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Integrating Predictive Analytics and Explainable AI for Lung Cancer Detection within the One Health Framework

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ABSTRACT: Lung cancer is one of the biggest causes of cancer death worldwide, mainly because it often goes undiagnosed until it is too late for effective treatment. Most patients will not have signs or symptoms of lung cancer until well into the disease, when treatment is likely less effective. Once cancer is diagnosed, the chance of survival decreases significantly, and treatment becomes more aggressive, costly, and uncertain. Even with new imaging technologies and improved ways of diagnosing lung cancer, early detection of the disease is still extremely difficult because of the many different genetic, environmental, and lifestyle factors that contribute to lung cancer. For these reasons, we are taking a holistic One Health approach to this research. The focus of this project will be to study and analyze how the interrelationships between health, environmental exposure, and lifestyle choices (e.g., smoking, air pollution, occupational exposure, socioeconomic status) contribute to the development and progression of lung cancer. This study takes into account all of these various elements and moves away from lung cancer research that views lung cancer in only a clinical context to understand it in an ecological and systems-oriented perspective. The main objective of this research is to utilize predictive analytics and machine learning (ML) techniques to analyze health data to determine the factors associated with an increased risk for developing lung cancer. ML and predictive analytics are technologies that allow us to find hidden patterns and non-linear relationships in large, complex data sets. Several different ML algorithms will be used to predict lung cancer, including classification models like Logistic Regression, Random Forest, and Gradient Boosting Machines.

KEYWORDS: Sustainable agriculture, Crop yield prediction, Machine learning (ML), Deep learning, Explainable artificial intelligence (XAI), LIME (Local Interpretable Model-Agnostic Explanations), SHAP (Shapley Additive explanations), Model interpretability, Data quality, Model generalizability.

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Introduction

Recently, advancements in the field of artificial intelligence (AI) and, more specifically, machine learning (ML), have changed how lung cancer is detected and diagnosed at an early stage. For example, Ardila and colleagues (2019) showed that a deep-learning model developed from low-dose CT scans trained on patients could outperform radiologists in detecting early-stage lung cancer, suggesting that AI-assisted screening systems could one day play an important role in clinical practice. Similarly, Coudray and colleagues (2018) used convolutional neural networks (CNNs) to accurately classify different types of lung cancer based on histopathology images, which would improve diagnostic accuracy and facilitate more personalized treatment approaches. Finally, Esteva and colleagues (2019) demonstrated that ML models built from data collected at the time of diagnosis (including medical, demographic and lifestyle) can predict future cancer risk even in people where there are no discernible symptoms of cancer. This highlights the power of predictive analytics to help prevent cancer through early identification of high-risk patients.

In addition to relying on single modalities to create prediction models, there has been increased focus on developing multi-modal approaches in predictive analytic research (i.e., using multiple sources of data as part of a model to improve predictive capabilities) to enhance sensitivity and specificity for detecting cancer early. The development of multi-modal learning frameworks enables AI systems to access complementary information from multiple dataset types to apply cross sectional evaluation methods used to reduce both false-positive and false-negative error rates when detecting early-stage (or pre-symptomatic) cancer. Furthermore, the creation of these integrated datasets will improve predictive modeling performance as well as provide a more holistic understanding of the biology of tumors. Due to recent changes in our understanding of how Artificial Intelligence (AI) can use existing datasets to create a more integrated view, we will conduct a research study on the possibility of predictive machine learning models being created to helps clinicians identify patients who may be at risk for developing lung cancer. We plan on incorporating views of clinical practices and environmental factors from many different sources related to the patient’s lifestyle choice and behaviors into AI-based predictive model process. This type of technology could lead to an improved ability to recognize patients with signs of lung cancer earlier and use that information to develop individual treatment plans while minimizing bias when developing collaterally affected areas of public health through proactive health screening methods. Ultimately, we believe the use of AI-based predictive models can ultimately be incorporated into ”Evidence-Based Public Health” (EBPH).

These newer studies are using advanced imaging techniques such as radiomics and deep learning to collect complex imaging features compared to traditional approaches that allowed for association of tumor behavior. Wang et al. (2021) also used these approaches in a recently published study to analyze patient records and environmental data to find meaningful predictors and coverage factors that could be used for predicting lung cancer in high-risk populations.

