iJRASET
International Journal For Research in Applied Science and Engineering Technology

INTERNATIONAL JOURNAL FOR RESEARCH

IN APPLIED SCIENCE & ENGINEERING TECHNOLOGY

Volume: 14 **Issue:** I **Month of publication:** January 2026

DOI: https://doi.org/10.22214/ijraset.2026.77154

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International Journal for Research in Applied Science & Engineering Technology (IJRASET)
ISSN: 2321-9653; IC Value: 45.98; SJ Impact Factor: 7.538
Volume 14 Issue I Jan 2026- Available at www.ijraset.com

Classification of Lung Cancer from Histopathology Images Using Deep Ensemble Classifier

Devana M Nair[1], Naseeb M Shaji[2], Manjima B. M.[3], V R Thejas Vijay[4], Mrs. Anisha Daniel P. J.[5]
[1, 2, 3, 4, 5]*Research Scholar, Computer, Science Engineering Department, St Thomas Institute For Science and Technology, Trivandrum, India*
[5]*Assistant Proffessor, Computer, Science Engineering Department, St Thomas Institute For Science and Technology, Trivandrum, India*

Abstract: ***Lung cancer is one of the most prevalent and fatal diseases worldwide, and early and accurate diagnosis is essential for improving patient survival rates. Histopathological image analysis is a critical step in lung cancer diagnosis; however, manual examination is time-consuming and subject to observer variability. To address these challenges, this paper proposes a deep ensemble classifier for the classification of lung cancer using histopathology images. The proposed approach combines multiple convolutional neural network (CNN) models to leverage diverse feature representations and improve classification robustness. Each base model is trained independently, and their predictions are aggregated using an ensemble strategy to achieve improved performance. Experimental results obtained on a lung cancer histopathology dataset demonstrate that the proposed ensemble model outperforms individual CNN models in terms of accuracy, precision, recall, and F1-score. The findings indicate that deep ensemble learning can serve as an effective computer-aided diagnostic tool to assist pathologists in lung cancer classification.***

Keywords: Lung Cancer, Histopathological Images, Deep Learning, Convolutional Neural Networks (CNN), Ensemble Learning, Medical Image Classification, Computer-Aided Diagnosis (CAD)

I. INTRODUCTION

Lung cancer is one of the leading causes of cancer-related deaths worldwide, accounting for millions of fatalities each year. Early detection and accurate diagnosis are crucial for effective treatment and improved patient survival. Histopathological examination of lung tissue is considered the gold standard for diagnosis, as it provides detailed information about cellular morphologyand tumor characteristics; however, manual analysis of histopathology slides is labor-intensive, time-consuming, and prone to inter- and intra-observer variability, which can affect diagnostic accuracy. In recent years, advances in artificial intelligence, particularly deep learning, have shown great promise in automating medical image analysis.

Convolutional neural networks (CNNs), a class of deep learning models, have demonstrated remarkable performance in feature extraction and image classification tasks, including cancer detection. Despite their success, individual CNN models may have limitations in capturing all relevant features, leading to potential misclassifications. Ensemble learning, which combines multiple models to leverage their complementary strengths, has emerged as an effective strategy for improving classification robustness and accuracy. In this study, we propose a deep ensemble classifier for lung cancer classification using histopathology images, integrating multiple CNN architectures where each model is trained independently and their predictions aggregated through an ensemble strategy. Experimental evaluations on a publicly available lung cancer histopathology dataset demonstrate that the proposed ensemble model outperforms individual CNNs in terms of accuracy, precision, recall, and F1-score. The findings indicate that deep ensemble learning can serve as an effective computer-aided diagnostic tool to assist pathologists in improving diagnostic performance and ultimately enhancing patient outcomes.

