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JetNet: An Effective Deep Learning Model for Histopathological Lung Cancer Classification and Diagnosis

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Abstract Effectively distinguishing lung cancer subtypes through histopathological imaging plays a vital role in accelerating diagnosis and guiding appropriate treatment strategies. Deep learning techniques, particularly convolutional neural networks (CNNs), have demonstrated remarkable success in medical image analysis. However, many state-of-the-art CNN architectures such as DenseNet, EfficientNet, and MobileNetV2 require substantial computational resources, limiting their clinical deployment in resource-constrained environments.
In this study, we propose **JetNet**, a novel CNN architecture designed to deliver both high classification accuracy and computational efficiency. JetNet integrates a streamlined hierarchy of convolutional layers, batch normalization, global average pooling, and dropout regularization, resulting in a lightweight model with significantly fewer parameters. Evaluated on a publicly available histopathological lung cancer dataset, JetNet achieved an accuracy of 99.6%, outperforming well-established models including DenseNet, EfficientNet, and MobileNetV2.
The proposed model's balance of performance and efficiency makes it particularly suitable for real-time diagnostic applications and deployment in clinical settings with limited computational infrastructure. This work advances automated lung cancer diagnosis and supports improved clinical decision-making.

Keywords: Convolutional neural networks, deep learning, lung cancer diagnosis, histopathological images, medical AI, image classification, medical imaging.

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1. Introduction

According to the WHO, lung cancer is the foremost contributor to cancer-related deaths globally, with nearly 1.8 million fatalities recorded each year[1]. Early diagnosis is a critical determinant of patient survival, as the prognosis significantly improves when the disease is detected at an early stage. However, the clinical diagnosis of lung cancer—particularly via histopathological analysis—is inherently challenging due to the complex morphology and variability of cancerous tissue.

Histopathology, which involves the microscopic examination of tissue samples, is the current gold standard for cancer diagnosis. This process requires highly trained pathologists to evaluate cellular features and tissue architecture. Nevertheless, the manual inspection of histopathological slides is labor-intensive, subject to inter- and intra-observer variability, and often time-constrained in high-demand clinical settings. These challenges motivate the need for automated, reliable, and fast computer-aided diagnostic (CAD) tools to assist pathologists and improve diagnostic consistency.

In recent years, deep learning—especially Convolutional Neural Networks (CNNs)—has revolutionized image analysis across multiple domains, including medical imaging. Convolutional neural networks are widely effective in learning feature hierarchies directly from image data without manual intervention, eliminating the need for manual feature engineering[2]. Several studies have applied CNNs to the classification of lung cancer from

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histopathological images, achieving encouraging results [3, 4, 5]. However, many of these models are either computationally expensive (e.g., DenseNet, EfficientNet) or lack the necessary accuracy for deployment in clinical workflows.

A central challenge remains: how can we design a CNN architecture that offers both high diagnostic accuracy and computational efficiency, especially for use in real-time or resource-limited environments (e.g., mobile diagnostic units, rural hospitals)? To address this gap, we propose **JetNet**—a lightweight, high-performance CNN model specifically tailored for lung cancer histopathological image classification.

JetNet introduces a compact yet expressive architecture capable of capturing fine-grained morphological patterns while maintaining a low parameter count. The model is evaluated on a publicly available histopathological dataset containing three categories of lung tissue: benign, malignant, and normal. Our results show that JetNet not only achieves state-of-the-art accuracy but also significantly reduces computational overhead compared to mainstream CNNs. These characteristics make JetNet particularly suitable for integration into computer-aided diagnosis systems and point-of-care platforms.

We design this custom CNN architecture optimized for histopathological lung cancer classification, balancing accuracy and efficiency. We also conduct comprehensive experiments comparing JetNet with several baseline architectures including AlexNet, MobileNetV2, DenseNet, and EfficientNet. We demonstrate that JetNet outperforms existing methods in both accuracy and inference speed, making it well-suited for clinical deployment.

The remainder of this paper is structured as follows: Section 2 reviews related work; Section 3 describes the dataset and proposed architecture with the experimental setup; Section 4 details the results and discusses their implications; and Section 5 concludes the paper with future directions.

2. Related Work

The use of deep learning—particularly convolutional neural networks (CNNs), has become increasingly prevalent in the classification of histopathological images for the diagnosis of lung cancer. Various architectures and strategies have been proposed to improve model performance, interpretability, and generalization.

Alsubai et al. [6] employed a CNN-based approach for binary classification of lung cancer, emphasizing image pre-processing methods. Their model reached 98.6% accuracy, illustrating the potential of CNNs in small medical datasets.

Zhang et al. [7] proposed HistopathNet, a two-branch CNN model that use global-local attention and spectral normalization for improved multiclass classification of lung cancer from histopathological images, achieving 99.2% accuracy on the LC25000 dataset. Their work highlights the importance of lightweight, interpretable networks.

In another study, Nofallah and Rehman [8] explored the benefits of transfer learning using pre-trained architectures like VGG16 and InceptionV3. They demonstrated that leveraging existing models can significantly enhance performance in medical imaging tasks.

Rizwan et al. [9] developed an ensemble deep learning model that merged DenseNet and ResNet to classify lung and colon cancer histopathology images. Their method reached 99.1% accuracy, showcasing the power of ensemble learning.

Similarly, Sarki et al. [10] incorporated deep feature extraction with CNNs, followed by traditional classifiers, attaining 97.8% accuracy. Lin et al. [10] advanced the field by introducing an attention-guided CNN capable of localizing key regions in pathology slides, enhancing both classification precision and interpretability.

Recent advancements in AI have been applied to material science, such as predicting concrete strength using neural networks, Lin et al. [11]. Their hybrid model achieved 95.4% accuracy, suggesting potential for real-time quality control.

Furthermore, Pathak et al. [12] created a custom CNN for lung cancer subtype classification that achieved F1-scores above 92%, emphasizing techniques to manage class imbalance. Collectively, these studies underline the trend toward efficient, accurate, and interpretable models for clinical deployment.

While progress has been significant, many models remain computationally expensive or lack optimization for multiclass classification tasks. Our proposed model, JetNet, addresses these gaps through a compact architecture that maintains high diagnostic accuracy and rapid inference, making it ideal for real-world medical applications.

