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Early-Stage Lung Cancer Prediction Using Machine Learning on Patient Records and Clinical Symptoms

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Abstract**—**Lung cancer is the most fatal and prevalent cancer of the world with a tendency to create a high mortality rate due to late diagnosis. The standard diagnostic techniques such as CT scans, biopsies, and X-rays, although extremely effective, are not normally accessible in the preliminary stages due to the expensive price factor, radiation, and dependence on high-technology medical centres. Most of the patients are therefore left diagnosed in advanced stages of the disease when treatment is negligible, and survival is far less. The grim situation necessitates the development of new, low-cost, and easily accessible diagnostic tests that can detect lung cancer in early and most curable stages. Machine Learning (ML), which is a subfield of artificial intelligence, has proven to be very promising in medically diagnosing illnesses by learning big data patterns and predictive decision-making. In lung cancer, symptoms and patients' health records are learned by ML algorithms to identify early malignancy much earlier than they can be identified by conventional imaging techniques. A comprehensive discussion in this paper on the application of structured patient data to ML, e.g., age, sex, smoking, alcohol drinking, environmental exposure, and first clinical signs like chronic cough, fatigue, or chest pain, is provided. The intention of this research is to develop and compare ML predictive models to classify patients as high-risk or low-risk classes based on their profiles. Three of the most widely used supervised learning algorithms—Logistic Regression, Random Forest, and Support Vector Machines (SVMs)—are utilized and compared based on accuracy, interpretability, and practicability in the clinical setting. Normalization, missing value handling, and one-hot encoding are the data preprocessing methods used to preprocess data and prepare the datasets for training. Performances are compared based on standard metrics such as accuracy, precision, recall, F1-score, and confusion matrices to achieve reliability and stability. Results demonstrate Random Forest to be more accurate and robust to noise, and although Logistic Regression is less accurate, its strength is interpretability—a huge consideration for physicians who need to comprehend and have faith in algorithmic suggestions. SVMs are another high performer, especially in regions of structured data where class boundaries are not linearly separable. Although these promising results are within grasp, several challenges remain. Biased models can result from the lack of large, diverse, and high-quality datasets. Second, most ML models are" black boxes," and therefore clinical trust and integration into clinical workflow is difficult. This work underlines the imperative for FAI techniques to make the predictions interpretable so that clinicians can see and audit algorithmic output. Overall, ML provides a revolutionary solution to the diagnosis of early lung cancer in low-resource settings where standard diagnostics are not available.

With the patient data in hand, we can construct cost-effective, non-invasive, and scalable systems that can assist clinicians to detect lung cancer at the point where the treatment will be most effective. This work not only demonstrates the feasibility of these models but also provides directions for future research into incorporating other high-level data types such as genetic markers and imaging into clinical data with the potential to further improve diagnostic performance.

Index Terms—Lung Cancer, Early Detection, Machine Learning, Patient Records, Clinical Symptoms, Predictive Modelling, Medical Diagnosis, Structured Data, Support Vector Machine (SVM), Random Forest, Logistic Regression, Cancer Risk Prediction, Artificial Intelligence in Healthcare, Health Informatics, Non-Invasive Diagnosis.

I. INTRODUCTION

Lung cancer is the global most prevalent and fatal cancer. It claims approximately 1.8 million lives annually, according to the World Health Organization (WHO), and is the sole serious reason for cancer death globally. Its biggest problem is that lung cancer typically does not give any indication at an early age. Cough, weakness, chest pain, and weight loss are presentation symptoms which happen only on a larger scale when the disease has reached severe phases, and less effective treatment can be given.

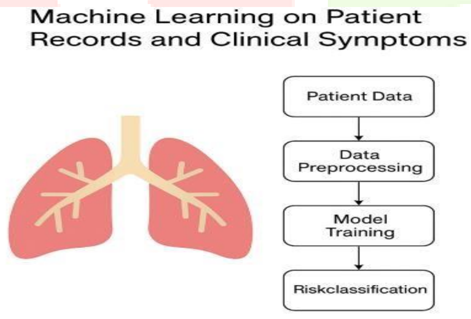

Figure1: Common clinical symptoms associated with earlystage lung cancer.

