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LUNG CANCER CLASSIFICATION BY USING TRANSFER LEARNING

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Abstract

Lung cancer poses a formidable global health challenge, necessitating advancements in diagnostic methodologies. This research addresses the exigency for efficient and accurate classification of lung cancer histopathological images by assessing the computationally streamlined ConvNeXtTiny model. The study meticulously examines the model's aptitude in differentiating amongst benign, squamous cell carcinoma, and adenocarcinoma, thereby obviating the constraints of computational intensity that encumber many contemporary deep learning architectures. Transfer learning is employed, leveraging the pre-trained ConvNeXtTiny model and refining it for lung cancer classification. The methodology encompasses a rigorous evaluation utilizing a curated dataset of histopathological images, with a focus on metrics pertinent to clinical applicability. The results evince the model's capacity to achieve high classification accuracy with reduced computational demands, thus underscoring its potential to facilitate the pragmatic deployment of AI in diverse medical facility settings, including those with inadequate resources. This study contributes to the persistent efforts to increase diagnostic precision and efficiency in lung cancer, offering a computationally viable solution that maintains clinical reliability. The research highlights the prospective of the ConvNeXtTiny model to serve as a valuable tool in assisting medical professionals in the accurate and timely diagnosis of lung cancer subtypes.

1. INTRODUCTION

In 2022, approximately 2.5 million new cases were reported, out of which 12.4% were all new cancer cases worldwide, which shows that lung cancer is the most commonly occurring. Likewise, in 2022 approximately 1.8 million deaths, which is 18.7% of total cancer deaths. According to the WHO (World Health Organization), findings highlight a continuous and critical need for advancements in the initial detection, diagnosis, and treatment of lung cancer globally [1]

AI is constantly evolving and developing at a rapid pace. AI also displays stunning expansion in the healthcare sector, especially in 2D biomedical imaging. The AI image architecture is assisting doctors and radiologists with better classification. Lung carcinoma is one of the major causes of cancer-related diseases worldwide has however continued to prove one of the hardest to diagnose. Histopathological image analysis is essential for identifying subtypes, including adenocarcinoma, benign, and squamous cell carcinoma, as these subtypes define the treatment approach. However, to perform conventional diagnostic assessments, the time and effort consumed, as well as, variability derived from interpretation differences, pose challenges. In the last few years, researchers have deployed deep learning (DL) strategies, especially the CNN, in the automation of this process with high accuracy. Nevertheless, the majority of current ones with well-developed DL architectures are still

computationally expensive and cannot be implemented in limited-resource contexts that may include rural hospitals or clinics with access to powerful computational hardware.[2]

These critical gaps are addressed by this study via the assessment of the computationally efficient ConvNeXtTiny model for lung cancer classification. Hence, supplementing computational gain with clinical significance, this work seeks to promote the pragmatic use of AI in healthcare environments.[3]

In this regard, analyzing the performance established by the ConvNeXtTiny model, which is a lightweight version of the ConvNeXt architecture family, becomes relevant. That is why its ability to obtain high classification accuracy with low computational complexity makes it. In this study, the effectiveness of the ConvNeXtTiny model in diffracting amongst squamous cell carcinoma, benign, and adenocarcinoma histopathological images will be examined.

The major purpose of this paper is to use transfer learning and evaluate a computationally efficient deep learning model, specifically the pre-trained ConvNeXtTiny, for classifying lung cancer histopathological images into three categories: adenocarcinoma, benign, and squamous cell carcinoma.