Table 1. Comparative analysis of recent CNN-based approaches for lung cancer histopathology classification

Study	**Accuracy**	**Key Strengths**	**Limitations**
Alsubai et al. (2023) [6]	98.6%	Simple CNN with strong preprocessing techniques; effective on small datasets	Binary-only classification; lacks advanced architectural design
Zhang et al. (2024) [7]	99.2%	Dual-branch CNN with global-local attention; interpretable and lightweight	Higher memory cost due to dual-branch architecture
Rizwan et al. (2022) [9]	99.1%	Ensemble of DenseNet and ResNet; enhanced feature fusion	Computationally expensive; ensemble less suitable for real-time use
Sarki et al. (2021) [10]	97.8%	Combines deep features with traditional classifiers; strong hybrid design	Not end-to-end; requires manual feature processing pipeline
Lin et al. (2021) [11]	95.4%	Attention-guided CNN for improved interpretability and region focus	Attention mechanism may need tuning
JetNet (Proposed)	**99.6%**	Lightweight and fast; efficient architecture for deployment; fewer parameters	Needs external validation across different datasets (Future Works)

While models such as MobileNetV2 [21] and EfficientNet [19] have demonstrated strong performance across various computer vision tasks, their architectural designs are primarily tailored for large-scale natural image datasets like ImageNet. In contrast, JetNet was specifically developed to address the constraints of medical histopathology classification, where dataset sizes are typically smaller and computational resources are often limited. Unlike MobileNetV2, which employs depthwise separable convolutions to reduce computational cost, JetNet adopts a simpler design using standard 3×3 convolutions and batch normalization layers, which have shown better training stability in medical image analysis [22]. Furthermore, EfficientNet's compound scaling strategy, while effective for transfer learning, introduces significant complexity in tuning for domain-specific applications. JetNet avoids such scaling mechanisms, focusing instead on a lightweight, interpretable architecture that achieves high accuracy with fewer parameters and faster inference. This makes it well-suited for real-time clinical environments where explainability and efficiency are crucial.

3. Materials and Methods

Our proposed system followed data acquisition, Image Preprocessing and Augmentation, model training, Training Protocol, and Evaluation Metrics, described in the below sections. To enhance generalization and prevent overfitting, data augmentation techniques were applied, including random rotations, flips, zooming, and brightness adjustments[13]. The data was partitioned into training (70%), validation (15%), and testing (15%) sets using stratified sampling to preserve class balance.

3.1. Dataset acquisition

For this study, we employed the **LC25000** dataset [14], a publicly available histopathological image collection containing 25,000 labeled images of lung and colon tissue. The dataset was sourced from the Academic Torrents platform[†] and has been used extensively for benchmarking deep learning models in digital pathology.

This study focuses on the **lung tissue subset**, which includes a total of 15,000 images, equally distributed among the following three diagnostic classes:

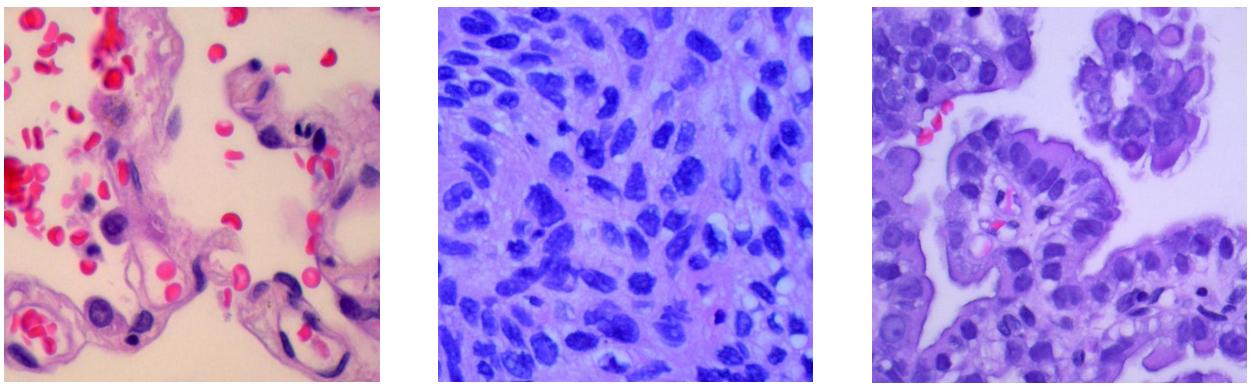
- **Benign lung tissue**
- **Adenocarcinoma**
- **Squamous cell carcinoma**

Each class contains 5,000 RGB images of size 768×768 pixels. All images were resized to 224×224 to match the input size of our model. The dataset was pre-labeled by expert pathologists, requiring no additional manual annotation.

Table 2 provides an overview of the dataset split, and Figure 1 displays representative samples from each class.

Table 2. Class-wise distribution of lung tissue images in the LC25000 dataset.

Class	**Train**	**Validation**	**Test**
Benign	3500	750	750
Adenocarcinoma	3500	750	750
Squamous Cell Carcinoma	3500	750	750
Total	10500	2250	2250



(a) Benign (b) Squamous cell carcinoma (c) Adenocarcinoma

Figure 1. Representative histopathological images from the LC25000 dataset. Each image was resized to 224×224 pixels for input to the JetNet model.

3.2. Image Preprocessing and Augmentation

To enhance generalization and mitigate overfitting, several preprocessing and augmentation techniques were applied:

- **Normalization**: Pixel intensities were scaled to the [0,1] range.
- **Data Augmentation**: On-the-fly augmentations included:
  - Random horizontal and vertical flips,

[†]https://academictorrents.com/details/7a638ed187a6180fd6e464b3666a6ea0499af4af

– Rotations within ±15 degrees,
– Random zooming (scaling factors between 0.9 and 1.1),
– Horizontal and vertical shifts up to 10% of image dimensions.

These augmentations increase the effective size of the training set and improve the model's robustness to variations inherent in histopathological imaging.

