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# An Effective Multi-Architecture Approach for Lung Cancer Detection

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**ABSTRACT**

Most of the traditional and existing methods in lung cancer detection suffer from challenges such as limited interpretability, delayed decision-making, limited diagnostic assistance, scope of misinterpretations, and single modality processing models. To address these, a hybrid deep learning model is required that consists of a 3 Dimensional Convolutional Neural Network (3D-CNN), a Transformer, and an RNN-LSTM pipeline for the identification of lung cancer. The hybrid model predicts the disease early and alerts so that the mortality rate is reduced. In these, 3D-CNN is used for volumetric CT images and nodules malignant processing, Transformer is used for processing genomics sequences, and the RNN-LSTM pipeline is used for temporal clinical data interpretation. The features from each section are fused using a multi-modal fusion layer for efficient lung disease classification. The results obtained over the LIDC-IDRI dataset (publicly available repository) of images, clinical/genomics data after preprocessing, and hybrid model processing, in terms of AUC, sensitivity, and specificity, are observed to be better than existing models used. The statistical test via DeLong would determine the effectiveness of the model. The interpretability is increased due to the usage of SHAP explainability by clinical and nodules features.

## 1. INTRODUCTION

Lung cancer is one of global cancer mortality affected disease, due to a lack of advanced screening methods and delayed decisions.

### 1.1 Background

Lung cancer results in the death of many people. In this, specific parameters are noted that are useful in estimating the risk, as well as rehabilitation would be preferred for recovery and mental support. Detecting lung cancer in the last stage is a high-risk scenario as well as the recovery rate is very low, which increases the mortality rate. In this, CT scans support clinical mechanisms for nodule detection, while genomics provides complementary information on risk assessment. Personalized treatments, as well as timely alerts, would improve the health of the patient with early prediction and accurate risk assessment. The available traditional methods suffer from a single modality and are limited in diagnostic power and interpretability.

### 1.2 Research gaps

The disadvantages of existing methods were demonstrated, such as: (i) support only a single modality like CT or genomics, which avoids rich information from cross-modality; (ii) limited integration of heterogeneous datatypes, which lacks advanced feature concatenation like multi-modal fusion; (iii) delayed decision-making due to dependent on radiologist reports, which involve manual or semiautomated mechanisms; (iv) insufficient interpretability, due to many DL methods behave as back boxes, and lack of agnostic explainability; and (v) limited statistical validation, due to not using statistical test like DeLong tests for AUC comparison.

### 1.3 Objectives

The proposed hybrid model would overcome and ensure objectives such as: (i) a hybrid architecture system that supports CT, clinical, and genomic data for accurate identification; (ii) use modality-specific models like 3 Dimensional Convolutional Neural Network (3D-CNN) for CT, Transformer for genomics, and LSTM-RNN for clinical; (iii) involve multimodal fusion that extracts cross-rich information from CT, clinical, and genomic data, for improvement of performance; and (iv) better interpretation using SHAP explainability usage.

### 1.4 Contributions

The key contributions are highlighted, for example, integration of a multi-modal architecture, which consists of 3D-CNN for CT image processing and nodule detection, Transformer for genomic analysis, and LSTM-RNN for temporal clinical data interpretation. The earlier significant contributions are demonstrated for the understanding of lung cancer identification. Although existing multimodal systems

exist, they still suffer from unified training and a lack of meaningful explainability. The existing DL models suffer from weak interpretation, limited modality use, and inadequate feature fusion support. Hence, a multi-architecture fusion with 3D-CNN, Transformer, and RNN-LSTM pipeline is to be integrated for enhancing lung disease prediction and better decision support. From a study made by Dritsas and Trigka [1], an ML model was used on a single modality, with low discrimination, hence requiring the motivation for multimodality support and hybrid models. From Gao et al. [2], although supporting clinical data and CT, the model suffers from lower accuracy, lacks genomic data and XAI, which motivates a hybrid approach that preserves all the positive aspects.

## 2. LITERATURE REVIEW

There are studies on the severity of lung cancer. The accurate prediction depends on the risks involved. The categories of parameters, if they are involved, would experience serious lung cancer. If they are in a smaller portion, it would help with expenditure forecasting. Existing systems face several key challenges: a lack of standardization, the need to handle large data volumes, and the requirement for multi-modal input support to enable efficient processing. Furthermore, they often exhibit limited external validation across diverse populations and provide inadequate support for low-resource settings in lung cancer detection.