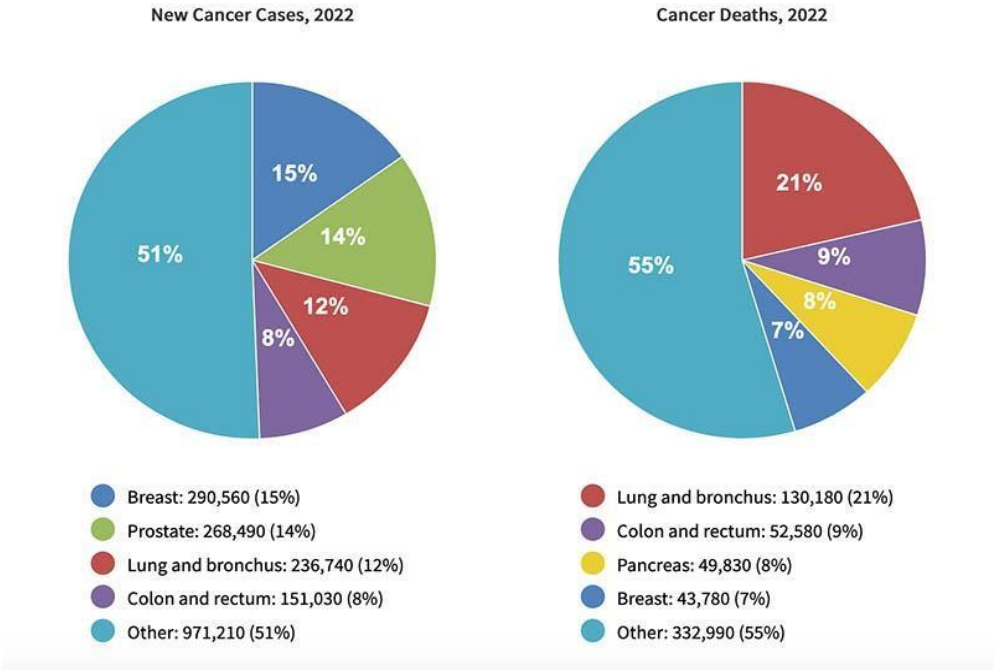


Figure 1: Distribution of new cancer cases and deaths in 2022, emphasizing the significant prevalence and mortality rate of lung cancer.[4]

The paper investigates the ConvNeXtTiny model for classifying lung cancer histopathological images into squamous cell carcinoma, benign, and adenocarcinoma. The model is adapted using transfer learning on a dataset sourced from Kaggle. Segment 2 presents the literature review, discussing computational challenges in CNN models. Segment 3 explains the methodology, including dataset details, data augmentation, and model Dense layers. Segment 4 covers the results and discussion, evaluating accuracy, precision, recall, and F1-score. Segment 5 concludes the whole paper.

2. Literature Review

Lung cancer, a malignant neoplasm leading to high cancer fatality, is subtyped according to histopathological features. Of these, adenocarcinoma and squamous cell carcinoma are the two most frequent subtypes of NSCLC, whereas benign lung diseases sometimes bear histopathological

resemblances with cancers, making diagnosis challenging. Adenocarcinoma originates from mucus-manufacturing glandular tissues and is usually diagnosed in the peripheral areas of the lungs, while squamous originates from flat cells lining the airspace and are often seen in the central region of the lung. Proper differentiation of these types is important in identifying adequate treatment plans for a patient.[5]

The SOTA DL models, especially the CNN, can work well to narrow down the morphological differences and thus help in the subtype categorization of lung cancer. Nonetheless, issues of limited data, classes that may not be evenly distributed, or the sheer computational intensity remain still demanding for the development of more efficient and effective solutions. These gaps are filled with this study as the ConvNeXtTiny model is employed in adenocarcinoma, squamous cell carcinoma, and benign classification, improving diagnosis accuracy and system availability.[6, 7]

However, difficulties like the cost involved in computational procedures, imbalance in datasets, and black box models have not been ignored. This research shows that a trained model can work on high as well as low computation with stunning benchmarks of evaluation metrics. These developments are taken forward, and the gaps left are filled in this study, where ConvNeXtTiny –an efficient architecture is used for classifying lung cancer, which is clinically feasible and requires low computational power.[8]

In a few years, CNN has gained prominence in classifying medical lung cancer images. Their capacity to acquire hierarchical features from raw image data has enabled them to excel in analyzing complicated histopathological images. In the detection of lung cancer, CNNs have been applied to distinguish between different subtypes, which include adenocarcinoma, squamous cell carcinoma, and benign lesions. AlexNet, VGG, ResNet, and DenseNet have shown that their morphological features of lung tissue samples can provide higher accuracy than conventional image analysis methods.[9]

Previous research has also confirmed the viability of transfer learning, in which pre-trained CNNs are retrained on a certain medical dataset; hence, model performance received can be achieved without requiring large labeled data. Nevertheless, the traditional architectures of CNN suffer from a problem of high computational complexity in which the deployment of such a system in a resource-limited environment such as rural hospitals is a challenge.[10] However, it is known that CNNs provide high accuracy, while the performance of models on clinically important characteristics such as precision and recall is often not disclosed to allow their use in practical tasks.