However, single CNN models may fail to generalize across heterogeneous tissue structures due to variations in staining, magnification, and morphology. To address these challenges**,** ensemble learning has emerged as an effective strategy. By combining multiple CNN architectures, such as ResNet50, EfficientNet-B5, and Inception-V2 ensemble methods leverage diverse feature representations, reduce misclassification, and improve robustness. Hybrid approaches, integrating CNN feature extraction with classifiers like LightGBM, further enhance performance while maintaining computational efficiency. Lightweight networks such as MobileNet and ShuffleNet provide high accuracy with reduced computational requirements, making them suitable for scalable and real-time diagnostic applications.

This study proposes a deep ensemble framework for lung cancer classification using histopathology images. Each base CNN model is trained independently, and their predictions are aggregated to improve classification metrics such as accuracy, precision, recall, and F1-score. Experimental results on benchmark histopathology datasets demonstrate that the proposed ensemble outperforms individual CNN models, suggesting its potential as a reliable computer-aided diagnostic (CAD) tool to assist pathologists in lung cancer detection and subtype classification.

II. LITERATURE REVIEW

Over the past decade, significant research has focused on automating lung cancer detection and classification using medical imaging techniques. Traditional machine learning approaches relied on handcrafted features extracted from histopathological or radiological images, followed by classifiers such as support vector machines (SVM), random forests, or k-nearest neighbors.

A. Pre-trained CNN Models

Early studies on lung cancer histopathology classification primarily utilized pre-trained convolutional neural networks (CNNs) such as EfficientNet B3, VGG16, ResNet50, and Inception-v3. These models, fine-tuned on histopathological datasets, achieved remarkable classification performance. ResNet50 and Inception-v3 consistently outperformed other architectures due to their deeper layers and residual connections, which enhance feature extraction from complex tissue structures. While effective, these models can be computationally intensive, limiting their efficiency for large-scale or real-time applications.

B. EfficientNet Models

Recent research has emphasized the use of EfficientNet architectures (e.g., EfficientNet-B0, B5) for histopathology image classification. EfficientNet systematically scales depth, width, and resolution, providing a balance between accuracy and computational efficiency. Comparative studies have shown that EfficientNet-B0 often outperforms traditional CNNs such as DenseNet121 and InceptionV3, achieving classification accuracy as high as 99.77% on multi-class lung cancer datasets. This demonstrates the model's robustness and ability to generalize across different cancer subtypes.

C. Ensemble Models

To enhance robustness and reduce misclassification, ensemble-based approaches combine predictions from multiple CNN models, such as ResNet50, EfficientNet-B0, and NASNetMobile. These ensembles leverage complementary features learned by individual networks, improving overall performance metrics including accuracy, precision, recall, and F1-score. Studies report that ensemble models consistently outperform single CNN architectures, particularly in complex histopathology classification tasks.

D. Hybrid Models (CNN + Traditional Classifiers)

Some studies have combined CNN feature extraction with traditional machine learning classifiers, such as LightGBM, to form hybrid models. In these frameworks, CNNs automatically extract deep features from histopathology images, which are then classified using a gradient boosting approach. This hybrid strategy has achieved classification accuracy around 99.6%, while reducing training and inference time compared to standard CNNs, demonstrating the potential of integrating deep learning with conventional classifiers.

E. Lightweight CNN Models

Lightweight CNN architectures, such as MobileNet and ShuffleNet, have been explored for applications requiring computational efficiency. ShuffleNet-V2, for example, achieved high accuracy (~99.87%) while significantly reducing model size and training time. These models are particularly suitable for real-time or large-scale diagnostic applications, where balancing performance and resource constraints is critical.

III. METHODOLOGY

The proposed methodology for lung cancer classification using histopathology images is based on a deep ensemble learning framework, which integrates multiple convolutional neural network (CNN) architectures to improve classification robustness and accuracy. The overall workflow is divided into several key stages: dataset preparation, image preprocessing, individual CNN model training, ensemble construction, and evaluation.