From Dritsas and Trigka [1], various machine learning models are demonstrated on the risk impact on lung cancer. The Rotation Forest is considered the most accurate detection approach in this domain of detection. The hyperparameters play the severity of risk prediction. Pathan et al. [3] demonstrated lung cancer disease prediction using various machine learning models such as Random Forest, decision tree, and SVM. The focus is on hyperparameter tuning, which results in better accuracy. Gao et al. [2] demonstrated two models compared with the Brock model, and noticed that the performance of the co-learning model on both images and CDEs is far better than individuals alone, such as images only or CDEs only. Hong Kong men's lung cancer was taken as a study, and the multivariate Logistic Regression was used for risk prediction with cross-validation regression by Tse et al. [4]. The performance is estimated via AUC, Confusion matrix, and ROCC in this study. As shown by Azhdarpoor et al. [5], there is a low impact and low effect of radon exposure on Iranians, in both the home living segment and the workers segment. This study observed 3 platforms, such as cutting stone, residents, and plant processing, as a base, and concluded that no impact on these due to environmental conditions.

Issanov et al. [6] demonstrated two review frameworks, such as PROBAST and CHARMS tools, for assessing the accuracy and performance of the model. The risk is high in the screening of smoking habits patients over lung cancer prediction (LCP). Feng et al. [7] demonstrated nine models in European countries, from which LLP has a lower risk performance, and the rest 8 are slightly different from the other 8 models but used for lung cancer risk prediction. Liao et al. [8] demonstrated the seven models, such as LLP and its versions, LC RAT, Bach, Pittsburgh, and PLCO approaches. The feature CanPredict() is assessed using these 7 models. Two significant factors, such as smoking, and the model's criteria in the evaluation of performance. Maurya et al. [9] demonstrated various ML models that are used for predicting the accuracy. These focused on classification and correlation. The clinical approach is a significant approach to take action at each stage for quick recovery. The two methods identified as K-nearest neighbor and Bernouli Bayes approaches produce better accuracy. Zhang et al. [10] demonstrated 4 models: Random Forest, Naive Bayes, Gradient Boosting, and Logistic Regression, in which performance and accuracy are assessed. The visualization is depicted using Shapley Additive Interpretation. Ostrowski et al. [11] demonstrated MOLTEST BIS people using three models, such as Back, LLP, and PLCO, in which another model called Tammemagi's risk model recommends that patients with minimal loss. Howell et al. [12] made a risk assessment over 16 factors covering aspects such as lifestyle, socioeconomic, demographic, clinical, and health data. The methodology used is linear regression to estimate the risk score. Feng et al. [13] demonstrated two risk models, such as smoking-based and proteomics-based, in terms of proteins. Based on 6 cohort studies, the protein-based risk model provides a standard model and is identified as a better risk prediction. Huang et al. [14] demonstrated many advancements in metabolism therapies, immunotherapies, radio therapies, etc. The need for AI and its importance were explored to help in plan preparation and personalized drug discovery for patient health recovery. AI predicts the immunoreactivity of patients and makes breakthroughs in lung cancer recovery. Yang et al. [15] demonstrated machine learning models in which decision trees and tree-based models are explored. The data of cell carcinoma and adenocarcinoma are integrated with clinical, genetic, and demographic details for determining the health status. It enables experts to make decisions on timeline, personalized care, and recovery plans.

A study made by Rubin et al. [16] demonstrated the Denmark population between specific years and applied Logistic Regression. By taking that specific dataset, an emerged model is derived that considers socio-demographic parameters and diagnostic parameters to determine the risk of patients' health stage. Chen et al. [17] demonstrated 4 European countries and their air pollution influence on lung cancer incidence. The components involved are particulate matter concentration, Nitrogen oxides, and black carbon are positive aspects, and negative aspects of ozone. The mortality rate and incidence rate based on demographics are compared and analyzed. Xue et al. [18] focused on using AI methods and deep learning models to improve the accuracy of the model for tumor detection. The application of radiomics is one of the accurate screening and diagnostic methods, with the collaboration of advanced centers, which would result in a breakthrough in accurate tumor detection. Elia et al. [19] focused on reducing false positives and the incidence of the disease. The lesions are initially benign, but they may turn into malignant ones, and surgeons would have a challenge in removing them accurately. The 3 ML models were used, in which J48 was found to be better in the prediction. Makubhai et al. [20] focused on lifestyle and medical diagnostic parameters as a basis for predictions. It uses XAI methods such as partial plots, feature significance, and decision trees to provide a clear and interpretable framework with the support of machine learning models. Kothari et al. [21] demonstrated a web application in which input is given and outputs a detailed description of the disease. In this, XAI is used to produce an understandable and transparent framework with descriptions of many aspects. The need of storing data, and retrieving the details on load balancing is demonstrated

