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THE ROLE OF ARTIFICIAL INTELLIGENCE IN THE EARLY DETECTION AND ANALYSIS OF LUNG CANCER IN PATIENTS

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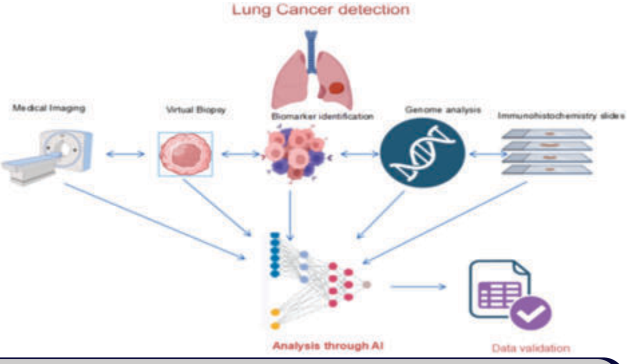
ABSTRACT Early detection of lung cancer can now be made possible with artificial intelligence through pulmonary nodule detection via analysis of CT scans and radiologist workflows. On the basis of the data combined from clinical processing and imaging, we can predict patient risk and differentiate benign and malignant nodules on the basis of the genomic profile and clinical history, leading to the development of personalized treatment plans. Current and ongoing research can integrate current biomarkers in cancer screening and preliminary results of bio-MILD on the basis of blood microRNA profiles followed by CT scanning and can help in choosing the correct screening interval. MicroRNA profiles can help distinguish symptomatic lung cancer patients from control patients, and blood-based biomarkers can help in nodule malignancy screening and characterization.



KEYWORDS : Lung cancer; MicroRNA profiles; Bio-MILD; Nodule malignancy; CT scanning

INTRODUCTION:

Scientists have recently used artificial intelligence and machine learning algorithms for predictive screening and precision oncology to improve accuracy and efficiency for the safe detection and treatment of cancer. All India Institute of Medical Sciences (AIIMS) in Delhi recently launched an AI system trained with 500,000 radiological and histopathological images from 1,500 cases of breast and ovarian cancer, the most prevalent form of cancer in India. Fullwood's team programmed a chromatin interaction neural network (ChINN), which is a convolutional neural network developed by training with DNA sequences to study chromatin interactions. This AI network may aid in targeted drug treatment by integrating genomic and epigenomic data [1].

New AI tools are available for studies such as cancer pathology and histology analysis, imaging results, and circulating tumor nucleic acid analysis, advancing early cancer detection and precision medicine. Machine learning in multiomics and combined data from genomes, transcriptomes, proteomes, epigenomes, and metabolomes can predict early detection, personalized treatment and targeted medicine[1]. Diagnosis through AI utilizes a range of imaging diagnostic methods, such as computed tomography, magnetic resonance imaging, positron emission tomography, ultrasound, and digital pathology, which play major roles in the early detection of cancers through deep learning networks[2].

Electronic health records, clinical notes, procedure reports, diagnostic notes and any unstructured data in human language can be converted into machine interpretation data via natural language programming (NLP)[3], an integral part of AI programming and machine learning[4]. Lung cancer prediction via AI allows early screening and detection, personalized treatment, targeted medicine and biomarker identification and treatment with precision.

AI Application In The Early Detection Of Lung Cancer:

The findings of the National Lung Screening Trial on lung cancer demonstrated that early detection of cancer can reduce mortality by approximately 20%, and updated screening methods for early diagnosis are necessary because high accuracy and extensive education can affect the prognosis and personalized treatment of patients affected with lung cancer. With the help of AI models, we can screen for lung cancer in an effective manner and include the benefits of minimized radiation exposure, accuracy in nodule characterization and segmentation, personalized screening schedules and LDCT interpretation where the availability of skilled radiologists is limited. Convolutional neural networks (CNNs) are a class of deep learning neural networks that can help in the early detection and screening of lung cancer by analyzing visual imagery collected from electronic medical records (EMRs) [5,6].

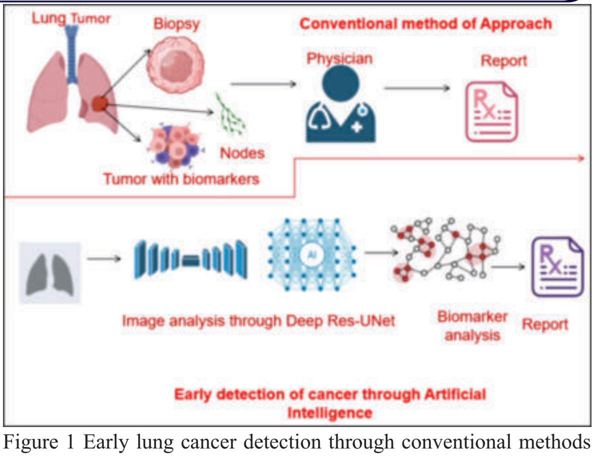


Figure 1 Early lung cancer detection through conventional methods and artificial intelligence. (Illustration developed using images from the Bio render app.)