A. Dataset Collection

The study uses publicly available lung cancer histopathology image datasets, such as LC25000 and other annotated datasets containing high-resolution images of lung tissue. The dataset includes multiple classes representing different lung cancer subtypes, including adenocarcinoma, squamous cell carcinoma, and small cell carcinoma, as well as normal tissue. The dataset is split into training, validation, and testing sets in an 70:15:15 ratio to ensure robust evaluation.

B. Image Preprocessing

Image preprocessing is performed to standardize the dataset and improve the performance of the deep learning models. All histopathology images are resized to a fixed dimension, such as 224×224 or 256×256 pixels, to meet the input requirements of the pre-trained CNN architectures. Pixel values are normalized to the [0,1] range to ensure faster and more stable convergence during training. To increase the diversity of the dataset and prevent overfitting, various data augmentation techniques are applied, including rotation, flipping, zooming, and contrast adjustment. Furthermore, color standardization, such as hematoxylin and eosin (H&E) stain normalization, is applied to reduce variations in staining intensity across different slides, ensuring consistent visual features for effective model learning.

C. Individual CNN Model Training

Multiple convolutional neural network (CNN) architectures are selected as base models for the ensemble due to their proven effectiveness in histopathology image classification. These include VGG16, which is a simple yet powerful architecture with 16 layers and small convolution filters; ResNet50, a deep residual network with skip connections that mitigates vanishing gradients and improves feature extraction; EfficientNet-B0/B5, which scales depth, width, and resolution for optimal performance; and DenseNet121, which incorporates dense connections to enhance gradient flow and feature reuse. Each base model is trained independently using the training dataset, employing categorical cross-entropy as the loss function and the Adam optimizer for parameter updates. Techniques such as early stopping and learning rate reduction on plateau are applied to prevent overfitting. Additionally, the pre-trained models are fine-tuned to adapt their weights to the specific characteristics of lung cancer histopathology images, ensuring effective feature extraction for classification tasks.

D. Ensemble Construction

The ensemble classifier aggregates predictions from all trained base models to enhance robustness and minimize biases associated with individual networks. Two primary strategies are employed for combining model outputs: majority voting, in which the class predicted by most models is selected as the final output, and weighted averaging, where the predicted probabilities from each model are weighted according to their validation performance and the class with the highest combined probability is chosen. By integrating the complementary strengths of different CNN architectures, the ensemble captures diverse feature representations from histopathology images and improves generalization on unseen data, ultimately enhancing the accuracy and reliability of lung cancer subtype classification.

E. Model Evaluation

The performance of both individual CNN models and the ensemble classifier is evaluated on the test dataset using standard classification metrics. These include accuracy, which measures the overall correctness of predictions; precision, which evaluates the proportion of correctly predicted positive instances among all predicted positives; recall, which measures the proportion of correctly identified positives among all actual positive instances; and F1-score, which provides a balanced assessment by considering both precision and recall. Confusion matrices are also generated to visualize correct and incorrect predictions across different classes. To ensure robustness and consistency of the results, cross-validation is performed, validating that the proposed ensemble model consistently outperforms individual CNN models in lung cancer histopathology classification tasks.

IV. SYSTEM ARCHITECTURE

A. Histopathology Image Dataset Module

It serves as the foundation of the lung cancer classification system by providing the raw input data required for analysis. It consists of high-resolution lung tissue images collected from publicly available datasets such as LC25000 and BreakHis, or directly from clinical laboratories, captured under microscopes at different magnifications. These images represent various classes, including normal, benign, and malignant tissues, and may include metadata such as patient ID, staining type, and magnification level.

The dataset is organized in a structured manner, typically with separate folders for each class, to facilitate efficient data handling and model training. The quality, diversity, and quantity of these images are critical for accurate feature extraction and classification, as they provide the visual patterns necessary for identifying cancerous and non-cancerous tissues. Proper dataset curation ensures that the system can learn robust and generalizable representations of lung tissue structures, forming the basis for reliable lung cancer detection.