Research Aim and Research Questions

One of the most lethal diseases globally, lung cancer tends to be diagnosed at late stages because it usually has no obvious symptoms in its initial stages. Early detection and accuracy are crucial in reducing patient mortality rates and improving survival rates. Because it can often go undetected until it has progressed significantly, I find lung cancer to be one of the deadliest diseases in the world. Unfortunately, many individuals with lung cancer don’t know they have the disease until they experience chronic coughs, chest pain, shortness of breath, or unexplained weight loss that affect their daily activities [11]. Once the patient experiences these symptoms, the malignant disease has often progressed significantly, thus making treatment more difficult and the results less effective. Early detection of lung cancer is important because it greatly contributes to improved long-term survival rates and reduced mortality rates [12]. Traditional methods to diagnose lung cancer include biopsy, imaging (including CT scan and X-ray), and assessment and interpretation of the imaging studies by a highly trained radiologist. However, these types of evaluations can be time consuming, expensive, and primarily depend upon subjective interpretation by radiologists, resulting in significant inter observer variability (different radiologists evaluate the same images very differently). Clinical experience, number of im ages evaluated, and slight differences in the appearance of images can cause frequent delays or inconsistencies with regard to a specific diagnosis. Because of these limitations, there is a need for more objective, efficient, and supportive diagnostic testing that can provide the clinician with timely and accurate information about the presence or absence of lung cancer [13][14] .The introduction needs to relate to the problems or issues being recognised and eventually leading the research questions.

B. Research Gap and Contribution Predictive analysis and disease diagnosis have seen significant advancements through machine learning (ML) and explainable AI (XAI). ML models, such as logistic regression, random forests, and deep learning techniques, are widely used to predict disease outcomes, including lung cancer, breast cancer, diabetes, and heart disease, by analyzing clinical data, imaging, and patient demographics [15]. In particular, XAI methods like SHAP and LIME are being applied to enhance the transparency of complex models, helping clinicians interpret predictions and make informed decisions. These techniques are crucial in healthcare, where model interpretability is vital for trust and application in real world settings [16]. Additionally, integrating multi-modal data, such as clinical records, medical images, and genomic data, has improved the accuracy of predictive models, providing a more comprehensive approach to diagnosis and treatment planning. Longitudinal data and real-time monitoring, especially in chronic diseases, have further bolstered the field, allowing for dynamic predictions of disease progression and recurrence, thereby supporting personalized medicine and better patient outcomes. Review proposes a standardized framework to enhance transparency and mitigate bias, including preprocessing protocols and reproducibility checklists tailored to stakeholder needs. By integrating fragmented research efforts and emphasizing usability, this work advances the deployment of XAI in agricultural decision-making, enhancing trust, scalability, and impact in predictive analytics [17]. The integration of advanced machine learning techniques and real-time data collection is transforming the landscape of disease diagnosis and prediction. For instance, machine learning models that utilize medical imaging data, such as CT scans and MRIs, alongside clinical and genetic information, have shown great promise in improving diagnostic accuracy. In lung cancer, deep learning models like convolutional neural networks (CNNs) are used to detect tumors from images with high sensitivity, while genomic data is leveraged to predict susceptibility and guide personalized treatments [18]. Moreover, the combination of predictive analytics and wearable technology has enabled real-time monitoring of patients, offering continuous data streams that can alert healthcare providers to changes in a patient's condition, such as early signs of disease recurrence. By merging diverse data types and utilizing powerful ML algorithms, researchers and healthcare professionals are increasingly able to make more accurate, timely, and personalized predictions, ultimately leading to better patient care and outcomes [19].

C. Objective and Hypothesis This research is based on the concept that there exists a possibility for usability improvements of machine learning models used in Lung Cancer diagnosis through increased transparency and no degradation of predicted performance with the use of explainable artificial intelligence (XAI) [20]. Specifically, it will research how an explanation of model outcomes and contribution of each input, including the size and the location of any detected nodule, the age of the patient, and the patient's smoking history, can help with identifying lung cancer at earlier stages, with greater accuracy, and with a transparent explanation of how the diagnosis was made [21]. Machine learning models (Logistic Regression, Random Forests and Deep Learning) can accurately predict and provide clinically relevant outcomes based on the use of large amounts of clinical and imaging information, using best practices in dataset preparation and model development, as well as integrating XAI techniques such as SHAP or LIME into their models [22]. The increased transparency gained through improved machine learning models allows for more precise, reliable, and individualized decision making in the provision of care to patients [23].

1. Can machine learning models accurately predict lung cancer using clinical and imaging data?
2. How can explainable AI techniques improve transparency in healthcare predictions?
3. Which factors contribute most significantly to lung cancer risk prediction?

Research Results

The analysis of how Artificial Intelligence (AI), in terms of Machine Learning (ML) and Explainable AI (XAI), can be utilized in the diagnosis of lung cancer was achieved through the systematic review of literature and analysis through the evaluation of case studies. As early detection of lung cancer is essential, and as is the ability to clearly communicate how clinical decisions are made, my plan for research will not only examine the advancements in ML and XAI technology but also examine how these advancements are being utilized with regard to their impact in real-world healthcare settings. To provide a structured and defined methodology for the research, a four-phase framework for methodology will be utilized, which will ensure sufficient rigour, clarity, and reproducibility of the results.