through the studies by Dey and Sangaraju [22, 23], in which the study [22] demonstrated the issues of using local, global load balancing strategies for the distribution of workload among the available entities over the cloud and the study [23] demonstrated effective mechanisms for evaluating the performance of load balancing involved over the cloud usage. Kumar and Raju [24] showed that identification of fraud using a combination of models, such as CNN, LSTM, and XGBoost, for quick processing and yielding of outcomes. From Basheer Ahmed [25], the study explored the risks of DR at an early stage in predicting diabetic surge during the COVID-19 pandemic, using a fuzzy logic mechanism with an aggregated operator called OWA. Ali et al. [26] demonstrated that blood vessel failure towards the brain results in brain stroke, which would be detected using various ML and NN models, in which K-means performs better than other models. Tables 1 and 2 demonstrate the methods used in LCP.

In Table 1, traditional methods lack complex interactions, ML and DL methods offer more accuracy but require complex datasets and expensive processing, multi-modal approaches lack training design, and XAI mechanisms would enhance interpretability and suffer from overhead.

Table 2 demonstrates specific deep-learning models whose description and demerits are mentioned.

**Table 1.** Assessment methodologies

| Methodology | Models Used | Description | Demerits |
|---|---|---|---|
| Statistical and traditional | LLP risk model, Bach model, and PLCOm2012 | Clinical, demographic, and behavioral | Lack of complex interactions, and less accurate |
| ML models | Random Forests, Logistic Regression, SVM, LightGBM, and XGBoost | Identify patterns and improve prediction accuracy | Require high-dimensional datasets, and less interpretable |
| DL models | CNN, RNN, and Transformers | Complex datatypes | Expensive, requires large datasets, and is difficult to interpret |
| Multimodal methods | Late, early, and hybrid fusions | Integrate multiple datatypes | Requires preprocessing and is complex to design and train |
| XAI technique | LIME, SHAP, GRAD-CAM | Interpretable explanations adopt clinical support and build trust | Overhead involved, and simply complex decisions |
| Clinical risk assessment | NLST, USPSTF, and AI-based | High-risk individuals use screening and interventions | Limited quality, and may not generalize |

**Table 2.** Specific DL methods

| DL Method | Description | Demerits |
|---|---|---|
| 3D CNNs | Ensures accuracy for imaging activities such as nodule detection and predicting the malignancy | Requires large volumetric data and is expensive |
| Transformers | Suitable for genomic data but requires fine-tuning for clinical data | Expensive to train, and limited interpretability |
| U-Net | Ensures accuracy for segmentation activities and is less suitable for classification | Pixel-level annotation is time-consuming, and can't handle other types except imaging |
| GNNs | Suitable for structured data and requires graphs for analysis | Computationally expensive for large graphs, with less interpretability |
| 1D CNNs | Suitable for genomic data and sequential data | May struggle with complex patterns and require careful parameter tuning |

## 3. METHODOLOGY

In this, the description of the dataset in the sense of primary, secondary, and significant in the risk prediction over lung cancer in Table 3. The modules identified for lung cancer detection are demonstrated in Figure 1. The flow of activities denoted in the order of their significance is demonstrated in Figure 2. From Table 3, the mixing of specific categories of attributes is considered, such as medical, demographic, environmental, behavioral, lifestyle, and socioeconomic aspects. The significant aspects that impact risk are behavioral and environmental. From Figure 1, the significant activities that must be prioritized in risk prediction over lung cancer are multi-modal adaptability, data preprocessing, model training, model evaluation, and applying the XAI technique.

The steps involved in this methodology are demonstrated as:

Step 1: Categorize the given data into 3 sets of features, like primary, secondary, and supporting factors.

Step 2: Start processing the given dataset over modules such as data processing. Feature extraction, multimodal fusion, training and evaluation, and explainability support.