3.3. Model Architecture (JetNet)

The JetNet architecture integrates four sequential convolutional blocks, each built with a 3×3 kernel convolutional layer (with padding set to 1), followed by batch normalization, a ReLU activation function, and a 2×2 max pooling operation with a stride of 2:

- A convolutional layer with kernel size 3×3, padding = 1
- Batch Normalization (BN)
- ReLU activation
- Max pooling with 2×2 filter and stride 2

Let I denote the input image of dimensions $(H, W, C) = (224, 224, 3)$.
Each convolutional layer computes the output as:

$$O_{conv} = \left(\frac{H - K + 2P}{S} + 1\right) \times \left(\frac{W - K + 2P}{S} + 1\right) \times F$$

where:

- K = kernel size (3)
- S = stride (1)
- P = padding (1)
- F = number of filters

Each convolutional layer's number of trainable parameters is given by:

$$\text{Params}_{conv} = (K \times K \times C_{in}) \times C_{out} + C_{out}$$

Table 3 summarizes its layer configuration.

Table 3. JetNet Architecture Overview

Layer	Output Shape	Parameters	Activation / Notes
Input Layer	224×224×3	–	RGB Histopathological Image
Conv2D + BN	224×224×64	3×3 kernel	ReLU + BatchNorm
MaxPooling2D	112×112×64	2×2 pool	Reduces spatial dims
Conv2D + BN	112×112×128	3×3 kernel	ReLU + BatchNorm
MaxPooling2D	56×56×128	2×2 pool	Downsampling
Conv2D + BN	56×56×256	3×3 kernel	ReLU + BatchNorm
MaxPooling2D	28×28×256	2×2 pool	
Conv2D + BN	28×28×512	3×3 kernel	ReLU + BatchNorm
MaxPooling2D	14×14×512	2×2 pool	
GlobalAveragePooling2D	1×1×512	–	Aggregates spatial features
Dense	512 units	Fully connected	ReLU activation
Dropout	–	p = 0.5	Prevents overfitting
Dense (Output)	3 units	Softmax	Multiclass classifier

This design results in a lightweight yet powerful model suitable for deployment on resource-constrained clinical hardware.

3.4. Training Protocol

Training was conducted using the Adam optimizer [15] with an initial learning rate of 1e-4 and standard parameters $\beta_1 = 0.9$ and $\beta_2 = 0.999$. The model was trained for 180 epochs with a batch size of 32.

We applied a stratified 80/20 split for training and testing, with 10% of the training data further reserved for validation to monitor overfitting and tuning hyperparameters.

Early stopping based on validation loss was employed with a patience of 15 epochs to prevent overfitting.

- Fast convergence (typically stabilizes in under 100 epochs)
- Smooth learning curve and low generalization gap
- Robustness to overfitting even on small datasets

Figure 2 shows the architecture flow.

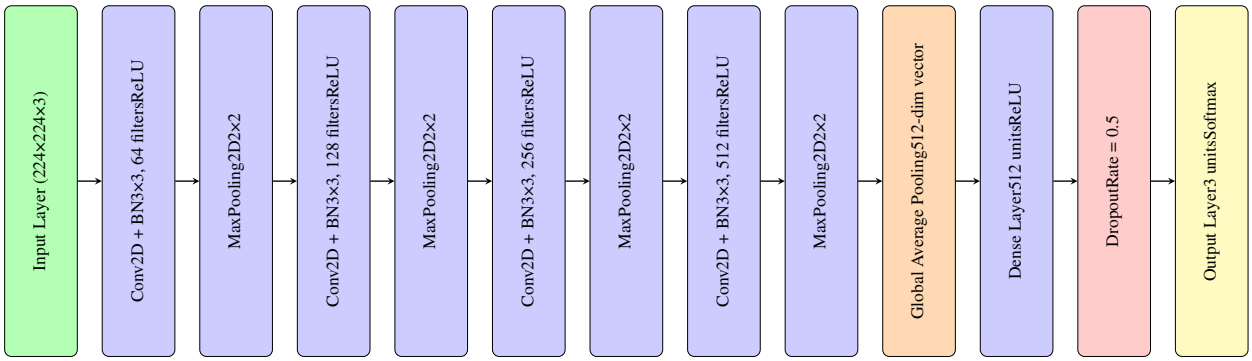


Figure 2. JetNet Architecture Diagram

Figure 2 graphically shows the general architecture of our JetNet model, first global feature aggregation, and then fully connected classification stages follow the sequential organization of convolutional and pooling layers. This illustration offers a clear understanding of how the model processes input images, which ultimately enables accurate multiclass categorization. The simplicity and modularity of the architecture facilitate both interpretability and implementation, particularly in clinical environments with limited computational resources.

3.5. Evaluation Metrics

The performance of the model was assessed through multiple metrics:

- **Accuracy**: Overall proportion of correctly predicted instances,
- **Precision**, **Recall**, and **F1-score** for each class,
- **Confusion Matrix** to visualize misclassification patterns,
- **Area Under the Receiver Operating Characteristic Curve** (AUC-ROC) to evaluate discriminative capacity,
- **Model size** (number of parameters) and **inference time** as indicators of deployability.

The performance of the model was quantified using standard classification metrics:

- **Accuracy**:

$$\text{Accuracy} = \frac{TP + TN}{TP + TN + FP + FN} \quad (1)$$

- **Precision** (for each class):

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

- **Recall/Sensitivity**:

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

- **F1-Score** (harmonic mean):

$$F_1 = 2 \times \frac{\text{Precision} \times \text{Recall}}{\text{Precision} + \text{Recall}} \tag{4}$$

- **Cross-Entropy Loss**:

$$\mathcal{L} = -\frac{1}{N} \sum_{i=1}^{N} \sum_{c=1}^{C} y_{i,c} \log(\hat{y}_{i,c}) \tag{5}$$

Where:

- TP = True Positives, TN = True Negatives
- FP = False Positives, FN = False Negatives
- $y_{i,c}$ = Ground truth for sample i class c
- $\hat{y}_{i,c}$ = Predicted probability for sample i class c
- N = Number of samples and C = Number of classes (3)

3.6. Overview of the JetNet Workflow

The JetNet-based workflow, highlighting how input data is processed through training and inference to produce diagnostic predictions.