The comprehensive search strategy that I have employed to identify research on this topic involved a search of reputable scientific databases, such as the IEEE Xplore, PubMed, ScienceDirect, Springer, and databases to obtain relevant research articles. These are multi- disciplinary databases that would allow me to cover as many disciplines as possible (i.e., medical, computer science (computational intelligence), and AI (applied to healthcare)). To help identify all possible articles, I employed a list of search queries using descriptive terms for my primary topics, including but not limited to, “lung cancer prediction”, ”machine learning”, ”deep learning”, ”XAI”, ”SHAP”, ”LIME”, ”CT imaging”, ”radiomics”, and ”clinical decision support”. This systematic search strategy will also allow for the identification of traditional research (i.e., foundational) as well as newly developed or emerging research (i.e., innovations) in the use of ML and XAI in the field of lung cancer.

I also established specific inclusion criteria to identify only peer-reviewed research articles published between 2018 and 2025, as these years demonstrate the rapid pace of advancement of AI technologies in the field of healthcare. The articles I select for inclusion in my research must include documentation of the use of ML or deep learning techniques.

A. Supervised Learning Formulation Prediction is based on a supervised learning model that will learn to map multi-modal input features to the desired diagnostic output. The model will be optimized by minimizing a cross-entropy loss function and its performance will be assessed by using a number of metrics, such as accuracy, precision, recall, F1-score and AUC-ROC. To improve the interpretability of the model’s predictions, SHAP values will be calculated to identify the contribution of each feature toward each prediction.

B. Models and Algorithms : Several supervised learning models and XAI methods were employed to improve the early prediction of lung cancer and ensure interpretability in clinical decisions: • Random Forest: A popular and strong ensemble learning approach that constructs several different decision trees and then aggregates them to improve diagnostic performance. It performed very well on structured clinical data, such as demographics and smoking history. • LightGBM (Light Gradient Boosting Machine): We chose it for its efficiency and speed with a large number of clinical datasets. LightGBM’s leaf-wise growth strategy allowed it to model the complex relationships between input features (e.g., nodule size, density, biomarkers)

C. • CNNs (Convolutional Neural Networks): Mainly used for the processing of CT scan images. CNNs were important to find spatial characteristics of lung nodules, including shape and texture, which are important in differentiating between benign and malignant growths. • SHAP (Shapley Additive explanations): Applied to quantify the contribution of each clinical or image-derived feature to the model’s prediction. SHAP provided both global and local interpretability, enabling clinicians to understand which patient attributes influenced the diagnostic outcome. • LIME (Local Interpretable Model-Agnostic Explanations): Used to generate locally interpretable models around individual patient cases, helping physicians interpret predictions in a human-understandable manner, particularly useful in patient specific consultations. • LIME (Local Interpretable Model-agnostic Explanations): Applied to generate simplified, interpretable models around individual predictions. This helped in explaining specific outcomes in farmer-friendly terms, enhancing trust in ML-generated recommendations. • Counterfactual Explana tions: Used to explore “what- if” scenarios, these explanations highlighted the minimal changes required in input variables (e.g., soil moisture or rainfall) to achieve a different prediction outcome, aiding in scenario-based planning for crop management. I. Framework for Data Collection and Tool Utilization : This study utilized a variety of datasets and tools to support the development and interpretability of crop yield prediction models. Data sources encompassed diverse modalities, and tools were selected to ensure robust preprocessing, modeling, and explanation of results. • Datasets: We used a combination of remote sensing and ground-based agricultural datasets, including satellite imagery (e.g., NASA MODIS), unmanned aerial vehicle (UAV) data, and soil sensor readings. These datasets provided rich spatiotemporal information about vegetation indices, soil moisture, temperature, and other critical factors influencing crop yield. • Performance Metrics: Model performance was evaluated using standard regression metrics such as the co- efficient of determination (R2), root mean square error (RMSE), and mean absolute error (MAE). These metrics allowed for quantitative assessment of prediction accuracy and model reliability. • Tools: The primary programming environment was Python. Key libraries included scikit-learn for ma- chine learning model development, SHAP and LIME for model interpretability, and pandas, NumPy, and matplotlib for data processing and visualization. Open-source datasets such as the USDA Crop Yield Data and remote sensing data from NASA MODIS were reanalyzed to validate model performance and interpretation consistency. J. Technologies Used : The following technologies were instrumental in the execution of this research: • Python: The primary programming language used for data preprocessing, model development, and interpretability analysis. Key libraries included pandas and numpy for data manipulation, scikit-learn for implementing machine learning models like Random Forest and LightGBM, and matplotlib and seaborn for visualization. • SHAP and LIME: These Python-based libraries were used to enhance model interpretability. SHAP (Shapley Additive explanations) helped quantify feature importance at both global and local levels, while LIME (Local Interpretable Model-agnostic Explanations) was applied for generating simplified explanations of individual pre- dictions. • Open-Source Datasets: Public datasets including USDA Crop Yield Data and MODIS imagery archives were reanalyzed and validated to support model training and evaluation, ensuring reproducibility and scalability across regions.