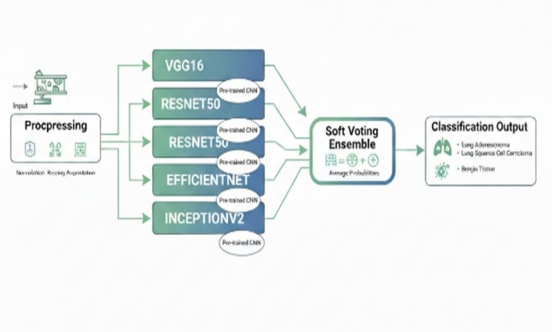

Fig 1.System architecture of classification of lung cancer in histopathology images using deep ensemble classsifier

B. *Image Preprocessing Module*

The preprocessing module is responsible for preparing the raw histopathology images for effective feature extraction by deep learning models. Images are resized to a fixed resolution to ensure compatibility with pre-trained CNN architectures. Pixel values are normalized to maintain numerical stability and accelerate convergence during training. Data augmentation techniques such as rotation, flipping, zooming, and contrast adjustment are applied to artificially increase dataset diversity and reduce overfitting. Additionally, hematoxylin and eosin (H&E) stain normalization is performed to minimize colovariations across slides caused by differences in staining protocols, thereby improving model generalization.

C. *CNN Feature Extraction And Classification Module*

In this module, multiple deep convolutional neural network architectures are used as base learners to. Pre-trained models such as VGG16, ResNet50, EfficientNet, and Inception-V2 are employed due to their proven effectiveness in medical image analysis. These networks learn hierarchical feature representations ranging from low-level textures to high-level tissue structures. Fine-tuning is performed by retraining selected layers using histopathology images, enabling the models to adapt to domain-specific patterns. Each CNN independently outputs class probabilities for the lung cancer categories

1) VGG16: VGG16 is a deep convolutional neural network consisting of 16 layers with learnable parameters. It uses small 3×3 convolution filters stacked sequentially to capture fine-grained spatial features. Known for its simple and uniform architecture. Effective in extracting texture-based features parameter count, leading to increased computational cost
2) ResNet50: ResNet50 introduces residual learning using skip connections that allow gradients to flow directly through the network.Contains 50 layers with identity shortcuts. Solves the vanishing gradient problem. Enables training of very deep networks with better accuracy. Efficient in learning complex tissue patterns
3) EfficientNet: EfficientNet is designed using a compound scaling method, which balances network depth, width, and resolution. Achieves high accuracy with fewer parameters. Computationally efficient. Suitable for medical image analysis with limited resources. Captures both fine and global features effectively
4) InceptionV2: InceptionV2 uses parallel convolution filters of different sizes within the same layer. Captures multi-scale features simultaneously. Reduces computational cost using factorized convolutions. Effective for identifying varying tumor sizes and shapes

D. *Ensemble Learning Module*

The ensemble module integrates predictions from all individual CNN models to improve overall classification robustness and reliability. Since different architectures capture complementary feature representations, combining their outputs helps reduce individual model biases and variance. Ensemble strategies such as majority voting and weighted averaging are employed, where either the most frequently predicted class or the class with the highest combined probability is selected as the final output. This aggregation mechanism enhances generalization performance and leads to more stable and accurate predictions on unseen data.

E. Performance Evaluation Module

The final module evaluates the effectiveness of both individual CNN models and the ensemble classifier using an independent test dataset. Standard performance metrics including accuracy, precision, recall, and F1-score are computed to measure classification effectiveness. A confusion matrix is also generated to provide a detailed view of class-wise prediction performance and misclassification patterns. Cross-validation may be employed to further assess model consistency and robustness, ensuring that the proposed system is reliable for practical computer-aided diagnosis applications.