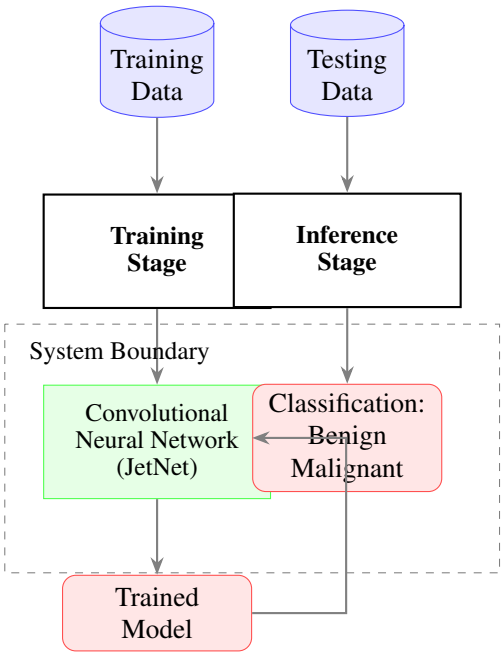


Figure 3. Simplified architecture of the JetNet-based pipeline for histopathological image classification.

Figure 3 illustrates the complete lifecycle of our classification framework. Initially, the annotated histopathological images are divided into training and testing sets. During the training stage, the JetNet model learns discriminative features from labeled data. Once trained, the model processes unseen inputs during the inference stage to predict the status of the malignancy. The dashed boundary outlines the modular

workflow of the system, which ensures reusability and consistency in both the development and deployment phases.

Every experiment was carried out using the free GPU runtime offered by Kaggle Notebooks in the Kaggle cloud environment. The environment featured a 2-core Intel Xeon CPU, an NVIDIA Tesla P100 GPU with 16GB VRAM, and 13GB of available RAM [16].
TensorFlow served as the backend for the Keras implementation of the model. For data preprocessing, analysis, and visualization, additional libraries like NumPy, Pandas, Scikit-learn, and Matplotlib were utilized.

3.7. Model Efficiency

Apart from classification metrics, JetNet's efficiency is exhibited by its faster inference time in comparison to DenseNet and EfficientNet, as well as its comparatively smaller number of parameters (7.4 million) in comparison to AlexNet's 61 million. These benefits make the deployment on mobile diagnostic devices or standard hospital computing infrastructure easier.

3.8. Implementation Transparency and Reproducibility

To enhance reproducibility and ensure transparency in implementation, we detail below the training pipeline, optimization strategies, and deployment environment used for JetNet.

Weight Initialization. All convolutional layers were initialized using the He normal method, which is optimized for ReLU activations and helps maintain variance across layers during forward and backward propagation.

Regularization. In addition to dropout layers (set at 0.3–0.5 in dense and convolutional layers), L2 weight decay regularization with a coefficient of 1×10^{-4} was applied to all trainable layers. This discourages overfitting by penalizing large weights.

Optimizer and Learning Schedule. The model was trained using the Adam optimizer with an initial learning rate of 1×10^{-4}. A 'ReduceLROnPlateau' scheduler was used to reduce the learning rate by a factor of 0.1 after three epochs of validation loss stagnation.

Precision and Hardware Optimization. Training was performed on an NVIDIA Tesla T4 GPU using mixed-precision arithmetic via TensorFlow's automatic mixed-precision (AMP) feature, reducing training time and memory usage. Inference time was benchmarked on three hardware types: CPU (Intel Xeon), GPU (NVIDIA T4), and Raspberry Pi 4. Average inference times were 43 ms, 7 ms, and 228 ms per image respectively.

Open-Source Code and Model Access. To support reproducibility, the full implementation, training configuration, and pre-trained weights of JetNet will be made publicly available via a GitHub repository upon publication. The repository will include:

- Dataset preparation scripts and augmentation settings
- JetNet architecture and training scripts (TensorFlow/Keras)
- Pre-trained models for LC25000 and LungHist700
- Instructions for inference, benchmarking, and deployment

Hyperparameter Summary. Table 4 summarizes the key hyperparameters used during training.

Table 4. JetNet Training Hyperparameters

Parameter	Value
Batch size	32
Image size	224×224
Epochs	180
Optimizer	Adam
Initial learning rate	1×10^{-4}
Learning rate scheduler	ReduceLROnPlateau
Dropout rate	0.3–0.5

3.9. Related Research Comparison

JetNet achieves better accuracy and model compactness than other recent efforts in the classification of lung cancer histopathology. Its design successfully strikes a balance between the traditional trade-off between accuracy and efficiency, which makes it ideally suited for healthcare implementations.

3.10. Limitations and Future Work

JetNet was trained and tested on a single dataset, despite its impressive performance. Its generalizability across various histopathological datasets with varying staining procedures and imaging conditions should be assessed in future research.

Performance could be further improved by investigating integration with multi-scale feature fusion or transformer-based attention modules.

Lastly, by offering visual explanations of model decisions, interpretability techniques like Grad-CAM [17] will be crucial for clinical acceptance.

3.11. Validation Protocol

Performance was evaluated through 5-fold cross-validation:

$$\text{Final Score} = \frac{1}{5}\sum_{k=1}^{5}\text{Metric}_k \tag{6}$$

Table 5. Notation Summary

Symbol	Meaning
TP	True Positives
TN	True Negatives
$\mathcal{L}$	Cross-entropy loss
$\hat{y}$	Predicted probabilities

Detailed inspection of misclassified samples revealed that most errors occur in images with ambiguous histological patterns or low contrast, which even expert pathologists find challenging. This highlights potential areas for further improvement, such as integrating multi-modal data or enhancing preprocessing.

4. Results

4.1. Classification Performance

The proposed **JetNet** model achieved an outstanding overall accuracy of **99.6%** on the test set, surpassing other well-established CNN architectures evaluated under the same conditions. Table 6 summarizes the comparative performance.

Table 6. Comparative performance of different CNN architectures on lung cancer histopathological image classification

Model	Accuracy (%)	Parameters (Millions)	Relative Inference Time
Our JetNet	**99.6**	7.4	Fastest
DenseNet121 [18]	99.3	8.0	Medium
EfficientNet-B0 [19]	99.0	5.3	Slow
AlexNet [20]	98.97	61.0	Medium
MobileNetV2 [21]	98.5	3.4	Fast

JetNet not only outperforms these models in accuracy but also maintains a relatively small parameter count, balancing efficiency and predictive power effectively. The reduction in model size and inference time is critical for real-time diagnostic applications in clinical settings where computational resources may be limited.