Following the enhancement of the CNN-based classification of lung cancer, this thesis presents the ConvNeXtTiny model. Because ConvNeXtTiny has a modified architecture for computations and takes up fewer resources than existing models, this CNN could stand as a solution to the issues associated with implementing CNNs in real-life healthcare settings for lung cancer detection.[11]

TABLE 1. Summarizing the entire Literature review.

Reference	Machine Learning Model	Results
Silva et al. [12]	PSO-based CNN	Accuracy 97.62%, Specificity 98.21%, Sensitivity 92.20%
Monkam et al. [13]	2D-CNN	Accuracy 88.28%, AUC 87%, F-score 83.45%, Sensitivity 83.82%
Song et al. [14]	CNN	Accuracy 84.15%, Sensitivity 83.96%, Specificity 84.32%
Sahu et al. [15]	MVCNN	Accuracy 93.18%
Bhandary et al. [16]	Modified AlexNet (MAN)	Accuracy >97.27%

Silva et al. [17]	CNN	Accuracy 82.3%, Sensitivity 79.4%, Specificity 83.8%
Ren et al. [18]	MRC-DNN	Accuracy 90%, Sensitivity 81%, Specificity 95%
Zhao et al. [19]	Hybrid CNN	Accuracy 88.1%
Masood et al. [20]	DFCNet	Sensitivity 84.58%
Nishio et al. [21]	2D-Deep CNN	Avg. validation accuracy 68%.
Alakwaa et al. [22]	3D-CNNs, U-Net	Accuracy 86.6%
Sasikala et al. [23]	CNN	Accuracy 96%
Sujata et al. [24]	KNN	Accuracy 98.30%
Qing et al. [25]	EDM	Accuracy 77.80%
Jayaraj et al. [26]	RF	Accuracy 89.90%

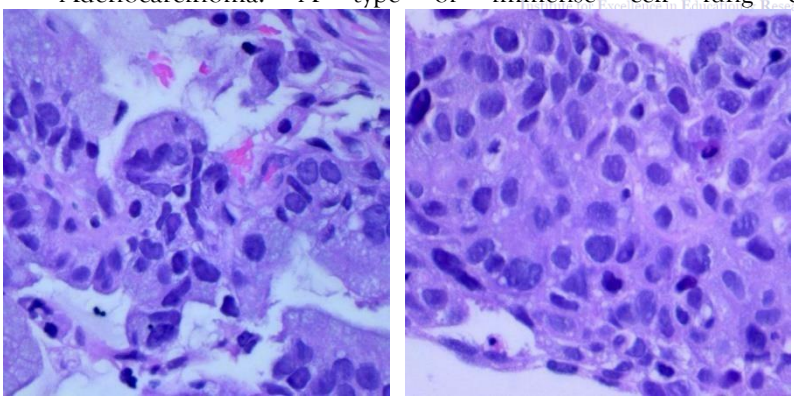
3. Methodology

The Lung Cancer (Histopathological Images) secondary dataset, accessible at Kaggle [27], is a curated collection of histopathological images aimed at facilitating the classification of lung tissue into three categories: adenocarcinoma, squamous cell carcinoma, and benign. According to researchers and physicians, this dataset single-mindedness has marvelous image resolution for ML models for lung cancer classification.

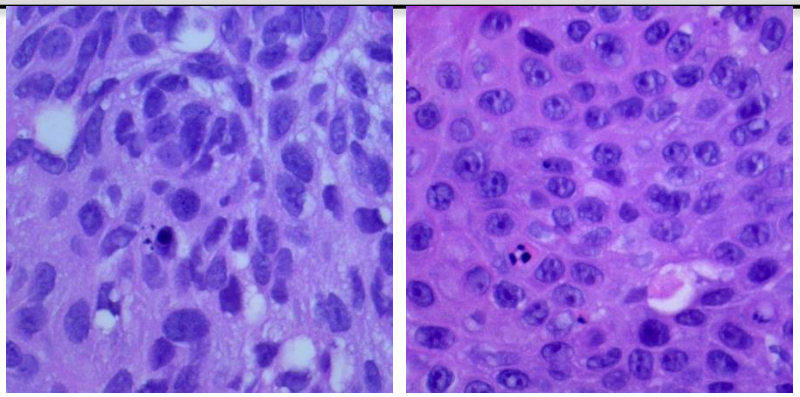
Dataset Composition:

Image Data: It comprises a considerable number of histopathological images, each labeled to indicate one of the three classes:

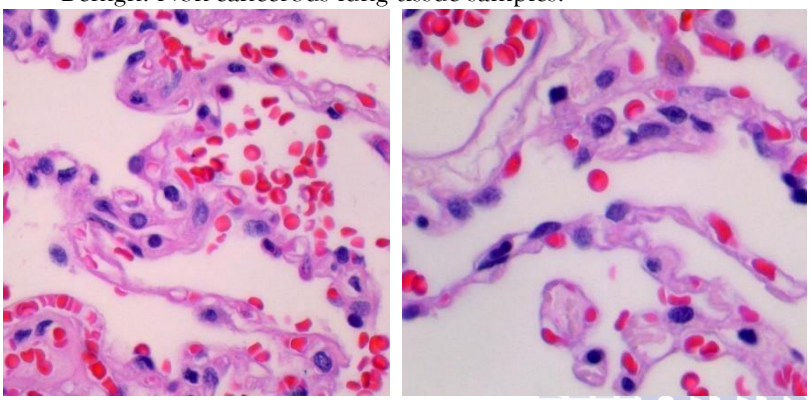
- Adenocarcinoma: A type of immense cell lung cancer originating in glandular cells



- Squamous Cell Carcinoma: Another form of immense cell lung cancer arising from squamous cells.



- Benign: Non-cancerous lung tissue samples.



Data Splitting:
The dataset is typically divided into the training and test sets in a 90:10 ratio to evaluate model performance while preventing data leakage. Stratified sampling is employed to maintain class balance.

Data Augmentation
Data augmentation is critical in medical image classification owing to the limited availability of labeled data and to avoid over-fitting in Real-time evaluation. Therefore, we employ the following technique on the training data
Key augmentation techniques include:

- Rescale = 1/255.0
- Rotation Range = 120
- Width Shift Range = 0.12
- Height shift Range = 0.12
- Shear Range = 0.12
- Zoom Range = 0.12
- Horizontal Flip = True
- Vertical Flip = Ture
- Brightness Range = [0.5, 2.5]
- Fill Mode = Nearest
- Image resize = 256^2

In contrast, we implement only rescaling the test data to make a difference between training and test sets. Thus, our evaluation should be very close to real-time. In transfer learning in this study, we utilized the ConvNeXtTiny model [25, 26]. The reason for this model is to avoid bigger computation costs.