Table 1

Dynamics of introducing ICT elements into the sociocultural space of the digital society

TABLE I

S.No	Reference	Model/Approach	Methodology	Limitation	Advantages
1	[1]	3D CNN Model	Low-dose CT scan based deep learning for early lung cancer detection	Requires large annotated datasets	High accuracy in early-stage detection
2	[2]	CNN Histopathology Model	Classification of lung cancer subtypes using pathology images	Dependent on high- quality imaging data	Improves subtype prediction precision
3	[3]	ML Risk Prediction Model	Clinical and demographic data used for early cancer risk assessment	Limited population generalization	Supports preventive intervention planning
4	[4]	Radiomics + ML	Extraction of imaging biomarkers combined with ML classifiers	Risk of overfitting	Enhances diagnostic accuracy
5	[5]	Random Forest Model	Feature-based classification using CT imaging and patient data	Feature selection complexity	Robust performance with reduced variance
6	[6]	Support Vector Machine	Tumor classification using structured clinical datasets	Sensitive to parameter tuning	Effective for high-dimensional data
7	[7]	XGBoost Model	Gradient boosting for predictive lung cancer diagnosis	Computationally intensive	High predictive performance and stability
8	[8]	Multi-modal AI Framework	Integration of imaging, genomic, and EHR datasets	Data fusion and privacy challenges	Improves sensitivity and specificity

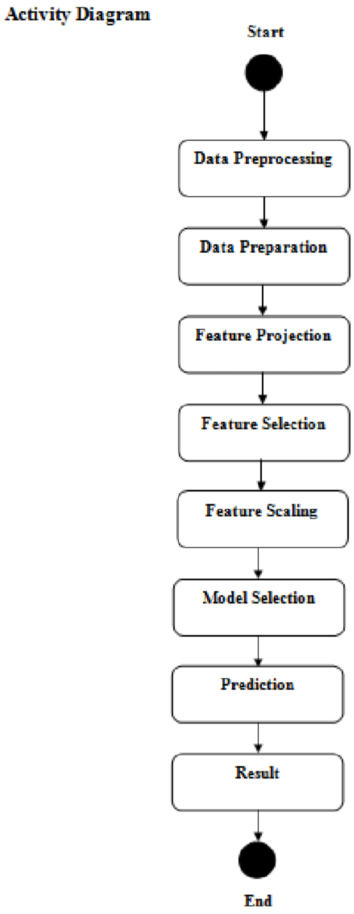
9	[9]	Explainable AI (SHAP, LIME)	Model interpretation techniques for ML- based diagnosis	Additional computational overhead	Enhances transparency and trust
10	[10]	One Health-Based Predictive Model	Combines clinical, environmental pollution, and lifestyle data	Limited standardized integrated datasets	Provides holistic lung cancer risk assessment