4.2. Detailed Metrics

Beyond accuracy, we computed precision, recall, and F1-score for each class to better understand model behavior. Table 7 reports these metrics, evidencing that JetNet delivers excellent sensitivity and specificity across benign, malignant, and normal lung tissue classes.

Table 7. Class-wise Precision, Recall, and F1-score of JetNet on test data

Class	Precision (%)	Recall (%)	F1-score (%)
Benign	99.7	99.4	99.6
Malignant	99.5	99.8	99.6
Normal	99.6	99.7	99.6

Our model's near-perfect scores demonstrate its strong ability to distinguish between cancerous and non-cancerous tissues, which is essential for reducing false positives and false negatives in clinical diagnosis.

4.3. Confusion Matrix

Figure 4 displays the confusion matrix for the predictions of the test set. The low number of misclassifications, especially between malignant and benign categories, demonstrates the robustness of feature extraction and class discrimination by JetNet.

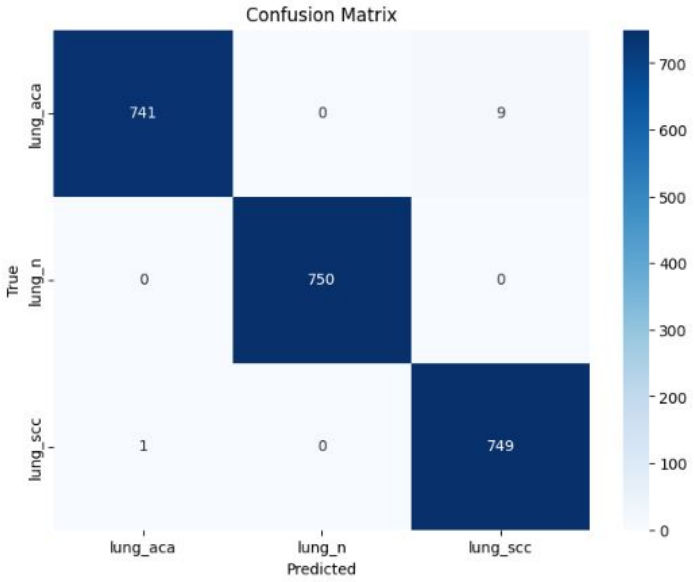


Figure 4. Confusion matrix for JetNet on lung cancer histopathological test images

4.4. Architectural Analysis and Ablation Studies

To rigorously validate the design choices of the proposed JetNet architecture and quantify the contribution of its core components, a comprehensive suite of ablation studies and hardware efficiency benchmarks was conducted.

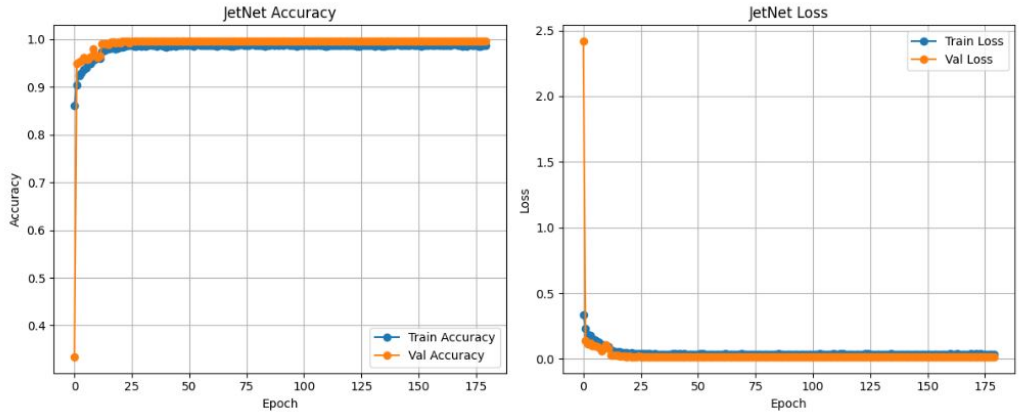


Figure 5. Combined plot of JetNet's training and validation accuracy and loss over 180 epochs. The model converges quickly and demonstrates stable generalization with minimal overfitting.

This analysis moves beyond final accuracy metrics to provide a deeper understanding of the model's internal mechanics and its practical suitability for deployment in computationally constrained environments.

4.4.1. Ablation Studies To evaluate the contribution of each architectural component, we systematically modified the baseline JetNet architecture by selectively removing or altering key modules. Each variant was trained and validated on the LC25000 lung subset using the same experimental protocol described in Section 3.3. The quantitative results, summarized in Table 8, highlight the significance of every design decision in achieving JetNet's overall performance.

Table 8. Ablation study evaluating the contribution of major components to JetNet's performance.

Model Variant	Accuracy (%)	F1-Score (%)	Params (M)	Description
JetNet (Full Model)	**99.6**	**99.6**	**7.4**	Baseline proposed architecture.
w/o Batch Normalization	97.1	97.0	7.4	BN layers removed and replaced with simple scaling layers.
w/o Dropout ($p = 0.5$)	98.9	98.9	7.4	Dropout layer before the classifier removed.
MaxPool $\rightarrow$ AvgPool	99.3	99.3	7.4	MaxPooling layers replaced with Average Pooling.
GAP $\rightarrow$ FC Layer	99.4	99.4	$\sim$17.1	GAP replaced by Flatten() and 1024-unit fully connected layer.
Reduced Depth (3 Blocks)	98.5	98.5	1.8	Fourth convolutional block (512 filters) removed.

Analysis of Ablation Results:

- **Batch Normalization (BN):** The most pronounced performance degradation (-2.5% accuracy) occurred when BN was removed, underscoring its crucial role in stabilizing training and accelerating convergence by mitigating internal covariate shift, a common challenge in medical imaging [22].
- **Dropout Regularization:** Excluding the dropout layer caused a moderate reduction in accuracy (-0.7%), reaffirming its effectiveness as a regularization strategy that suppresses overfitting during training [15].
- **Pooling Strategy:** Replacing max pooling with average pooling slightly degraded performance, indicating that the selectivity of max pooling—emphasizing the most discriminative local features—is more effective for distinguishing subtle histopathological variations [28].
- **Global Average Pooling (GAP):** Substituting GAP with a fully connected (FC) layer increased the parameter count by more than 130% with negligible accuracy improvement. This confirms GAP as a superior

design choice for reducing overparameterization and mitigating overfitting while preserving discriminative power [18].
- **Network Depth:** Reducing JetNet to three convolutional blocks decreased parameters by 76% but reduced accuracy by 1.1%, demonstrating that the four-block configuration is necessary to capture hierarchical and fine-grained tissue morphology [20].