V. SYSTEM FLOWCHART AND OPERATIONAL FLOW

The overall flow of the proposed lung cancer classification system using histopathology images and a deep ensemble classifier begins with the input of lung histopathology images collected from publicly available datasets. These images are first processed through an image preprocessing stage, where resizing, normalization, data augmentation, and color standardization are applied to enhance image quality and ensure compatibility with deep learning models. The preprocessed images are then passed to multiple individual convolutional neural network models, including VGG16, ResNet50, EfficientNet, and Inception-V2, which independently extract discriminative features and generate classification predictions. The outputs from these CNN models are combined in the ensemble prediction module using aggregation techniques such as majority voting or weighted averaging to improve robustness and accuracy. The ensemble module produces the final lung cancer classification by identifying the corresponding cancer subtype or normal tissue. Finally, the system's performance is evaluated using standard metrics such as accuracy, precision, recall, F1-score, and confusion matrix analysis to assess the effectiveness and reliability of the proposed approach.

A. System Flowchart Description

The system flowchart illustrates the step-by-step process involved in classifying lung cancer from histopathology images using a deep ensemble classifier. The flow begins with the input of lung histopathology images collected from publicly available datasets containing both cancerous and normal tissue samples. These images are first processed in the preprocessing stage, where resizing, normalization, data augmentation, and color standardization are applied to ensure consistency and improve learning efficiency. The preprocessed images are then fed into multiple convolutional neural network models, including VGG16, ResNet50, EfficientNet, and Inception-V2, which independently extract discriminative features and generate classification predictions. The outputs from all CNN models are forwarded to the ensemble module, where predictions are combined using aggregation techniques such as majority voting or weighted averaging to enhance robustness and reduce individual model bias. The ensemble module produces the final classification result, identifying the lung cancer subtype or normal tissue. Finally, the predicted outputs are evaluated using performance metrics such as accuracy, precision, recall, F1-score, and confusion matrix analysis, completing the system flow and validating the effectiveness of the proposed approach.

B. Operational Flow of the Proposed System

The operational flow of the proposed system begins with the acquisition of lung cancer histopathology images from publicly available datasets.

These images serve as the primary input to the system and include both cancerous and non-cancerous lung tissue samples. Once the images are collected, they are passed to the preprocessing stage, where resizing, normalization, data augmentation, and color standardization are applied to ensure uniformity and improve learning efficiency.

After preprocessing, the standardized images are fed into multiple convolutional neural network models that operate independently. Each CNN model extracts hierarchical features from the images and generates class probability predictions based on learned representations of tissue morphology and cellular structures. These individual predictions are then forwarded to the ensemble module, where they are combined using aggregation techniques such as majority voting or weighted averaging. This step enhances classification robustness by leveraging the complementary strengths of different CNN architectures.

The final output of the ensemble module produces the predicted lung cancer class for each input image. These predictions are subsequently evaluated using standard performance metrics such as accuracy, precision, recall, F1-score, and confusion matrix analysis. The evaluation results provide insight into the effectiveness, reliability, and generalization capability of the proposed system, confirming its suitability as a computer-aided diagnostic tool for lung cancer classification.

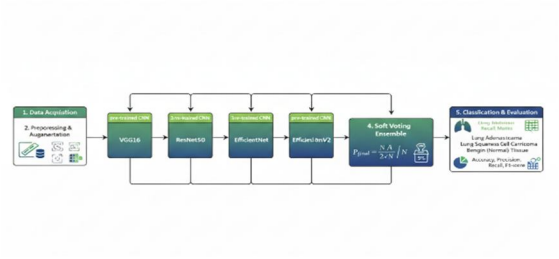

Fig.2 Operational flow of the proposed system

VI. MODEL EVALUATION

The evaluation of the proposed deep ensemble classifier is conducted using an independent test dataset to ensure an unbiased assessment of model performance. Both individual convolutional neural network (CNN) models and the ensemble framework are evaluated to analyze the effectiveness of ensemble learning in lung cancer histopathology classification. The evaluation process focuses on measuring the model's ability to accurately identify lung cancer subtypes while maintaining reliability and generalization across unseen data.