Step 3: Call PS1 for multimodal fusion, which calls PS2 for 3D-CNN, then calls PS3 for Genomic data, and calls PS4 for temporal clinical data.

**Table 3.** Factors impacting the severity of risk

| Attribute | Risk Factor Type |
|---|---|
| Cigarette smoking | Behavioral |
| Secondhand smoke exposure | Environmental/behavioral |
| Family history of lung cancer | Genetic/hereditary |
| Occupational exposures | Environmental |
| Radon exposure | Environmental |
| Asbestos exposure | Environmental |
| Age (65 years and older) | Demographic |
| Chronic Obstructive Pulmonary Disease (COPD) | Medical history |
| Personal history of cancer | Medical history |
| Socioeconomic status | Socioeconomic |
| Diet and nutrition | Lifestyle |
| Physical inactivity | Lifestyle |
| Air pollution | Environmental |

Step 4: Training and evaluation follow 70%, 15%, and 15%. It uses features such as Dropout and L2 regularization, cross entropy loss, early stopping, and back propagation.

Step 5: Perform hyperparameter tuning using grid search

over layers, batch size, attention heads, epochs, learning rate, and cross-fold-validation, as well as L2 weight decay.

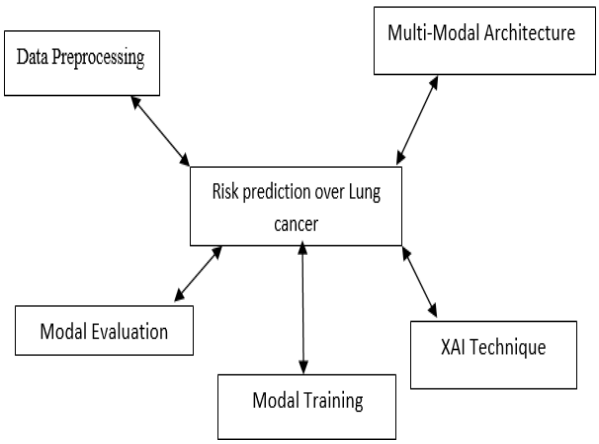


**Figure 1.** Demonstration of proposed system modules

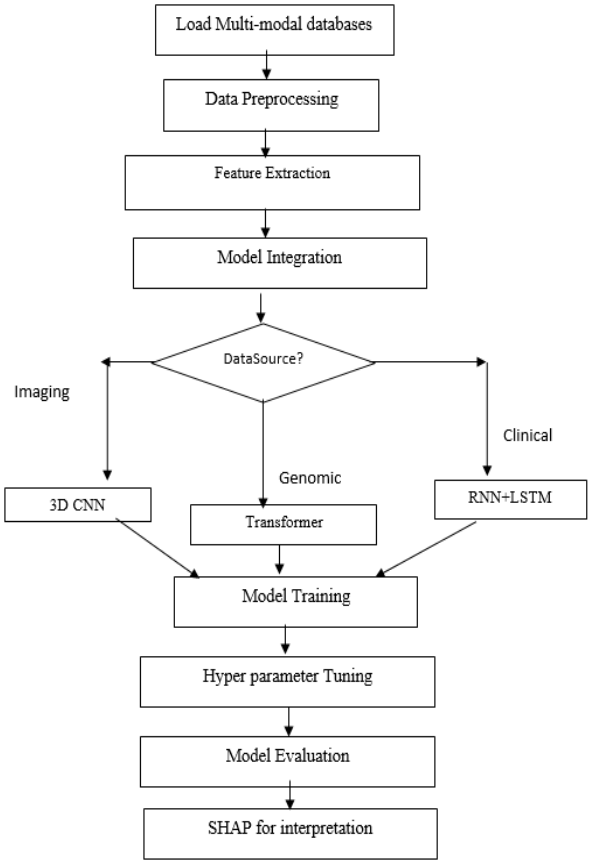


**Figure 2.** Flow of activities of the hybrid approach

The pseudo procedure for demonstration of a multi-architecture approach for multi-modality is demonstrated as follows:

**PS1: Pseudo_Procedure Multi_architecture_multi_modality(dataset1[][][],dataset2[][][],dataset3[][][])**

**Input**: Different Datasources for imaging, genomics, and clinical data, such as dataset1[][]: Imaging data, dataset2[][]: Genomic data, dataset3[][]: Clinical data