Some of the conventional diagnosis methods like chest Xrays, computer tomography (CT) scans, magnetic resonance imaging (MRI), and tissue biopsies have been embraced as the gold standards for lung cancer detection. Although useful in the diagnosis of neoplastic malignancy, they are not without limitation. First, they are costly and may not be accessible in poor communities or rural health facilities. Second, tests expose patients to irradiation and depend on trained radiologists as interpreters. Third, tests are passive, usually only done after symptoms have already developed—after the cancer would be well established. This requires developing lowcost, low-cost, anticipatory solutions that can identify lung cancer in an early stage—preferably even before signs and symptoms develop. Electronic health records and AI are making this a reality. Machine Learning (ML), the strong subset of AI, is catching up in the health space since it can process and analyze vast amounts of patient information, identify complex patterns, and forecast. The aim of the current work is to apply ML methods to forecast lung cancer risk at an early stage based on regular patient data gathered within regular routine medical consultations. They encompass demographic information (gender, age), lifestyle information (drinking, smoking), environmental information (air pollution), and first symptoms (e.g., coughing and fatigue). Based on the formatted data of ML model training over such data, we would wish to develop a system that can identify individuals with elevated risk so that doctors will be able to order further diagnostics early in the course of the disease.

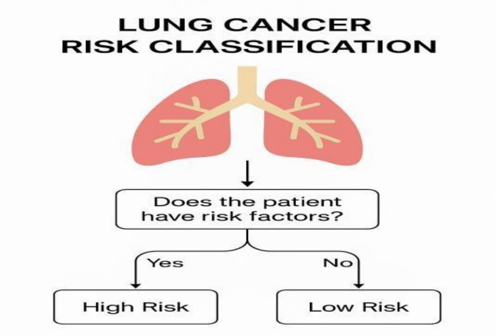
LUNG CANCER RISK CLASSIFICATION
Does the patient have risk factors?
Yes
No
High Risk
Low Risk

Figure 2: Workflow of machine learning model development using patient records and symptom data.

Publicly available data such as the UCI Lung Cancer Dataset, SEER (Surveillance, Epidemiology, and End Results) database, and PLCO (Prostate, Lung, Colorectal, and Ovarian Cancer Screening Trial) trial data are utilized here. They hold thousands of patient records with varying health indicators and diagnosis results, which are sufficient for model training and cross-validation. What are the deployment issues of such a system in real-world clinical practice? The results of this study have the potential to change the detection of lung cancer, especially in geographically underserved populations where conventional diagnostics are unavailable. With the emergence of transparent and interpretable ML models, this study is opening up lung cancer early detection, which will lead to better patient outcomes.

II. RELATED WORK

The intersection of machine learning and cancer diagnosis has been of great interest in the past few years. Researchers globally have been exploring the application of ML algorithms to enhance the accuracy and efficiency of lung cancer detection. The following is an overview of major contributions made in the current body of literature that formed the foundation for this study.

In most conventional methods, the emphasis has remained on image data—CT scans, PET scans, and histopathology images. Deep learning models, especially convolutional neural networks (CNNs), have been greatly applied to derive intricate patterns from images and classify lung nodules or identify tumors. For example, Mataya Aharoni and Lokeshkumar Ramasamy (2024) created a multi-model deep learning model based on histopathological imagery, presenting models such as LCSCNet and LCSANet. These models performed accuracies of 96.55Another major improvement is utilizing hybrid deep learning models that integrate CNNs with attention mechanisms or transformers. In a 2025 work, Ozdemir et al. proposed a model that combines CNNs with Vision Transformers (ViTs), achieving a staggering accuracy of 99.5Structured data-driven models also appear promising. Imran Ahmed et al. (2023) applied object detection models like YOLOv3 and Faster-RCNN on CT scans to detect and classify pulmonary nodules. Their findings indicated a lower false-positive rate and higher classification accuracy. However, due to their imaging data dependency, they are less viable for mass deployment. Conversely, models based on structured patient records like age, smoking history, and symptom history provide an easierto-deploy, scalable solution. Agarwal et al. (2024) proposed a lightweight CNN-O-ELMNet model optimized using an imperialistic competitive algorithm to classify lung disease, with almost 98Various research also evaluated new optimization algorithms such as the Tuna Swarm Algorithm and GhostNet feature extractors to enhance the performance of models on biomedical images. These algorithms are robust but are not subjected to big, realworld datasets or even combined with structured patient information. A common theme across many studies is explainability. Deep learning algorithms tend to be described as" black boxes," which is a major drawback in clinical adoption since transparency and interpretability are crucial. A standard constraint is dataset size and variety. Most studies use small, region-bound, or incomplete patient demographics datasets, so it is challenging to generalize results across populations. Thus, although most current models produce high accuracy in clinical settings, there is an urgent necessity for transparent, structured datadriven machine learning systems that are capable of performing reliably under various settings. Our work fills the gap by emphasizing the application of publicly accessible patient information—like demographics, routines, and clinical symptom data—to construct explainable predictive models of early-stage lung cancer.