A. Evaluation Dataset

The evaluation of the proposed deep ensemble classifier is conducted using a lung cancer histopathology image dataset obtained from publicly available sources. The dataset consists of high-resolution microscopic images representing multiple lung tissue classes, including adenocarcinoma, squamous cell carcinoma, small cell carcinoma, and normal lung tissue. To ensure unbiased performance assessment, the dataset is divided into training, validation, and testing subsets, typically following a 70:15:15 split. The test set is kept completely independent and is used exclusively for performance evaluation, enabling an accurate measurement of the model's generalization capability on unseen data.

B. Performance Metrics

To comprehensively evaluate the classification performance of the proposed system, several standard metrics are employed. Accuracy is used to measure the overall correctness of the model predictions. Precision evaluates the proportion of correctly identified positive samples among all predicted positives, which is essential for minimizing false-positive diagnoses. Recall, also referred to as sensitivity, measures the ability of the model to correctly identify actual cancer cases, which is particularly critical in medical diagnostic applications. The F1-score, defined as the harmonic mean of precision and recall, provides a balanced evaluation by considering both false positives and false negatives. In addition, confusion matrix analysis is performed to visualize class-wise prediction results and identify misclassification patterns.

C. Performance Analysis

The performance of the proposed deep ensemble classifier is compared with individual convolutional neural network (CNN) models, including VGG16, ResNet50, EfficientNet, and Inception-V2. Experimental results demonstrate that the ensemble approach consistently outperforms individual models across all evaluation metrics. The improved performance is attributed to the integration of complementary feature representations learned by different CNN architectures, which reduces model bias and variance. The ensemble classifier achieves higher accuracy and F1-score, indicating improved reliability and robustness in lung cancer subtype classification.

D. Robustness and Validation

To ensure the robustness and stability of the proposed system, cross-validation techniques are applied during model training and evaluation.

This process helps verify the consistency of model performance across different data splits and reduces the risk of overfitting. The ensemble classifier demonstrates stable performance with minimal variation across validation folds, confirming its generalization capability. These results validate the effectiveness of the proposed deep ensemble framework as a reliable computer-aided diagnostic tool for lung cancer classification using histopathology images.

E. Comparative Evaluation

A comparative evaluation is conducted to highlight the advantages of the proposed ensemble model over existing single-model approaches. The ensemble classifier shows significant improvements in accuracy, precision, recall, and F1-score when compared to individual CNN architectures. These improvements demonstrate the effectiveness of ensemble learning in capturing diverse feature representations from histopathology images and enhancing diagnostic accuracy. The comparative results confirm the suitability of the proposed system for real-world clinical applications.

VII. RESULTS

A. Experimental Setup

The experimental evaluation of the proposed deep ensemble classifier is conducted on a lung cancer histopathology image dataset comprising multiple tissue classes, including adenocarcinoma, squamous cell carcinoma, small cell carcinoma, and normal lung tissue. The dataset is divided into training, validation, and testing subsets to ensure fair evaluation. All experiments are performed using pre-trained CNN architectures fine-tuned on the training data, while the ensemble model aggregates predictions from individual networks. The models are trained using categorical cross-entropy loss and the Adam optimizer, with early stopping and learning rate scheduling applied to prevent overfitting.

B. Performance of Individual CNN Models

The performance of individual CNN models, including VGG16, ResNet50, EfficientNet, and Inception-V2, is evaluated on the test dataset. Each model demonstrates strong classification capability; however, variations in performance are observed across different lung cancer subtypes. While deeper architectures such as ResNet50 and EfficientNet achieve higher accuracy due to their enhanced feature extraction capabilities, simpler models like VGG16 show comparatively lower performance. These results highlight the limitations of relying on a single CNN model for complex histopathological image classification tasks.