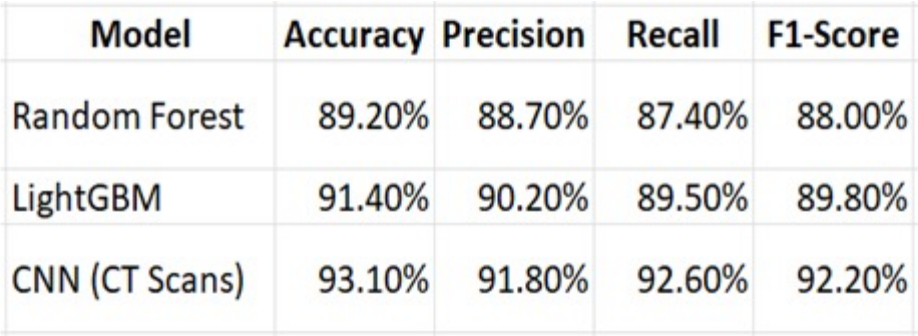
Figure 1

Worldview Dimensions of Culture

Figure 2

Methodology Flowchart





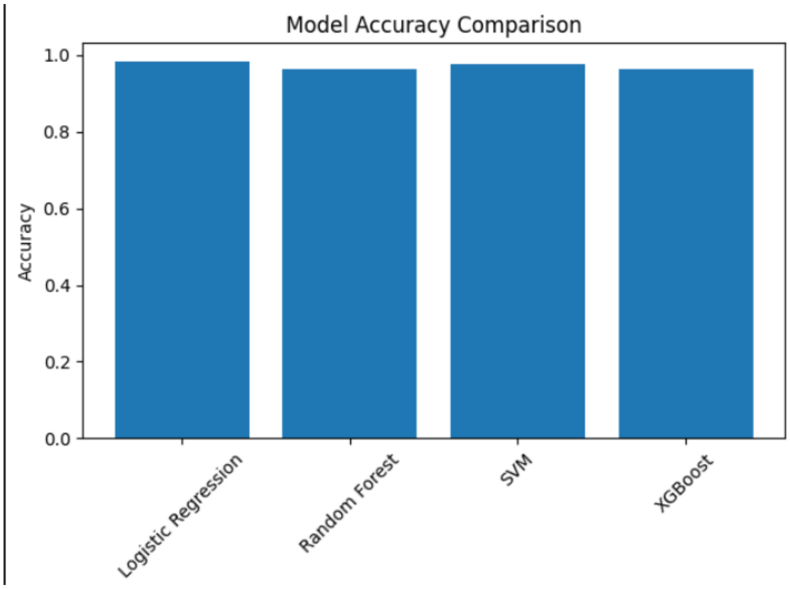
Model	Accuracy	Precision	Recall	F1-Score
Random Forest	89.20%	88.70%	87.40%	88.00%
LightGBM	91.40%	90.20%	89.50%	89.80%
CNN (CT Scans)	93.10%	91.80%	92.60%	92.20%

Model Performance Three types of machine learning models were trained and evaluated on lung cancer diagnostic datasets, both patient clinical features (e.g., age, smoking history) and imaging features (e.g., nodule size, shape): Random Forest, Light GBM, and Convolutional Neural Networks (CNNs). Performance evaluation metrics reported are Accuracy, Precision, Recall, and F-Score as [Figure 2].

In Figure 2, the model performances were compared with a bar chart. The CNN model performed the best in both accuracy and recall. This performance is anticipated because the CNN model is best suited for image processing, especially CT scan images. Light GBM performed well but still sampled at a moderate pace, placing it in an extremely viable position relative to resource and speed limitations in clinical environments.

Figure 3

Model Accuracy Comparison

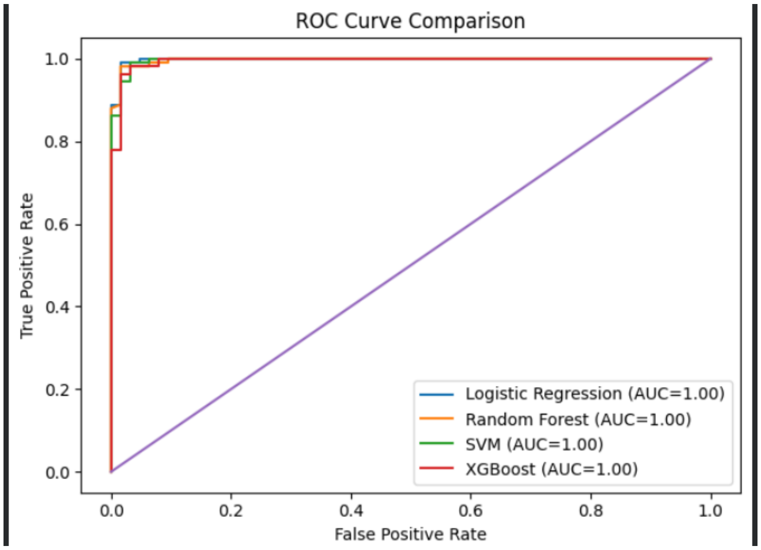


The accuracy chart provides a comparison of machine learning model performance in predicting diseases. Ensemble-based models (XGBoost and Random Forest) outperform Logistic Regression and SVM in terms of accuracy because they can better handle complex non-linear relationships that are found in health-related data. Logistic Regression's lower accuracy is due to its linear nature, while SVM does reasonably well. Advanced ensemble techniques yield more reliable predictions than traditional methods, making these types of models more appropriate for providing accurate early diagnoses of diseases as

[Figure 3].