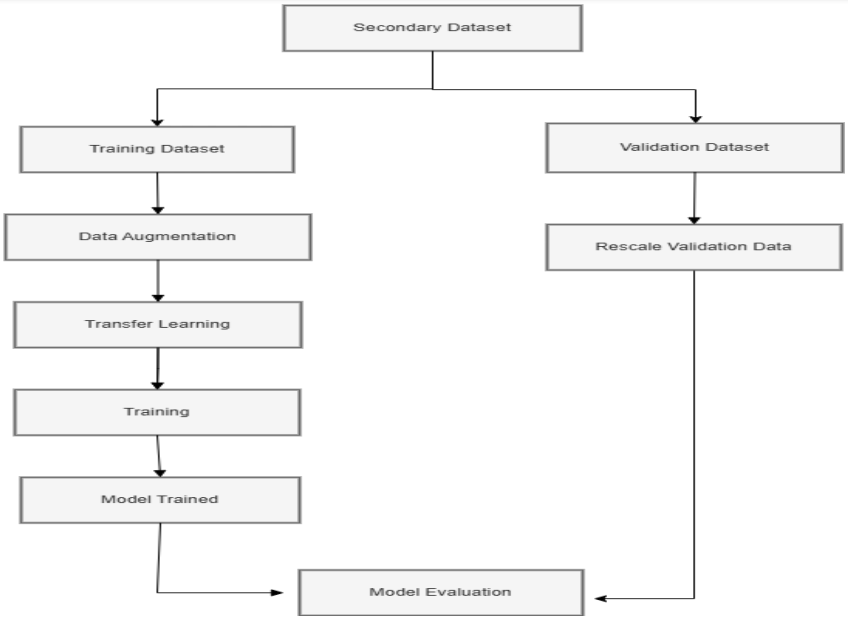


Figure 2: The Flowchart shows how the methodology of this study work

To adapt the ConvNeXtTiny model for the classification of lung cancer. The convolutional base of ConvNeXtTiny was retained, excluding the classification head (include_top=False). This allowed the model to utilize the rich feature representations learned from ImageNet. Global Average Pooling: The base model's output was passed through a GlobalAveragePooling2D layer to reduce spatial dimensions and retain essential feature maps. A flattening layer was applied to transform the pooled feature maps into a 1-D feature vector. A Dense layer with 1234 units and an ELU activation function to introduce non-linearity and enable the model to capture complex patterns. A Dense layer with 1024 units and an ELU activation function to further refine learned features. A final Dense layer with 3 units and a softmax activation function to produce probabilistic outputs corresponding to the three lung cancer classes (adenocarcinoma, benign, and squamous cell carcinoma). We use ELU instead of ReLU because it helps prevent neurons from dying, unlike ReLU, which can deactivate neurons. For training, we employed the ADAM optimizer [28] and a learning rate of 0.0001, We utilized the callback to capture the best model with good accuracy and avoid wasting computation units.

For evaluation purposes, we exploit the following evaluation metrics.

Accuracy:

The ratio of correct-predicted lung cancer images to the total number of lung cancer images

$$Accuracy = \frac{True\ predicted\ images}{Total\ number\ of\ images}$$

Precision:

Precision measure depicts how many of the lung cancer images foreseen as positive are positive.

$$Precision = \frac{TP}{TP + FP}$$

Recall:

Recall determining the proportion of actually positive lung cancer images is correctly identified by the model.

$$Recall = \frac{TP}{TP + FN}$$

F1-Score

The F1 score is the harmonic mean of the precision and recall, balancing both of the matrices into a single value.

$$F1\ score = \frac{2 \times Precision \times Recall}{Precision + Recall}$$

4. Discussion and results

Although accuracy is used frequently in the evaluation of the performance of a model, for better and more extensive evaluations of a model, we also

used precision, recall, F1-score, and loss function categorical cross-entropy. These metrics are invaluable in the management of clinical decisions as they reflect the capability of the model to precisely classify the number of positive cases and exclude as many negative cases as possible, which can be useful in medical imaging. We exploit these evaluation metrics on training and testing datasets. In this study, we achieved stunning numbers of metrics.

TABLE 2. Results of the model.

Evaluation Matric	Training data Evaluation	Testing Data evaluation
Accuracy	*0.9847*	*0.9831*
Categorical Cross-Entropy Loss	*0.0375*	*0.0572*
Precision	*0.9847*	*0.9831*
Recall	*0.9847*	*0.9831*
F1 score	*0.9847*	*0.9843*

5. Conclusion

This study has demonstrated the effectiveness of the ConvNeXtTiny model that classifies lung cancer histopathological images. The model's efficient computational requirements, combined with its strong classification performance, fill an important gap in the use of deep learning within resource-limited healthcare settings. By achieving a high F1-score, accuracy, precision, and recall, the ConvNeXtTiny model not only aids in the accurate differentiation of adenocarcinoma, benign lesions, and squamous cell carcinoma but also improves the viability of implementing AI-driven diagnostic tools in clinical environments where computational resources may be scarce. This study contributes to the ongoing advancement of medical image analysis, offering a pathway for more accessible and effective lung cancer diagnosis.

REFERENCES

[1] "Global cancer burden growing, amidst mounting need for services." Accessed: Mar. 16, 2025. [Online]. Available: https://www.who.int/news/item/01-02-2024-global-cancer-burden-growing--amidst-mounting-need-for-services

[2] X. Zhang *et al.*, "Deep Learning With Radiomics for Disease Diagnosis and Treatment: Challenges and Potential," *Front. Oncol.*, vol. 12, p. 773840, Feb. 2022, doi: 10.3389/fonc.2022.773840.