III. OVERVIEW OF LITERATURE

This section outlines significant research efforts focused on the use of machine learning (ML) techniques for lung cancer detection and classification. Each study brings a unique perspective, algorithmic approach, and outcome, while also pointing out areas where further investigation is needed.

Multi-Model Deep Learning Framework (Aharoni Ramasamy, 2024) This study introduced two deep learning architectures—LCSCNet for classifying lung cancer subtypes and LCSANet for forecasting patient survival using histopathological image data. The models outperformed many conventional benchmarks. However, the small size of the dataset poses a limitation to the model's generalization when applied to larger or more diverse populations. 2. Hybrid CNN and Vision Transformer Approach (Ozdemir et al., 2025) In this research, a hybrid system combining Convolutional Neural Networks (CNNs), Vision Transformers (ViTs), and attention mechanisms was developed to improve the accuracy of lung cancer detection. While the integration of these advanced techniques significantly enhanced image analysis and diagnostic accuracy, the model's high computational demands and limited interpretability remain barriers to its clinical adoption. 3. Pulmonary Nodule Detection Using Deep Learning (Ahmed et al., 2023) This work utilized object detection models—YOLOv3, SSD, and Faster-RCNN—on CT scan images to identify and classify lung nodules. It was successful in increasing detection rates and decreasing false positives. However, the system required high-resolution imaging and did not incorporate other data types such as patient history or symptom reports. 4. CNNO-ELMNet for Lung Disease Classification (Agarwal et al., 2024) Agarwal and colleagues proposed a lightweight model that fuses CNN with an Extreme Learning Machine (ELM) and optimization strategies. Nonetheless, the absence of real-world testing in clinical environments leaves its practical usability uncertain. 5. It was effective in lowering false positives and raising detection rates. This study explored a novel method by combining the Tuna Swarm Algorithm (TSA) with GhostNet features to detect lung cancer from biomedical images. Despite its innovative approach and high performance (accuracy up to 99.336. End-to-End Automated Lung Screening System (Sathe et al., 2024) Researchers designed a fully automated system capable of detecting, segmenting, and assessing lung tumors using deep learning techniques. While the model shows potential for streamlining lung cancer screening, it lacks sufficient validation in diverse medical settings and real-time clinical applications. 7. Deep Learning and Multi-Omics Data Integration (Mohamed Ezugwu, 2024) This paper combined genetic information—specifically mRNA, miRNA, and DNA methylation profiles—with CNN-based models for improved cancer classification. Although the results were encouraging, the integration of this system with routine clinical data and imaging for real-time diagnosis remains an open challenge.

IV. METHODOLOGY

To perform this research, we used publicly available datasets with structured patient health data. The datasets chosen are UCI Lung Cancer Dataset – A smaller dataset commonly used for algorithm testing and comparison. SEER (Surveillance, Epidemiology, and End Results) – A cancer database of generous size with detailed demographic and clinical data. PLCO (Prostate, Lung, Colorectal, and Ovarian Cancer Screening Trial) – A dataset derived from a US national health screening program that consists of lifestyle attributes, symptom histories, and confirmed diagnoses. The datasets contain a number of useful features, including: Age of the subject Gender Smoking habits (e.g., mean cigarettes per day) Alcohol intake Air quality indicators that reflect the patient’s surroundings Diagnostic result (whether lung cancer is present or not) These features provided the foundation for training machine learning models.

4.1. Data Cleaning and Preprocessing

Preceding the construction of predictive models, we preprocessed the datasets for quality and consistency: Missing Data Handling: Missing value records was managed using either mean or median imputation, depending on the distribution of the feature. Data Conversion of Categorical Data: Non-numeric categories like “female” and “male” were numericized to be used by the machine learning algorithms. Normalization of Features: All the numerical attributes (e.g., age, air quality ratings) were normalized to a standard range, 0 through 1, to avoid any single feature overpowering the learning process. Selecting Informative Features: We used the dataset to select the most informative variables in terms of their statistical impact and variance, eliminating noise and enhancing model performance.