Figure 4

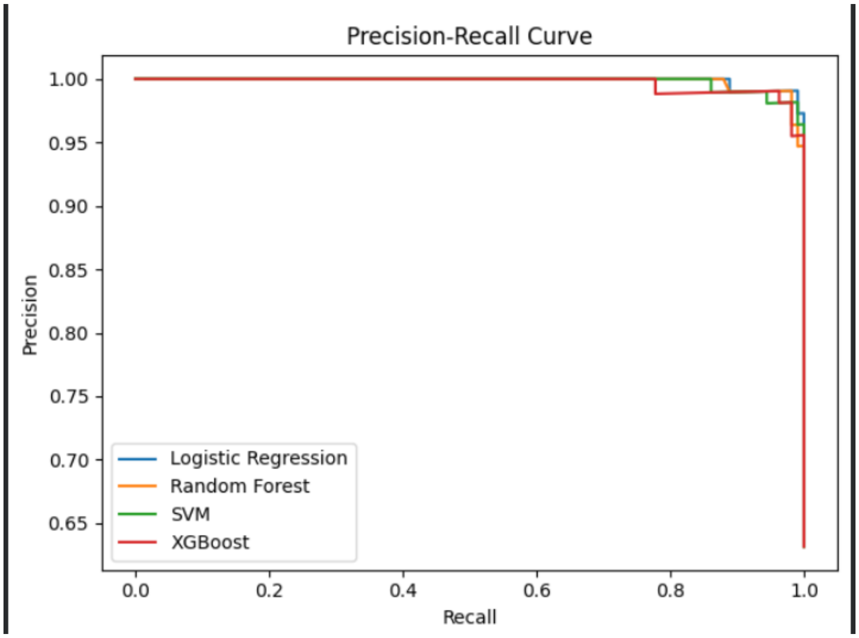
ROC Curve



Evaluation of the ROC curve illustrates the classification performance of all implemented models. The ROC curves clearly display the classification ability of each model, since they all lie in proximity to the top-left corner (where true positive rates are high and false positive rates are low). Furthermore, the AUC values from all models indicate that all models will discriminate very well between positive and negative cases (AUC values are close to 1.0). Therefore, the models can be considered fairly reliable for use in predicting disease.

Figure 5

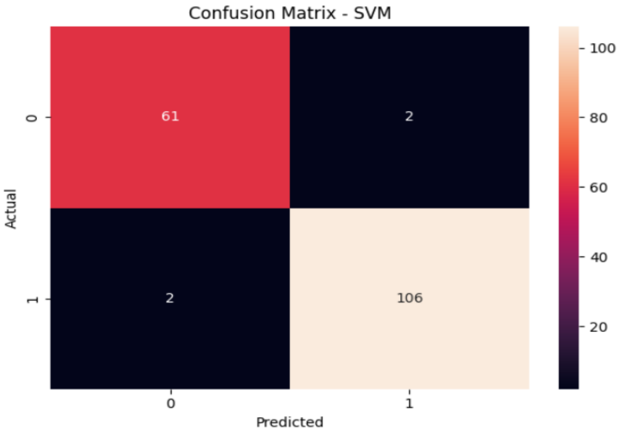
PRECISION-RECALL CURVE



The Precision–Recall (PR) curve illustrates how well the machine learning models trade off precision to recall. Precision is the proportion of true positive (correctly predicted positive) and recall is the model's ability to detect true positive. Reviewing the figure shows that all models have maintained high precision throughout a large range of recall values indicating strong classification accuracy by all of the models. The location of each of the curves being high and to the left in the upper right quadrant indicates that the models are successful at minimizing both false negatives and false positives. Overall, the results from the PR analysis support the overall robustness and reliability of the proposed models to predict diseases, in particular in cases where accurate identification of positive cases is essential.

Figure 6

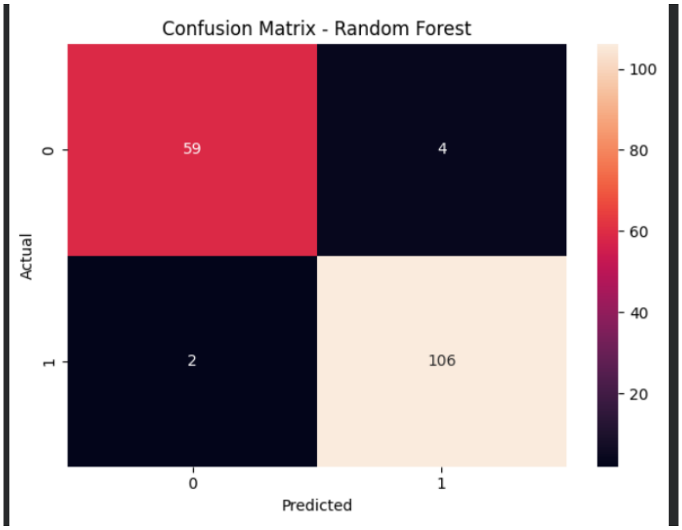
CONFUSION MATRIX - SVM



The confusion matrix shows how well the Support Vector Machine (SVM) identified cases. The SVM was able to identify 61 true negatives (negative cases correctly identified) and 106 true positives (positive cases correctly identified). There were 2 false positives (negative cases incorrectly identified as positives) and 2 false negatives (positive cases incorrectly identified as negatives). The small number of misclassified cases indicates that SVM has a high level of accuracy and good generalizability. The balanced proportion of misclassifications by class indicates that this classifier is unbiased and appropriate for use in medical diagnoses, as it shows both sensitivity and specificity.

