) (b)

Fig. 3: Confusion matrices of feature selection methods: a) SVM, b) XGBoost



(a) (b)

Fig. 4: Confusion matrices of feature selection methods: a) CNN, b) EfficientNetB0

V. Result

The performance of the four models — Convolutional Neural Network (CNN), XGBoost, Support Vector Machine (SVM), and CNN-based EfficientNetB0—was assessed using key standards such as accuracy, precision, recall, and F1-score. The outcomes are outlined in Table 2.

EfficientNetB0 outperforms CNN, XGBoost, and SVM in overall accuracy, achieving 99.54%, which is significantly higher than CNN's 95.60%, XGBoost's 91.48%, and SVM's 73.56%. It also maintained high F1-scores, with a peak of 1.00 for most classes except "Lung ACA" (0.99). CNN performed well, especially in the "Lung N" class with an F1-score of 1.00, while XGBoost showed moderate performance, excelling in the "N Lung" class (F1-score of 0.99) but struggling with "Colon ACA" (F1-score of 0.87).

SVM recorded the lowest accuracy at 73.56%. While it performed reasonably well in the "N Lung" class (F1-score of 0.96), the results are poor in "Lung ACA" (F1-score of 0.64) and "Colon ACA" (F1-score of 0.69), indicating challenges with complex datasets.

Regarding efficiency, CNN required approximately 9 seconds per epoch, making it the most computationally intensive. XGBoost was faster than CNN but more resource-intensive than SVM. EfficientNetB0 had a training time of around 5 minutes per epoch. SVM, with its simpler structure, was the fastest but traded off accuracy for speed.

VI. Conclusion

EfficientNetB0 is recommended for applications where accuracy is critical, particularly in medical diagnostics.CNN provides an optimal trade-off between accuracy and efficiency,

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making it well-suited for environments with moderate computational resources. XGBoost is appropriate for scenarios demanding faster execution with acceptable accuracy. However, SVM's poor classification performance makes it unsuitable for complex datasets.

Future research may focus on optimizing EfficientNetB0's training time while maintaining accuracy. Additionally, hybrid approaches combining CNN and XGBoost could be explored to capitalize on their strengths. Efficient hardware implementations and further hyperparameter tuning may also enhance model performance.

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