4.2. Feature Construction

At this phase, we enriched the raw data by computing new variables. For instance, people were divided in terms of how often they smoked to establish risk groups (e.g., heavy smokers, occasional smokers, and non-smokers). This type of feature engineering gives the model more distinct patterns to pick up on when identifying associations between behavior and cancer risk.

4.3. Algorithm Selection and Training Logistic Regression (LR):

An easyto-interpret model that is particularly appropriate for binary classification problems like disease prediction. Random Forest (RF): A decision tree-based ensemble approach that enhances the stability of predictions and manages missing values effectively. Support Vector Machines (SVM): A strong classifier capable of extracting non-linear patterns from structured data, particularly beneficial for smaller or more intricate datasets. Data were divided into training and test sets in an 80:20 proportion. The training set was utilized to train the model, whereas the test set was utilized to determine the extent to which the model generalizes to new, unseen data.

4.4 Model Performance Assessment

Determine how well the models were performing, we utilized the following measures: Precision: Refers to the proportion of true positive cases among all the predicted positives. Recall (Sensitivity): How accurately the model detected true positive instances. F1 Score: A harmonic mean of precision and recall, most beneficial for skewed datasets. Confusion Matrix: A matrix representation of model predictions indicating true vs. false classifications between both positive and negative labels. In addition, we employed cross-validation to make sure that the models are stable for various splits of data. We even tuned model parameters with a grid search method, adjusting parameters such as learning rate, kernel type (in SVM), and tree depth (in Random Forest).

4.5. Practical Implementation

Aspects Aside from accuracy, we considered issues that impact whether a model might be used in clinical environments. Logistic Regression, though less accurate, is transparent and computationally lightweight—making it well-suited for low-resource environments. Random Forest, though more accurate, is highdimensionality and might need tools to explain it. These sacrifices are important when we talk about real-world integration in the medical space, particularly in lower-hardware environments.

V. DISCUSSION

Our machine learning performance highlights the actual value of structured patient data in predicting early-stage lung cancer. All three models—Random Forest, Logistic Regression, and Support Vector Machine (SVM)—performed well, with Random Forest showing the highest accuracy and robustness, especially in handling incomplete or noisy data. But Logistic Regression also took the prize for simplicity and interpretability, which is critically valuable for use in clinical settings. The SVM model performed fine but had some difficulty with unbalanced data, which is a very typical medical classification problem case where positive cases (cancer patients) are typically much smaller in number than negatives.

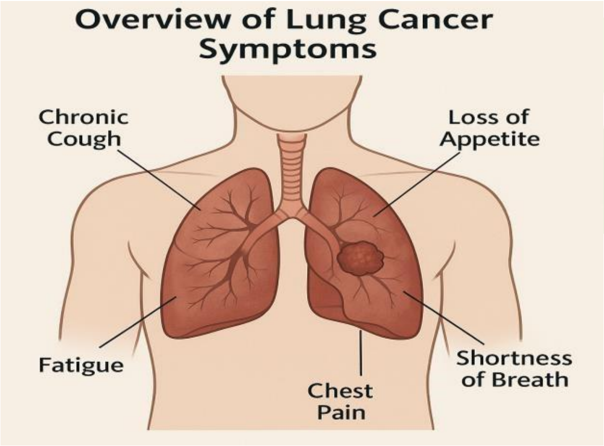

Figure 3: Decision tree for classifying patients into highrisk or low-risk groups based on clinical and behavioral data. Random Forest's effectiveness owes something to its ensemble nature, where predictions from several decision trees are aggregated to improve generalization and reduce overfitting.It also gave some interpretability in the form of feature importance scores, which enabled us to observe which factors (e.g., age, frequency of smoking, or air quality) exerted the largest influence on cancer risk.