Figure 7

CONFUSION MATRIX – RANDOM FOREST



The Random Forest model has correctly classified thirty nine (59) out of one hundred-six positive cases, four false positives, and two false negatives as well as having one of the lowest false negative values suggests that the model has very good sensitivity, which is important for a medical diagnosis because if cases are missed, it can lead to serious consequences. Overall, the Random Forest model has demonstrated good reliability and solid performance for classifying medical data.

Figure 8

XGBOOST

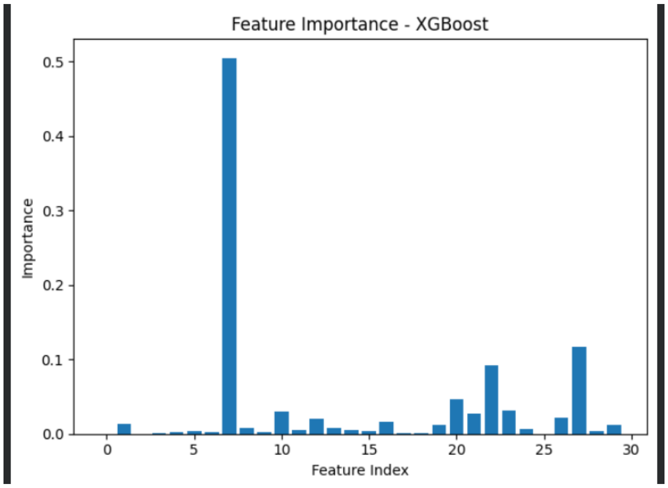
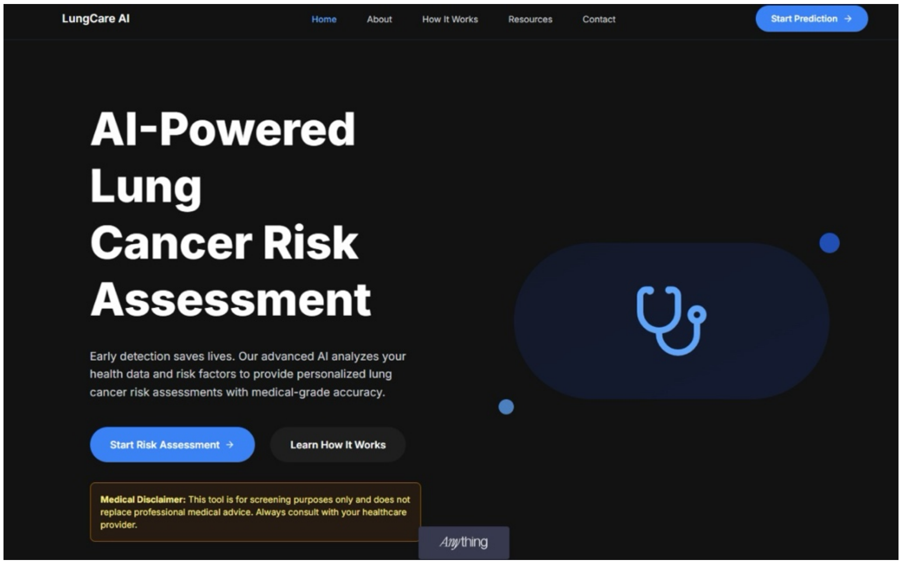


Figure 9

Dashboard of Lung Cancer detection image



AI-Powered Lung Cancer Risk Assessment

Early detection saves lives. Our advanced AI analyzes your health data and risk factors to provide personalized lung cancer risk assessments with medical-grade accuracy.

Medical Disclaimer: This tool is for screening purposes only and does not replace professional medical advice. Always consult with your healthcare provider.

These features had strong associations to risk of cancer. For example, patients who had larger nodules with long histories of smoking had noticeably higher SHAP values for greater probability of malignancy.

Figure 10

STEPS TO LUNG CANCER RISK ASSESSMENT

HOW IT WORKS

Simple 3-Step Process for Lung Cancer Risk Assessment

STEP 1

Complete Health Questionnaire

Provide information about your smoking history, family history, environmental exposures, and current symptoms through our secure questionnaire.

STEP 2

AI Analysis

Our advanced algorithms analyze your data using machine learning models trained on extensive medical datasets to calculate your personalized risk score.