**Output**: Accuracy

**Step 1**: Apply data preprocessing
- 1.1 Apply uniform voxel spacing, Normalization, and augmentation for standardizing imaging
- 1.2 Apply one-hot encoding for encoding genomic data into numerical
- 1.3 Clean clinical by handling missing and categorical values using imputation, and min-max

**Step 2**: Apply CNN
- 2.1 Extract spatial features from imaging
- 2.2 Capture sequential patterns using Transformers
- 2.3 Use CNN for clinical data
- 2.4 Apply PCA as a feature selection technique for extracting relevant features

**Step 3**: For integrated data, combine features of imaging, genomics, and clinical data
- 3.1 For visualization and compatibility, apply UMAP on integrated data

**Step 4**: Model design
- 4.1 For imaging, use CNN, call PS2
- 4.2 For genomic, use Transformer, call PS3
- 4.3 For clinical use Fully Connected neural network, call PS4
- 4.4 Use an attention mechanism over significant features from each modality with weight

**Step 5**: Training
- 5.1 Split the integrated dataset into training, validation, and testing in a 70,15,15 fashion
- 5.2 For classification and feature representation, use a hybrid model to get trained
- 5.3 For classification, use cross entropy loss
- 5.4 To avoid overfitting, use dropout and L2 regularization

**Step 6**: Tuning hyperparameters
- 6.1 For tuning hyperparameters, use the grid search technique over learning rate, number of layers, batch size, dropout, epochs, etc.
- 6.2 For robustness, use K-fold cross-validation
- 6.3 Use early stopping, use L2 weight decay

Step 7: Apply SHapley Additive exPlanations (SHAP) to interpret model predictions and identify key features

In PS1, three datasets are used, like imaging, genomics, and clinical. Data preprocessing is applied to make a quality dataset by removing noise if it exists. Apply multi-architectures like 3D-CNN for imaging, Transformer for genomics, and RNN+LSTM for the clinical set. The extracted features are integrated in processing models in the further step, and analyze interpretation is analyzed using Shapley as an XAI technique.

**PS2: Pseudo_Procedure 3D_CNN(dataset1[][][])**

**Input**: Dataset1: Imaging

**Output**: Prediction1

**Step 1**: Resample volumes into consistent resolution
- 1.1 Apply augmentation for data diversity

**Step 2**: Construct 3D CNN using layers such as
- 2.1 Input layer, contains 3D volumes
- 2.2 3D CNN, used to extract spatial features
- 2.3 3D Pooling, to reduce dimensionality
- 2.4 Fully Connected layers, to combine the features
- 2.5 Based on significant factor values, the higher the value, the higher the risk. Based on binary classification, risk is outputted as Low or High

**Step 3**: In training, use the categorical cross-entropy loss for classification and Dice loss for segmentation
- 3.1 Use Adam optimizer
- 3.2 Iterate till convergence is reached

**Step 4**: Use early stopping to avoid overfitting

**Step 5**: Compute accuracy, precision, recall, and F1-Score

**Step 6**:

$$Accuracy = \frac{True\ Positives + True\ Negatives}{Total\ Number\ of\ Cases}$$

where,

$$\text{Precision} = \frac{True\ Positives\ (TP)}{(True\ Positives\ (TP) + False\ Positives\ (FP))}$$

$$\text{Recall (Sensitivity)} = \frac{True\ Positives\ (TP)}{(True\ Positives\ (TP) + False\ Negatives\ (FN))}$$

$$\text{F1 Score} = \frac{2 \times (Precision \times Recall)}{Precision + Recall}$$

From PS2, 3D CNN is constructed using Inut, CNN, Pooling, Fully Connected, and Output layers. Based on hyper parameter tuning, classified the sample as High risk or Low risk.