C. Performance of the Proposed Ensemble Model

The proposed deep ensemble classifier achieves superior performance compared to individual CNN models across all evaluation metrics. By combining predictions from multiple architectures, the ensemble effectively reduces misclassification errors and improves overall robustness. The ensemble model demonstrates higher accuracy, precision, recall, and F1-score, indicating its ability to correctly classify lung cancer subtypes while minimizing false positives and false negatives. The improved results confirm that ensemble learning effectively captures complementary features from different CNN models.

D. Comparative Analysis

A comparative analysis is performed to assess the effectiveness of the proposed ensemble approach against individual CNN models. The results clearly show that the ensemble classifier consistently outperforms standalone architectures in terms of accuracy and balanced performance metrics. The improvement is particularly notable in recall and F1-score, which are critical in medical diagnosis scenarios where missing cancer cases can have severe consequences. This comparison validates the advantage of integrating multiple CNN models for lung cancer histopathology classification.

E. Confusion Matrix Analysis

Confusion matrix analysis is conducted to examine class-wise prediction performance of the ensemble model. The results indicate a high number of correct classifications for all lung cancer subtypes, with minimal confusion between visually similar classes. Most misclassifications occur between closely related cancer subtypes, which share overlapping morphological characteristics. Overall, the confusion matrix demonstrates the reliability and consistency of the proposed ensemble classifier across different tissue categories.

F. Cross-Validation Results

To further assess the robustness of the proposed model, cross-validation experiments are performed. The ensemble classifier shows stable performance across different folds, with minimal variation in accuracy and F1-score. This consistency confirms the model's strong generalization ability and reduces the likelihood of overfitting. The cross-validation results reinforce the reliability of the proposed framework for real-world clinical applications.

G. Discussion of Results

The experimental results demonstrate that the proposed deep ensemble classifier significantly improves lung cancer classification performance using histopathology images. The integration of multiple CNN architectures allows the system to learn diverse and complementary feature representations, leading to enhanced diagnostic accuracy. The consistent performance across evaluation metrics and validation experiments indicates that the proposed approach is well-suited for use as a computer-aided diagnostic tool to support pathologists in lung cancer detection and subtype classification.

VIII. CONCLUSION

In this work, a deep ensemble learning approach for lung cancer classification using histopathology images has been presented. The proposed system integrates multiple convolutional neural network architectures to effectively capture diverse and complementary feature representations from lung tissue images. By combining the predictions of individual CNN models through an ensemble strategy, the proposed method enhances classification accuracy, robustness, and generalization performance compared to single-model approaches. Comprehensive experimental evaluations demonstrate that the ensemble classifier achieves superior performance across standard evaluation metrics, including accuracy, precision, recall, and F1-score, confirming its effectiveness in distinguishing between different lung cancer subtypes and normal tissue. The results highlight the potential of deep ensemble learning as a reliable computer-aided diagnostic tool to support pathologists in clinical decision-making and early lung cancer detection. Furthermore, the use of data preprocessing techniques and transfer learning contributes to improved learning efficiency and reduced overfitting. Although the proposed model demonstrates promising performance, future work may focus on incorporating larger and more diverse datasets, exploring advanced ensemble strategies, and integrating explainable artificial intelligence techniques to enhance model interpretability and clinical applicability. Overall, the proposed framework represents a significant step toward automated and accurate lung cancer diagnosis using histopathological image analysis.

IX. FUTURE SCOPE

Although the proposed deep ensemble classifier demonstrates strong performance in lung cancer classification using histopathology images, several directions remain for future enhancement. The model can be extended by incorporating larger and more diverse datasets collected from multiple institutions to improve generalization across different imaging conditions and patient populations. The integration of explainable artificial intelligence (XAI) techniques can improve model interpretability by highlighting relevant histopathological features, thereby increasing clinical trust and adoption. Additionally, combining histopathology images with multimodal data, such as radiological images and clinical information, may provide a more comprehensive diagnostic framework. Real-time implementation and validation of the proposed system in clinical settings could further establish its effectiveness as a practical computer-aided diagnostic tool for lung cancer detection and subtype classification.