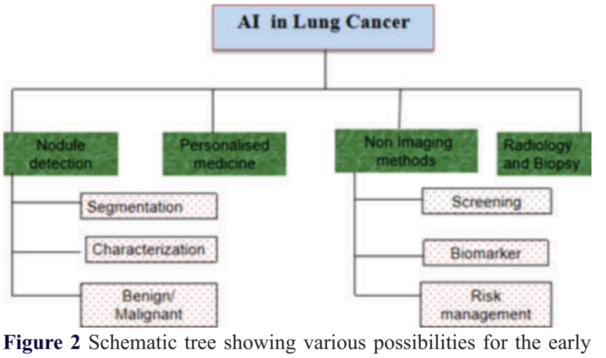


Figure 2 Schematic tree showing various possibilities for the early detection of cancer

Early Pulmonary Nodule Detection Of Lung Cancer Via AI:

Figure 1 AI algorithms with deep learning models can detect and localize small pulmonary nodules automatically through CT and X-ray images to predict the primary initial onset of lung cancer. Detecting cancerous regions is the most challenging and basic task of the deep learning process in cancer pathology, and accuracy depends on the quality and quantity of data generated through the differential status of malignant cells. Figure 1 shows that the model combines the detection, segmentation and subtyping of histological samples, but histological subtyping of cancer tissues is not possible unless specific methodologies such as immuno histochemical typing are used. The AI model can help reduce errors and predict data with precision and has a greater detection rate of single-cell metastasis or micro-metastasis. As shown in Figure 2, we can interpret and diagnose lung cancer early through both imaging and non imaging techniques.

It is difficult to obtain precise nodule segmentation in lung cancer because parameters such as small size and position, especially those located near the edge of the lungs or blood/lymph vessels, are needed. Segmentation systems vary according to architecture, techniques of image preprocessing and training strategies. Two different approaches can be possible, such as multi-view or general neural network architectures, and multi-view methods consider data collected from multiple lung nodules to combine them and use them as input signals. Figure 3 shows that few of the models similar to the general neural network work via traditional CNNs through the addition/modification of certain components. Lung nodule shape and size influence the choice of segmentation, and several studies are based on conventional methodology. In addition, the traditional CNN architecture is one of the advancements in AI for better nodule segmentation results [7,8]. Two commonly used basic structures are the U-Net (Figure 4) and fully convolutional neural network (FCN) architectures.

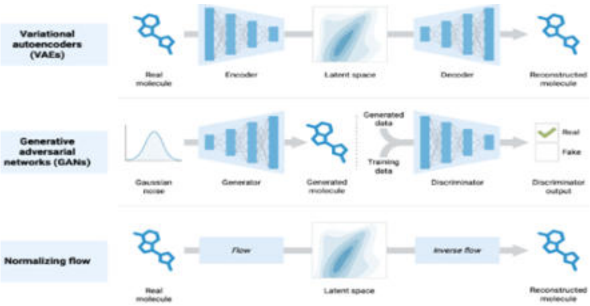


Figure 3: Generative models for molecular discovery

Figure of reference Bilodeau, C., Jin, W., Jaakkola, T., Barzilay, R., & Jensen, K. F. (2022). Generative models for molecular discovery: Recent advances and challenges. Wiley Interdisciplinary Reviews: Computational Molecular Science, 12(5), e1608. https://doi.org/10.1002/wcms.1608

Usman et al. proposed a dynamic modified ROI (region of interest) algorithm that works with Deep Res-U Net as per figure: 4 architectures for better segmentation, localization and calculation of the volume of lung nodules. It is a two-step approach with first-stage training and predicting the axial axis with respect to Deep Res-U Net through focusing on new ROIs, and the second approach is based on training the network according to Deep Res-U Net [9,10]. The main limitations of the study include difficulty in nodule characterization from non-nodular areas due to difficulty in predicting margins and the small diameter associated with them.

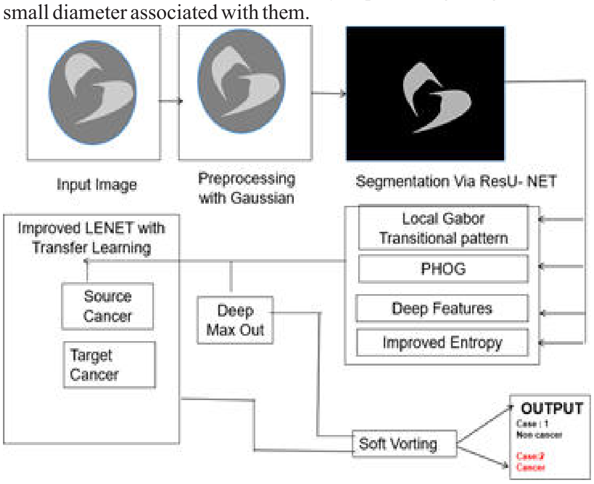


Figure:4 Transfer learning-based deep architecture using CT images

Reference figure from R, N., C. M, V. Transfer learning based deep architecture for lung cancer classification using CT image with pattern and entropy-based feature set. *Sci Rep* **15**, 28283 (2025). https://doi.org/10.1038/s41598-025-13755-0 (Remodeled and modified).