**PS3: Pseudo_Procedure Transfomer(dataset2[][])**

**Input**: Dataset2: Genomics

**Output**: Prediction2

**Step 1**: Convert the genomic into the required format
- 1.1 Use K-mer embeddings for DNA sequences
- 1.2 Use pre-trained embeddings like DNABERT
- 1.3 Combine this genomic with clinical if the complete suite of input is required

**Step 2**: The Transformer model is constructed
- 2.1 Input layer in which genomics is to be auto-encoded
- 2.2 For long-range dependencies and relational mapping, use techniques such as
  - 2.2.1 multi-head self-attention mechanism
  - 2.2.2 Positional encoding for retaining the sequences
- 2.3 Use Fully Connected layers
- 2.4 Output layer for prediction, such as High or Low

**Step 3**: Model training
- 3.1 Cross-entropy loss for classification and MSE for regression
- 3.2 Appy AdamW optimizer
- 3.3 Iterate for some epochs till convergence is reached

**Step 4**: For hyperparameter tuning, use the number of layers, no of attention heads, the batch size, and learning rate

**Step 5**: Compute measures for classification

$$Accuracy = \frac{True\ Positives + True\ Negatives}{Total\ Number\ of\ Cases}$$

where,

$$\text{Precision} = \frac{True\ Positives\ (TP)}{(True\ Positives\ (TP) + False\ Positives\ (FP))}$$

$$\text{Recall (Sensitivity)} = \frac{True\ Positives\ (TP)}{(True\ Positives\ (TP) + False\ Negatives\ (FN))}$$

From PS2, specific and pre-trained embeddings are used for encoding, then a Transformer model with input uses positional encoding and multi-head self-attention for contextual relationship, Fully Connected layers, and output layers. The model is trained, then fusion the significant parameters, and evaluate the model performance.

**PS4: Pseudo_Procedure RNN+LSTM(dataset23[][])**

**Input**: Dataset3: Clinicaldata

**Output**: Prediction3

**Step 1**: Convert clinical data into a time-series format
- 1.1 Use embedding layers to denote categorial data into a dense vector space
- 1.2 Combine the statistical data with time-series details if the complete suite of input is required

**Step 2**: The Transformer model is constructed
- 2.1 Input layer in which the preprocessed data is accepted
- 2.2 For temporal dependencies, an RNN is used
- 2.3 For enhancing the model's capability, use an LSTM layer
- 2.3 Use Fully Connected layers, for combined features regarding classification
- 2.4 Output layer for prediction, such as High or Low

**Step 3**: Model training
- 3.1 Binary cross entropy loss for classification and MSE for regression
- 3.2 Appy Adam optimizer
- 3.3 Iterate for some epochs till convergence is reached

**Step 4**: For hyperparameter tuning, use the number of RNN, LSTM layers, no of hidden units, batch size, and learning rate

**Step 5**: Compute measures for classification

$$Accuracy = \frac{True\ Positives + True\ Negatives}{Total\ Number\ of\ Cases}$$

where,

$$\text{Precision} = \frac{True\ Positives\ (TP)}{(True\ Positives\ (TP) + False\ Positives\ (FP))}$$

$$\text{Recall (Sensitivity)} = \frac{True\ Positives\ (TP)}{(True\ Positives\ (TP) + False\ Negatives\ (FN))}$$

From PS3, convert clinical data into time-series data, then construct the required model using RNN and LSTM layers, then train the model, then fine-tune the model, and evaluate the model's performance.

From Figure 2, the activities mentioned in the order such as data sources are loaded, then preprocessing such sources for quality, then feature extraction, then combining the significant features for model training based on data source type, then hyperparameter tuning, then model evaluation, and providing interpretation using the SHAP model.

## 4. RESULTS

This section is decomposed into four aspects: analysis of evaluated factors (accuracy, robustness, interpretability),

analysis of performance measurement, assessment of tools for lung cancer diagnosis, and analysis of statistical tests. The evaluation of the proposed multi-architecture model against existing models, such as ML, DL methods, medical diagnostic tools, multimodal approaches, and other models. In this, the significant factors considered, such as accuracy, robustness, interpretability, and performance (precision and recall), are demonstrated in Table 4, in which such measures are compared and visualized in Figure 3, which highlights the best values for the multi-architecture model on multi-modalities. Table 5 demonstrates the AUC, sensitivity, and specificity values against the considered methods against the multi-architecture modal. Table 6 demonstrates the key features, the type of domain/specialization, and accepted input. When it transforms the multi-architecture into a UI tool, input the values, it produces a risk that is high or Low after processing the combined data. Table 7 demonstrates the accuracy of the tools considered against the proposed model tool, in which specific measures such as sensitivity, specificity, and AUC are evaluated for the analysis in the future.

### 4.1 Analysis of evaluated factors (accuracy, robustness, interpretability)

Table 4 demonstrates accuracy, robustness, interpretability, and performance (precision and recall), which determines the effectiveness of the models.