[3] M. Q. Shatnawi, Q. Abuein, and R. Al-Quraan, "Deep learning-based approach to diagnose lung cancer using CT-scan images," *Intell.-Based Med.*, vol. 11, p. 100188, 2025, doi: 10.1016/j.ibmed.2024.100188.

[4] CCCN, "Comprehensive Cancer Encouraged by Lung Cancer Survival Rate Increasing by 21%," Comprehensive Cancer Centers. Accessed: Apr. 02, 2025. [Online]. Available: https://cccnevada.com/comprehensive-cancer-encouraged-by-lung-cancer-survival-rate-increasing-by-21/

[5] Y. Han *et al.*., "Histologic subtype classification of non-small cell lung cancer using PET/CT images," *Eur. J. Nucl. Med. Mol. Imaging*, vol. 48, no. 2, pp. 350–360, Feb. 2021, doi: 10.1007/s00259-020-04771-5.

[6] N. F. Noaman, B. M. Kanber, A. A. Smadi, L. Jiao, and M. K. Alsmadi, "Advancing Oncology Diagnostics: AI-Enabled Early Detection of Lung Cancer Through Hybrid

Histological Image Analysis," *IEEE Access*, vol. 12, pp. 64396–64415, 2024, doi: 10.1109/ACCESS.2024.3397040.

[7] Y. Zhang *et al.*, "Histopathology images-based deep learning prediction of prognosis and therapeutic response in small cell lung cancer," *Npj Digit. Med.*, vol. 7, no. 1, p. 15, Jan. 2024, doi: 10.1038/s41746-024-010030.

[8] R. Javed, T. Abbas, A. H. Khan, A. Daud, A. Bukhari, and R. Alharbey, "Deep learning for lungs cancer detection: a review," *Artif. Intell. Rev.*, vol. 57, no. 8, p. 197, Jul. 2024, doi: 10.1007/s10462-024-10807-1.

[9] S. L. Tan, G. Selvachandran, R. Paramesran, and W. Ding, "Lung Cancer Detection Systems Applied to Medical Images: A State-of-the-Art Survey," *Arch. Comput. Methods Eng.*, vol. 32, no. 1, pp. 343–380, Jan. 2025, doi: 10.1007/s11831-024-10141-3.

[10] H. Huang, Y. Song, J. Yang, G. Gui, and F. Adachi, "Deep-Learning-Based Millimeter-Wave Massive MIMO for Hybrid Precoding," *IEEE Trans. Veh. Technol.*, vol. 68, no. 3, pp. 3027–3032, Mar. 2019, doi: 10.1109/TVT.2019.2893928.

[11] P. Hao *et al.*, "Advancing EGFR mutation subtypes prediction in NSCLC by combining 3D pretrained ConvNeXt, radiomics, and clinical features," *Front. Oncol.*, vol. 14, p. 1464555, Nov. 2024, doi: 10.3389/fonc.2024.1464555.

[12] G. da Silva, A. Silva, A. de Paiva, and M. Gattass, "Classification of malignancy of lung nodules in CT images using Convolutional Neural Network," in *Simpósio Brasileiro de Computação Aplicada à Saúde (SBCAS)*, SBC, Jul. 2016, pp. 2481–2489. doi: 10.5753/sbcas.2016.9894.

[13] P. Monkam, S. Qi, M. Xu, F. Han, X. Zhao, and W. Qian, "CNN models discriminating between pulmonary micro-nodules and non-nodules from CT images," *Biomed. Eng. OnLine*, vol. 17, no. 1, p. 96, Jul. 2018, doi: 10.1186/s12938-018-0529-x.

[14] "Using Deep Learning for Classification of Lung Nodules on Computed Tomography Images - Song - 2017 - Journal of Healthcare Engineering - Wiley Online Library." Accessed: Mar. 02, 2025. [Online]. Available: https://onlinelibrary.wiley.com/doi/full/10.1155/2017/8314740

[15] P. Sahu, D. Yu, M. Dasari, F. Hou, and H. Qin, "A Lightweight Multi-Section CNN for Lung Nodule Classification and Malignancy Estimation," *IEEE J. Biomed. Health Inform.*, vol. 23, no. 3, pp. 960–968, May 2019, doi: 10.1109/JBHI.2018.2879834.