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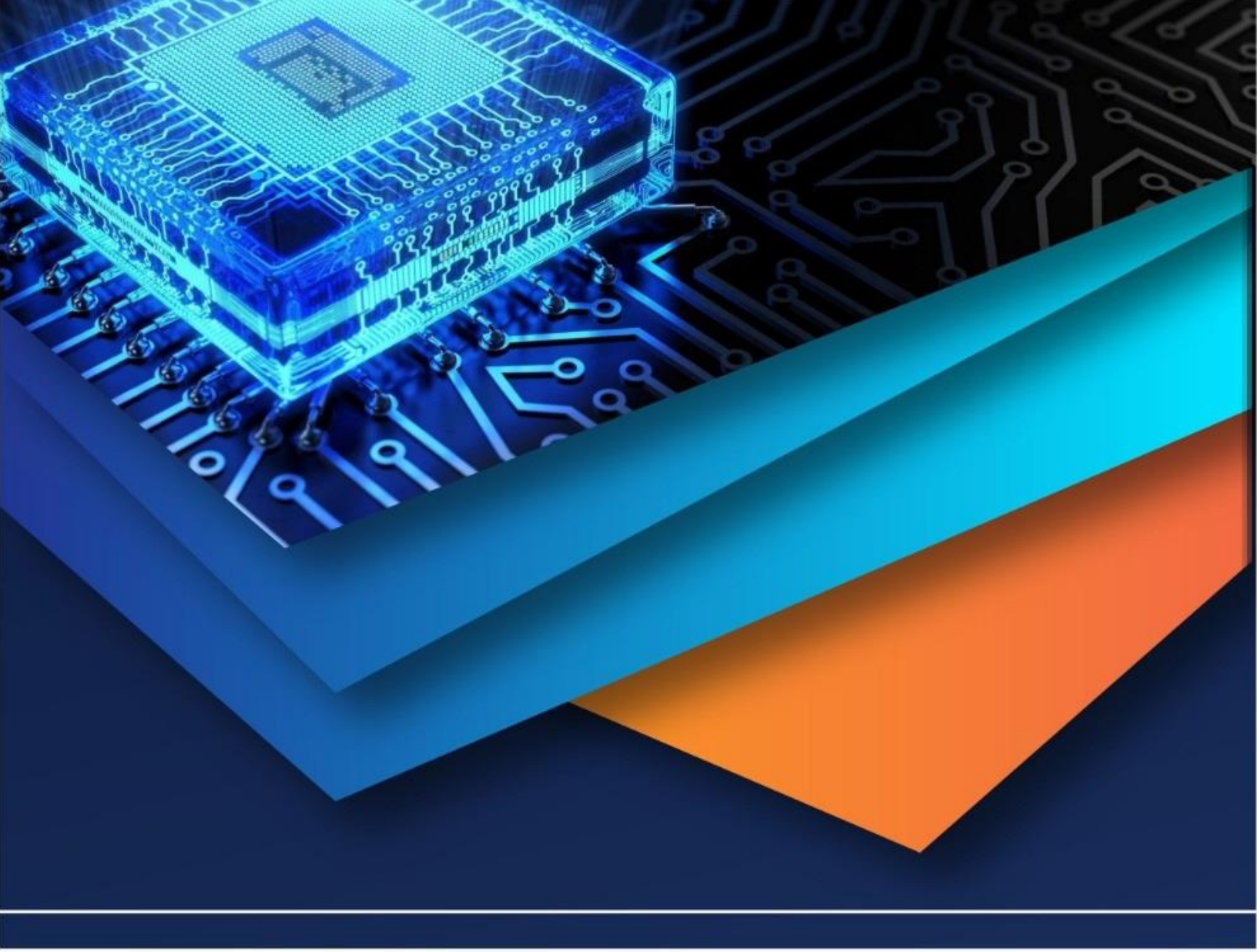

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