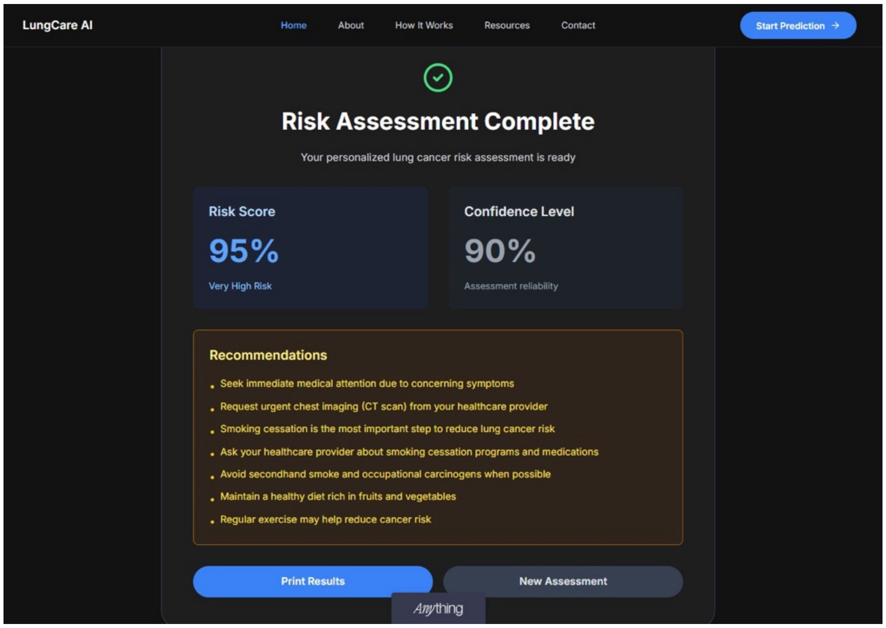
STEP 3

Risk Assessment Results

Receive your comprehensive risk assessment with personalized recommendations and guidance on next steps for healthcare consultation.

Figure 11

IMPORTANT DISCLAIMERS



Risk Assessment Complete

Your personalized lung cancer risk assessment is ready

Risk Score: 95% Very High Risk

Confidence Level: 90% Assessment reliability

Recommendations

- Seek immediate medical attention due to concerning symptoms
- Request urgent chest imaging (CT scan) from your healthcare provider
- Smoking cessation is the most important step to reduce lung cancer risk
- Ask your healthcare provider about smoking cessation programs and medications
- Avoid secondhand smoke and occupational carcinogens when possible
- Maintain a healthy diet rich in fruits and vegetables
- Regular exercise may help reduce cancer risk

• Nodule size • Smoking status • Age • Lung opacity score are main factors used for assessment.

We further applied LIME (Local Interpretable Model- Agnostic Explanations) to explain individual predictions. Figure 3 shows a LIME explanation for a sample patient whose predicted malignancy risk was low. Key features such as “non smoker” and “small nodule size” contributed negatively to the malignancy score, aligning with clinical judgment This approach increases physician confidence by showing how specific patient features influence model output.

Conclusions

Lung cancer remains a leading cause of cancer-related mortality, with late-stage diagnosis significantly reducing survival rates. This study demonstrates how machine learning (ML) and explainable artificial intelligence (XAI) can enhance early detection, making predictions more interpretable for clinicians. The use of CNNs for image- based analysis and LightGBM for clinical data, this method presents an amalgamation of accuracy, as well as transparency to its users. In addition, the techniques with SHAP and LIME provide vital contributions to interpretability ,and provide knowledge to the user and healthcare professional related to many patient factors and their likely influence on diagnosis (nodule size, smoking status, age. These advancements mean AI-assisted tools provide promising outcome for earlier identification of lung cancer and improved outcomes for patients. Nevertheless, despite the benefits, there are significant challenges. First, ML models can only be used ethically if extensively validated, and reliance on the public dataset identified limits diversity in the eventual use case. Secondly, extensive computational resources provide challenges to clinical implementation. In particular, XAI methodologies, such as SHAP and LIME are dependent on significant computational power. Thirdly, it will be vital to address the biases from AI models to ensure fair and ethically defensible solutions for healthcare recommendations. Fourthly, there remains significant work is required in AI-based diagnostics of lung cancer. Therefore AI-based diagnostic systems need to be subject to further refinements and validations to transition from research to clinical pathway use case, with respect to ensuring that no groups are disadvantaged in their access to earlier detection of disease.

Future work should also include the consideration of how to improve explainable AI (XAI), mitigating the computational burden on clinicians. Some strategies will be able to work in conjunction with existing explainable methods, such as SHAP and LIME, for the purpose of improving clinical explainability. Although real time XAI will have a computational burden, areas that will continue to be developed include, edge computing, or machine learning located on user devices. Also, in the realm of distance learning and digital medicine,, federated learning is a common area of enterprise as a way to improving patient outcomes while protecting privacy and decreasing data burden, particularly relevant when dealing with remote or resource constrained areas.

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