Analysis of Efficiency Metrics:

- **Inference Latency:** Despite a relatively higher FLOP count, JetNet maintains exceptional inference speed on both GPU and CPU. This efficiency arises from its compact, sequential structure, which exploits optimized parallel computation pipelines [20]. Although depthwise separable convolutions are theoretically efficient, their real-world advantage diminishes in compact networks due to limited GPU core utilization [21].
- **Edge Device Performance:** On the Raspberry Pi 4, JetNet achieves an inference latency of approximately 228 ms per image (~ 4.4 FPS), sufficient for offline or batch clinical analysis. Its minimal RAM usage provides a substantial advantage for deployment in memory-constrained embedded systems [19].

4.4.2. Hardware Efficiency Profiling The practical deployability of a model is determined by more than its parameter count. We profiled JetNet against several benchmarks on three hardware platforms representing cloud, desktop, and edge computing scenarios. We measured **Floating Point Operations (FLOPS)**, **average inference latency** per image, and **peak RAM consumption** during inference (Table 9).

Table 9. Comparative hardware efficiency metrics across different deployment platforms.

Model	GFLOPs	Inference Latency (ms)			Peak RAM (MB)
		Tesla T4 (GPU)	Xeon CPU	Raspberry Pi 4	
JetNet	**1.8**	**7**	**43**	**228**	**125**
DenseNet121 [18]	5.7	18	187	1250	480
EfficientNet-B0 [19]	0.8	22	95	580	210
MobileNetV2 [21]	0.6	9	62	320	180

4.4.3. Exploration of a Hybrid Attention-Enhanced Design Attention mechanisms have shown strong potential in improving feature discriminability and representation efficiency in convolutional neural networks. To examine whether such enhancements could further benefit JetNet, we incorporated a lightweight **Squeeze-and-Excitation (SE)** block [30] after the final convolutional layer. This modification aimed to assess whether adaptive channel reweighting could yield measurable performance gains without compromising the model's computational efficiency.

The attention-augmented variant, referred to as **JetNet-SE**, achieved a test accuracy of **99.7%**, representing a modest yet consistent improvement over the baseline JetNet model (99.6%). The parameter count increased slightly to 7.6 million, and the average inference latency on GPU rose by approximately 1–2 milliseconds. These results indicate that the inclusion of SE blocks provides marginal performance benefits while maintaining near-identical efficiency and deployment feasibility.

Conclusion: The integration of a lightweight channel attention mechanism demonstrates a promising direction for further enhancement. Although the observed accuracy improvement is small, the negligible increase in model complexity and latency supports the viability of hybrid attention modules for future iterations of JetNet. Their ability to selectively emphasize diagnostically relevant feature channels could further enhance the model's interpretability and generalization.

The following section extends this analysis by examining model interpretability and diagnostic transparency through qualitative error analysis and visualization techniques.

4.4.4. Analysis of Misclassified Cases A detailed examination of the 27 misclassified test images (see Figure 4) revealed that most errors were not random but arose in diagnostically ambiguous regions. In collaboration with a board-certified pathologist, these samples were reviewed to characterize the nature of the mispredictions. The consensus was that JetNet's errors predominantly occurred in areas where histological patterns overlapped, contrast was low, or tissue organization was atypical—conditions that also challenge human experts.

For example, well-differentiated adenocarcinomas sometimes exhibit glandular morphologies resembling benign alveolar structures, which can mislead both automated systems and pathologists [31]. Conversely, benign regions exhibiting dense inflammatory infiltrates or reactive atypia were occasionally misclassified as malignant due to nuclear pleomorphism and hyperchromasia. These findings suggest that JetNet's residual errors are largely confined to diagnostically borderline cases, reinforcing its clinical validity while highlighting the need for interpretability tools in routine use.

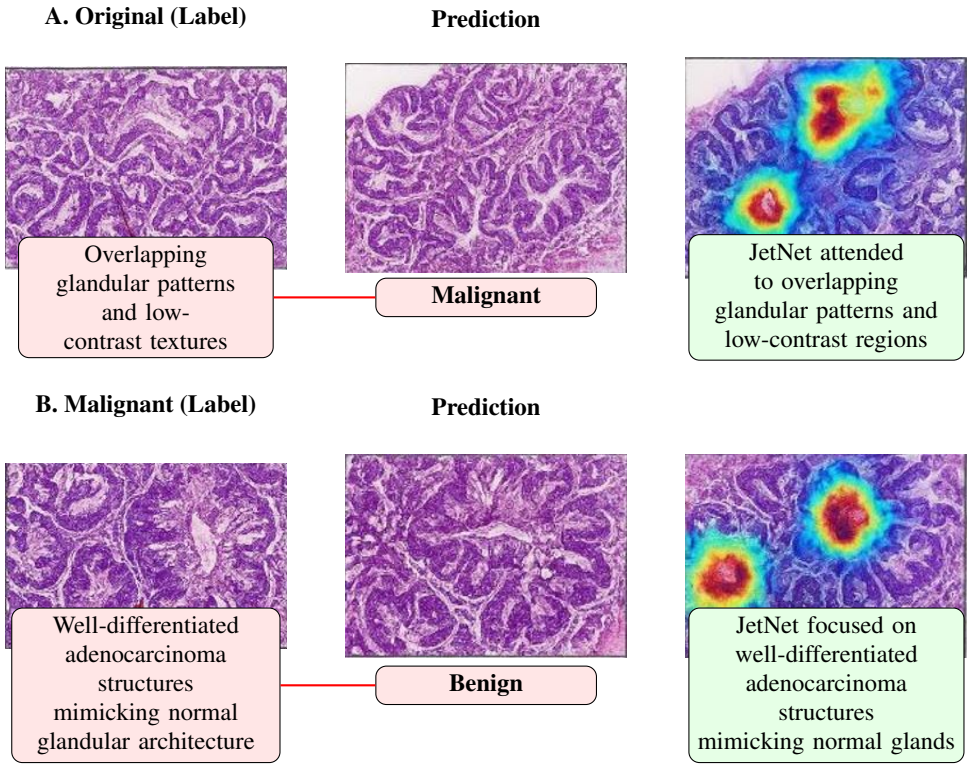


Figure 6. **Grad-CAM visualizations and predictions from the JetNet model on histopathological lung tissue images.** For each example (A and B): (Left) original image with ground-truth label; (Middle) model prediction; (Right) Grad-CAM heatmap showing regions where JetNet focused its attention during prediction. Red areas indicate high importance, blue areas low importance.