[16] A. Bhandary *et al.*, "Deep-learning framework to detect lung abnormality – A study with chest X-Ray and lung CT scan images," *Pattern Recognit. Lett.*, vol. 129, pp. 271–278, Jan. 2020, doi: 10.1016/j.patrec.2019.11.013.

[17] G. L. F. da Silva, T. L. A. Valente, A. C. Silva, A. C. de Paiva, and M. Gattass, "Convolutional neural network-based PSO for lung nodule false positive reduction on CT images," *Comput. Methods Programs Biomed.*, vol. 162, pp. 109–118, Aug. 2018, doi: 10.1016/j.cmpb.2018.05.006.

[18] Y. Ren *et al.*, "A manifold learning regularization approach to enhance 3D CT image-based lung nodule classification," *Int. J. Comput. Assist. Radiol. Surg.*, vol. 15, no. 2, pp. 287–295, Feb. 2020, doi: 10.1007/s11548-019-02097-8.

[19] X. Zhao, L. Liu, S. Qi, Y. Teng, J. Li, and W. Qian, "Agile convolutional neural network for pulmonary nodule classification using CT images," *Int. J. Comput. Assist. Radiol. Surg.*, vol. 13, no. 4, pp. 585–595, Apr. 2018, doi: 10.1007/s11548-017-1696-0.

[20] A. Masood *et al.*, "Computer-Assisted Decision Support System in Pulmonary Cancer detection and stage classification on CT images," *J. Biomed. Inform.*, vol. 79, pp. 117–128, Mar. 2018, doi: 10.1016/j.jbi.2018.01.005.

[21] "Computer-aided diagnosis of lung nodule classification between benign nodule, primary lung cancer, and metastatic lung cancer at different image size using deep convolutional neural network with transfer

learning | PLOS One." Accessed: Mar. 02, 2025. [Online]. Available: https://journals.plos.org/plosone/article?id=10.1371/journal.pone.0200721

[22] W. Alakwaa, M. Nassef, and A. Badr, "Lung Cancer Detection and Classification with 3D Convolutional Neural Network (3D-CNN)," *Int. J. Adv. Comput. Sci. Appl.*, vol. 8, no. 8, 2017, doi: 10.14569/IJACSA.2017.080853.

[23] P. Naresh and D. R. Shettar, "Early Detection of Lung Cancer Using Neural Network Techniques," vol. 4, no. 8, 2014.

[24] "Molecular Insights and Therapeutic Implications of Nanoengineered Dietary Polyphenols for Targeting Lung Cancer: Part II: Nanomedicine: Vol 17, No 23." Accessed: Mar. 03, 2025. [Online]. Available: https://www.tandfonline.com/doi/abs/10.2217/nnm-2022-0117

[25] Q. Wu and W. Zhao, "Small-Cell Lung Cancer Detection Using a Supervised Machine Learning Algorithm," in *2017 International Symposium on Computer Science and Intelligent Controls (ISCSIC)*, Oct. 2017, pp. 88–91. doi: 10.1109/ISCSIC.2017.22.

[26] D. Jayaraj and S. Sathiamoorthy, "Random Forest-based Classification Model for Lung Cancer Prediction on Computer Tomography Images," in *2019 International Conference on Smart Systems and Inventive Technology (ICSSIT)*, Nov. 2019, pp. 100–104. doi: 10.1109/ICSSIT46314.2019.8987772.

[27] "Lung Cancer (Histopathological Images) | Kaggle." Accessed: Mar. 02, 2025. [Online]. Available: https://www.kaggle.com/datasets/rm1000/lung-cancer-histopathological-images/data

[28] I. Sinha Roy, K. Acharjya, and A. K. Singh, "Comparative analysis of Deep CNN Models for Pancreatic Cancer with Adam Optimizer," in *2024 Second International Conference Computational and Characterization Techniques in Engineering & Sciences (IC3TES)*, Nov. 2024, pp. 1–6. doi: 0.1109/IC3TES62412.2024.10877609.