Risk Stratification:

AI can be used for risk stratification on the basis of medical processing (Figure 4) and can aid in nodule detection and characterization, as discussed in the previous section. Furthermore, it helps in the prediction of malignancy through radiological images and can help in personalized treatment by screening plans and the inclusion/exclusion of patients for further treatment. The patient outcome can also be improved by integrating medical data and deep learning image analysis to study the overall survival rate of patients.

Pulmonary nodules diagnosed via CT scan imaging can be used for risk stratification to differentiate malignant lesions from benign lesions through medical images and radiomic data and can be used for routine clinical risk assessment [11].

Screening Of Lung Cancer Through AI:

AI analyses low-dose CT scan images and can predict the future risk of developing lung cancer through the identification of patterns that cannot be detected or differentiated by the human eye. Personalized screening is possible with data from preclinical risk analyses through AI and can avoid unwanted multiple scans in patients with future risk. In addition to imaging, AI can predict future risk through the integration of clinical data and demographic data obtained from patients, such as patient age, smoking history and blood biomarkers.

Image analysis through computer-aided detection is possible through automatic nodule detection and characterization with reduced dosage and improvement in image quality. Automatic nodule detection and characterization are possible with AI-powered CAD systems by radiologists to reduce observational errors during diagnosis. AI-powered characterization of nodules will help in distinguishing the malignancy from benign lesions through quantitative data generated by analyzing the size, volume, shape and density of the tumor via virtual biopsy.

Enhanced diagnostic applications using radiomics can help in screening for lung cancer before biopsy and can also help in the prediction of genetic mutations in tumors. Through AI, it is possible to perform comorbidity analysis by training simultaneously to detect other physiological conditions, such as cardiovascular disease and emphysema, and early treatment before cancer screening. Reporter generation with AI helps radiologists reduce backlogs with accurate diagnoses in patients with abnormal observations.

Early Detection Of Lung Cancer Through Biomarker Screening:

Using the genome data of lung cancer patients, it is possible to design personalized medicines on the basis of biomarkers that are uniquely expressed in lung cancer tissue. Biomarkers can include proteins, enzymes, transporters, signaling proteins, proteins associated with EMT, or anti-apoptotic proteins with abnormal expression. Figure 5 Genomic profiling of lung cancer patients can help in pharmacogenomic studies and the design of anti-toxoid antibody drugs that can act on cancer cells with specific receptors or targeting proteins that act at immune checkpoints or signaling pathways, leading to improved survival and prognosis. AI analysis of immunohistochemistry slides can detect peculiar biomarkers expressed in lung tissue, and the integration of genome profiling with pharmacogenomic personalized medicine can yield positive therapeutic outcomes.

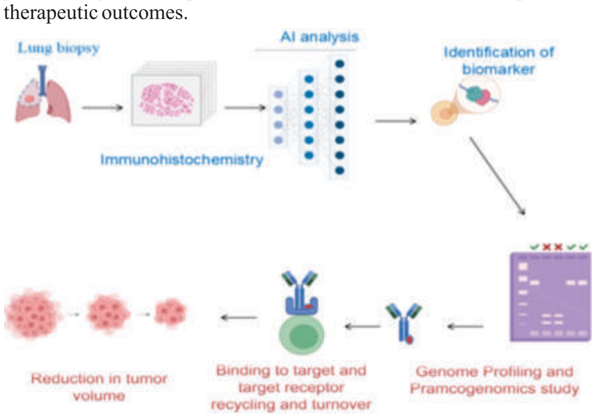


Figure 5 Overall process of personalized treatment through biomarker identification via AI. (Illustration developed using images from the Bio render app.)

DISCUSSION AND CONCLUSION:

Despite the advancements and advantages of AI in detecting lung cancer, it faces several challenges and limitations. Owing to high sensitivity, false positives may sometimes lead to unnecessary follow-up. Variability and bias in AI-based cancer detection due to the inability of individuals to handle them, image quality and equipment used may lead to inconsistent data and inadequate data. AI still faces difficulty in reading certain nodules of highly complex anatomization with tissues such as the heart and diaphragm. Owing to the challenges and limitations faced, highly robust validation in terms of algorithms that can benefit and address real-world challenges is still needed. The future of AI in lung cancer screening includes the development of versatile algorithms and validation using various populations and the integration of multi-module data, including pharmacogenomic data and biopsy data, ultimately resulting in truly personalized treatment and precise screening programs.

Declarations:

Ethics statement for the use of human and animal subjects: Not Applicable

Consent For Publication:

As an author, I strongly agree and accept the publication of the paper in the Journal Advanced Biotechnology.

Competing Interest:

As an author, I do not have any competing interests.

Author Contributions:

As an author of the paper, I wrote the paper, reviewed the literature, included our own perspectives and submitted it to the journal.

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