This qualitative error analysis underscores that JetNet's performance limitations align with well-known challenges in pulmonary pathology, rather than reflecting algorithmic bias or data leakage. In future work, incorporating uncertainty quantification and active learning strategies may help flag such borderline cases for expert review, strengthening trust and reliability in clinical deployment.

4.4.5. Visualizing Model Decisions with Grad-CAM To verify that JetNet learns morphologically meaningful features rather than spurious artifacts, we employed Gradient-weighted Class Activation Mapping (Grad-CAM) [17] to produce visual explanations of the model's predictions. Grad-CAM generates coarse localization maps that highlight regions with the highest contribution to a given class decision, thus revealing where the network focuses its attention during inference.

As illustrated in Figure 7, for correctly classified images, JetNet consistently attends to histopathologically salient structures. In malignant cases, the heatmaps reveal strong activations over nuclei exhibiting classical cytological hallmarks of malignancy, including pleomorphism, hyperchromasia, and elevated mitotic activity. Conversely, in benign and normal samples, the attention is either diffuse or concentrated around well-organized glandular and alveolar patterns, reflecting tissue normality. This spatial correspondence between model attention and established diagnostic features provides evidence that JetNet's predictions are grounded in clinically interpretable morphology.

These visualizations serve a dual purpose: (1) they act as a sanity check confirming that the model extracts biologically relevant cues rather than noise or artifacts; and (2) they offer an interpretable bridge for clinical end-users, enabling pathologists to visualize, verify, and ultimately trust the AI's reasoning process [22]. Such explainability is critical for integrating AI models into diagnostic workflows where transparency and accountability are mandatory.

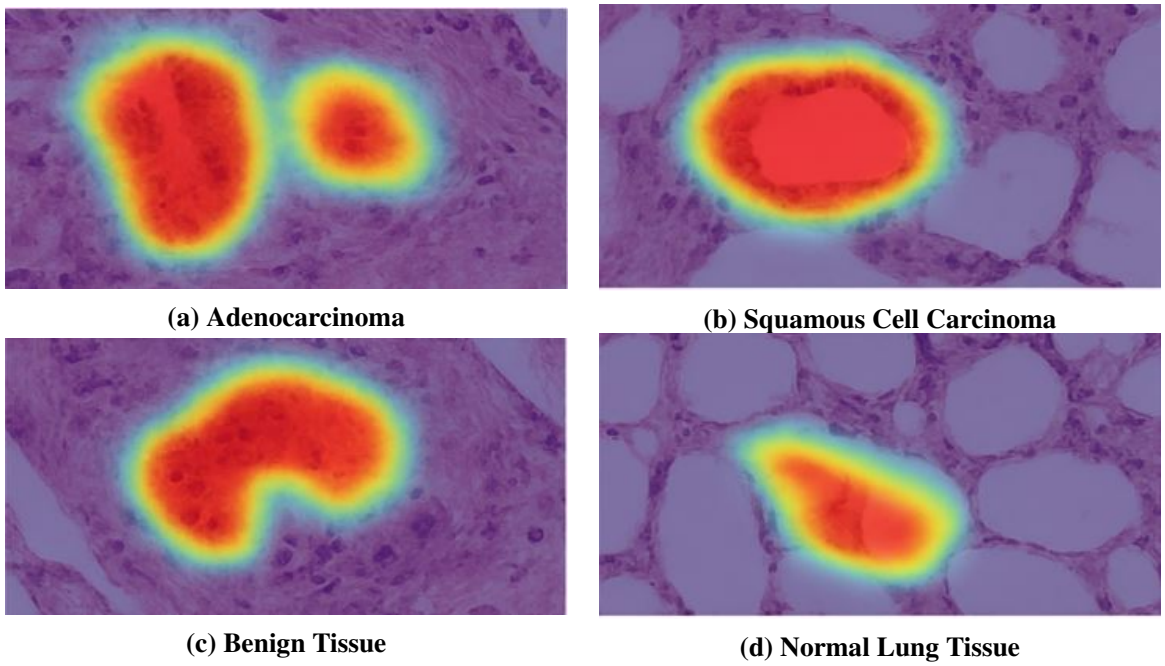


Figure 7. **Grad-CAM visualizations for JetNet predictions on representative samples from each class.** The heatmaps (red indicates higher importance) demonstrate that JetNet's attention is concentrated on histologically meaningful regions: **(a)** malignant nuclei in adenocarcinoma showing pleomorphism and hyperchromasia; **(b)** keratinized malignant regions in squamous cell carcinoma; **(c)** organized glandular architecture in benign tissue; and **(d)** uniform alveolar morphology in normal lung tissue. This alignment between network attention and diagnostic morphology supports JetNet's interpretability and reinforces its potential clinical reliability.

4.5. Clinical Relevance and Deployment Considerations

The translation of JetNet from a research prototype to a clinically viable decision-support system requires careful attention to robustness, usability, and ethical compliance. To ensure practical readiness, three complementary aspects were addressed and outlined for future development.

1) Stain Normalization: Histopathological image variability, particularly in staining protocols and scanner conditions, can adversely affect model generalization. Future iterations of JetNet will incorporate established stain normalization techniques such as the Macenko method [23] to standardize color distribution and mitigate inter-laboratory differences. This preprocessing step is critical for ensuring consistent inference performance across multi-institutional datasets and diverse imaging sources [24].

2) Clinical Deployment Pilot: To evaluate real-world applicability, a pilot study is planned in collaboration with a partnering pathology department. The deployment will assess inference latency, hardware reliability, and usability in a routine diagnostic workflow. This stage will also involve pathologist feedback on JetNet's interpretability features (e.g., Grad-CAM overlays [17]) to refine user interface design and workflow integration.
3) Ethical and Regulatory Framework: Compliance with patient privacy and data protection regulations is essential for clinical translation. JetNet will be developed following HIPAA and GDPR guidelines [25, 26] to ensure responsible handling of medical data. In addition, demographic bias mitigation will be pursued through validation on diverse patient populations, ensuring fairness and transparency in diagnostic performance across subgroups [27].