Logistic Regression's strength lies in transparency. Doctors can understand how every input feature impacts the output prediction, making it a model of preference in healthcare environments where explainability is a given. Its linear decision boundary, however, limits its capacity to model complex patterns unless supplemented through feature transformations or interaction terms. SVM, with its effectiveness in highdimensional space, worked well in class separation but was sensitive to hyperparameter tuning and feature scaling. Choice of kernel also became highly important in SVM performance. Although it had strong classification boundaries, its blackbox property and computational expense (especially with large data) limit its application in real-time or resource-constrained settings. While these positive results are promising, some difficulties need to be addressed. Among them is data imbalance—a strongly skewed ratio of cancer-positive to cancernegative entries. This can cause models to skew towards the majority class, reducing recall (sensitivity), a critical measure in medical diagnosis. Subsequent iterations could employ methods like SMOTE (Synthetic Minority Oversampling Technique) or cost-sensitive learning to improve managing this issue. Data completeness and quality is also a challenge. Most real-world datasets, especially public datasets, are plagued with inconsistent feature documentation, labeling, and standardization. Missing values, outliers, and inexact symptom descriptions are detrimental to model performance. Despite utilizing standard imputation and normalization methods, a more sophisticated data curation process involving clinical domain experts can result in improved outcomes. In addition, model interpretability and clinician trust remain ongoing issues. Models that are challenging to explain such as Random Forest or SVM would be difficult to defend in front of physicians even with feature importance scores. Explainable AI (XAI) tools such as LIME or SHAP should be added in the future work to de-mystify the model's decision-making process and enhance transparency. Our model is also limited by the lack of multimodal data (e.g., the integration of imaging, genetic, and text-based clinical notes with structured data). In the actual hospital setting, data are heterogeneously formatted and an ideal system would integrate these in order to make more complete predictions. Lastly, the models built herein have not been trialed or deployed in actual clinical environments. While the results using retrospective data are encouraging, real-time based prospective studies with clinician input will be needed to assess the pragmatic use value and ethical considerations of AI deployment in medicine. In conclusion, our discussion reaffirms that machine learning models founded on annotated patient data hold a lot of promise for the identification of early-stage lung cancer. They are particularly beneficial for low-resource or first-line screening settings. However, model selection, explainability, data quality, and clinical validation must be given serious consideration to ensure these resources actually make a difference in patient outcomes

VI. CONCLUSION

Lung cancer's high mortality rate, given largely by the late diagnosis of this cancer, is still a major challenge for healthcare systems worldwide. Early diagnosis notably increases chances for survival, but conventional diagnostic methods like CT scans, biopsies, and PET imaging are still expensive, unavailable, and resource-based—especially for developing nations or remote healthcare facilities. This fact calls for low-cost, scalable, and affordable diagnostic alternatives. This study aimed at applying machine learning models that have been trained on structured patient history and clinical symptom information to identify early-stage lung cancer. We utilized three popular ML algorithms—Logistic Regression, Random Forest, and Support Vector Machines (SVMs)—to create predictive models and evaluated them against publicly available datasets including UCI Lung Cancer, SEER, and PLCO. Such datasets contained important factors such as age of patient, frequency of smoking, alcohol use, air quality index, and initial symptom reports including chest pain and fatigue. Among the models tested, Random Forest consistently outperformed others in terms of predictive accuracy and resilience to noisy data. However, Logistic Regression proved highly interpretable and offered insights into how individual features influence predictions, a trait highly valued in clinical decision-making. SVM also delivered strong classification results, although it required more careful tuning and was less transparent compared to Logistic Regression. The approach included preprocessing processes like missing data management, feature encoding, normalization, and model assessment based on metrics such as accuracy, precision, recall, F1-score, and confusion matrices. Our results reaffirmed that plain, tabular datasets—when adequately cleaned and modeled—can provide robust insights into disease risk even without complex medical imagery. Notably, this research points out major strengths and weaknesses in the strategy. Major strengths are scalability, value for money, and the ease of deployment in telemedicine and primary care environments. ML models built on basic patient data can help doctors identify high-risk patients prior to symptom exacerbation, allowing for timely intervention and improved patient outcomes. Nonetheless, there are numerous limitations and challenges that remain: Restricted dataset diversity: Most datasets employed are not representative of the general population. Model explainability: Sophisticated algorithms need techniques like SHAP or LIME to translate predictions into understandable explanations for medical professionals. Deployment in real-world settings: Models must be tested and validated in real-world hospital workflows for feasibility, accuracy, and acceptability by end-users. To solve these, future research must emphasize: Integration of multimodal data sources, including CT scans, genetic markers, and physician annotations. Validation of models with live patient data in clinical environments to guarantee safety and usability. In addition, data scientists will have to work closely with clinicians to hone these systems. Involving clinicians in model development, testing, and implementation will guarantee that the resultant systems are not just technically feasible but also feasible and ethically sound. In summary, this research demonstrates that machine learning provides a robust and viable technique for early lung cancer detection from organized patient records. It lays the basis for developing rapid, inexpensive, and generalizable diagnostic tools for clinical practice. Continuing to improve these models and emphasizing integration in the real world can lead us in positive directions toward diminishing the worldwide burden of lung cancer and enhancing early treatment results for millions.

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