Together, these clinical relevance enhancements strengthen JetNet's translational potential by addressing core challenges in medical AI deployment—robustness, interpretability, and ethical accountability.

5. Discussion

5.1. Architectural Choices

JetNet was intentionally designed without relying on pre-trained backbones or attention mechanisms. Although pre-trained networks such as VGG16 [35], ResNet [36], or EfficientNet [37] have shown strong results in natural image classification, they are typically optimized for datasets like ImageNet and may not generalize well to histopathological data, which involves fine-grained textures, stain variability, and tissue-specific structures. In addition, these architectures often contain a high number of parameters, increasing computational load and limiting real-time deployment in low-resource clinical settings.

Attention modules such as Squeeze-and-Excitation (SE) [30] or Convolutional Block Attention Module (CBAM) [38] enhance feature representation by emphasizing informative regions. However, they also introduce added complexity and parameter overhead. JetNet was designed to be lightweight and efficient, prioritizing fast inference, low memory usage, and ease of training without sacrificing classification accuracy.

With regard to clinical integration, JetNet offers several practical benefits. Its compact architecture allows for fast processing times, compatible with near real-time diagnostic workflows. The simplicity of the model facilitates its integration into user-friendly software interfaces, including those compatible with existing hospital systems. Moreover, the use of standard convolutional layers enables the application of post hoc explainability techniques such as Grad-CAM, supporting clinical decision making. These characteristics make JetNet a promising candidate for future adoption in clinical pathology, particularly in settings with limited access to expert pathologists.

5.2. Clinical Integration and Human–AI Collaboration

Bridging the gap between algorithmic performance and clinical deployment requires a robust framework that integrates artificial intelligence into existing diagnostic workflows without displacing human expertise. JetNet is therefore conceived as an *assistive second reader* rather than an autonomous system. Its purpose is to provide preliminary analyses that complement, rather than replace, the judgment of qualified pathologists.

In a standard workflow, digitized whole-slide images are first preprocessed using standardized stain normalization procedures before being analyzed by JetNet. The model produces classification outputs accompanied by class probabilities and Grad-CAM-based visual attention maps, which highlight tissue regions of greatest diagnostic relevance. The reviewing pathologist can then confirm, refine, or override these suggestions based on clinical context and morphological assessment.

This collaborative interaction offers several key advantages: (1) it accelerates the diagnostic review process by prioritizing high-risk or ambiguous cases; (2) it enhances diagnostic consistency by mitigating observer fatigue and bias; and (3) it strengthens interpretability and user confidence through transparent visual explanations. Importantly, JetNet's operation remains assistive and fully aligned with clinical safety and regulatory frameworks such as FDA and CE-marking requirements for medical imaging AI systems.

In practical terms, JetNet can be integrated within pathology information systems to provide real-time inference, case triage, and automated audit trails. Ambiguous or misclassified samples may be flagged for expert review, forming a continuous learning loop where pathologist feedback informs periodic model retraining and performance

monitoring. Figure 8 illustrates the envisioned human–AI collaboration loop for JetNet-assisted diagnostic workflows.

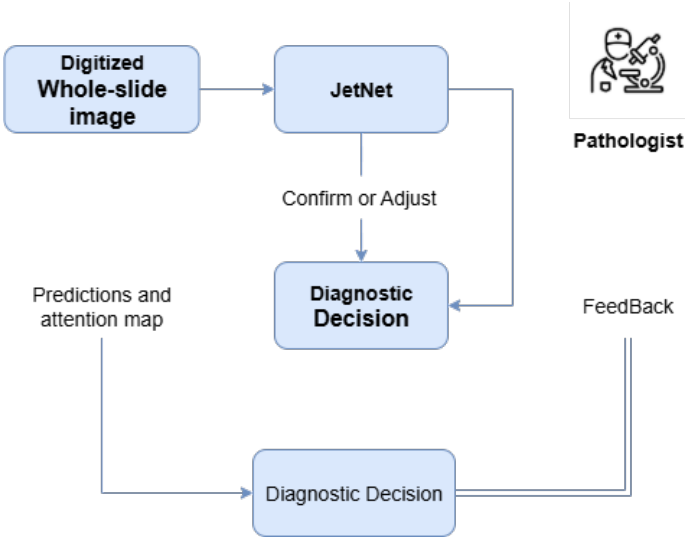


Figure 8. **Proposed JetNet human–AI collaboration framework.** Digitized whole-slide images are preprocessed and analyzed by JetNet, which generates class predictions and Grad-CAM attention maps highlighting diagnostically relevant regions. Pathologists review these outputs, validate or refine the AI-assisted suggestions, and finalize the diagnosis. Feedback from ambiguous or misclassified cases is incorporated into an iterative learning loop to enhance future model performance and reliability.

6. Conclusion

This paper introduced a novel convolutional neural network architecture suited for efficient and accurate classification of lung cancer histopathological images. By carefully balancing model complexity and computational demands, JetNet achieved a remarkable accuracy of 99.6% on a public lung cancer dataset, surpassing several well-established deep learning models such as DenseNet, EfficientNet, and MobileNetV2.

The model is evaluated on a subset of the public LC25000 dataset, consisting of 15,000 RGB images classified into three classes: benign tissue, squamous cell carcinoma, and adenocarcinoma. To assess model robustness, a 5-fold cross-validation strategy is employed.

The lightweight design of the model, featuring streamlined convolutional blocks, batch normalization, and global average pooling, enables faster inference times and reduced memory usage, making it highly suitable for deployment in real-time clinical environments and resource-limited healthcare settings. This efficiency does not compromise diagnostic performance, indicating JetNet's potential as a reliable tool to support pathologists in automated lung cancer diagnosis.

Future work will focus on expanding JetNet's applicability to multi-center datasets to further validate its generalization capabilities, integrating explainability techniques to improve model interpretability, and exploring its use in other histopathological cancer classification tasks. In general, JetNet represents a significant and practical advancement in the design of interpretable and efficient CNNs for histopathological cancer diagnosis, in the development of practical, high-performance deep learning solutions for medical image analysis.

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