Table 4 and Figure 3 demonstrate the effectiveness of the models in terms of accuracy, performance, robustness, and interpretability. The multi-architecture model (hybrid model) is observed to have better computed values than other considered methods.

**Table 4.** Evaluated factors against the considered models

| Method | Accuracy | Performance | Robustness | Interpretability |
|---|---|---|---|---|
| Statistical and traditional models | 85 | 85 | 75 | 100 |
| ML models | 90 | 90 | 80 | 80 |
| DL models | 95 | 95 | 85 | 30 |
| Multimodal methods | 97 | 97 | 95 | 85 |
| XAI technique | 85 | 85 | 90 | 100 |
| Clinical risk assessment | 85 | 85 | 75 | 100 |
| 3D CNNs | 95 | 95 | 85 | 30 |
| Transformers | 90 | 90 | 90 | 85 |
| U-Net | 95 | 95 | 90 | 80 |
| GNNs | 85 | 90 | 75 | 80 |
| 1D CNNs | 85 | 85 | 80 | 80 |
| Multi-architecture model | 98 | 98 | 95 | 100 |

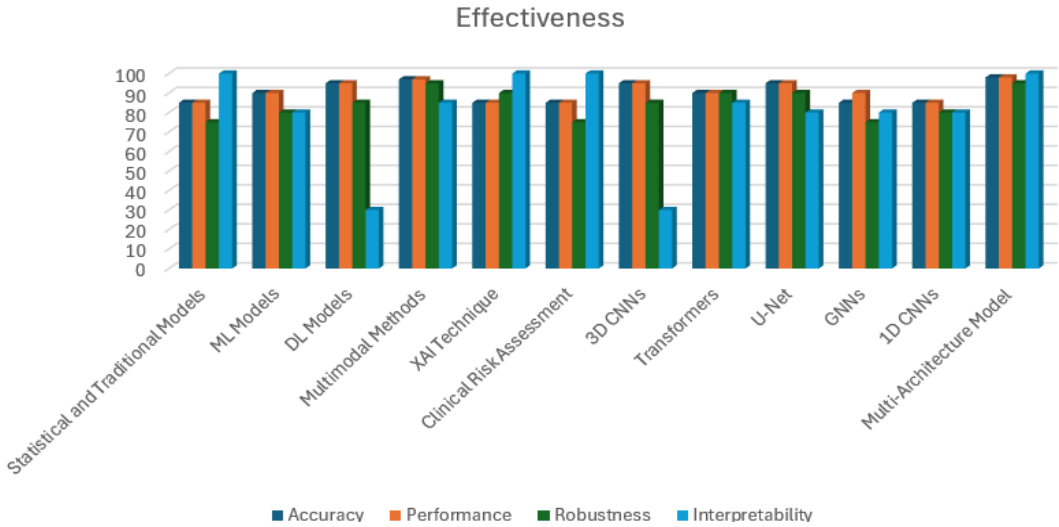


**Figure 3.** Effectiveness of the methods considered against the multi-architecture model

### 4.2 Analysis of performance measurement

Table 5 explores that traditional and ML-based models achieve moderate AUC (0.85–0.90), DL and multimodal architectures exhibit significantly better discriminative ability (0.94–0.96), and 3D-CNNs and Transformer models independently achieve high AUC (0.95–0.96). The proposed multi-architecture model ensures superior performance arises from combining spatial features from CT imaging, sequence patterns from genomic data, and temporal dependencies from clinical histories.

### 4.3 Assessment of tools for lung cancer diagnosis

The existing diagnostic tools, Lung-RADS, NLST, PLCOm2012, Brock University, LCP, DL tools, and CAD systems, are explored in terms of data input and type of prediction method.

Table 6 demonstrates tools in categories such as risk prediction, diagnostic aid, and risk assessment, the type of modality supported, and the domain of technique used for processing.

From Table 7, the tools listed along with their accuracies are demonstrated, in which the multi-architecture model sustains

better and satisfactory accuracy than other models.

From Figure 4, the order of tools that ensure better accuracy is multi-architecture models as the first, outperforming tool than other considered models.

**Table 5.** Performance against considered approaches

| Model/Method | AUC | Specificity | Sensitivity |
|---|---|---|---|
| Statistical, traditional models | 0.85 | 85 | 80 |
| ML models | 0.90 | 90 | 85 |
| DL models | 0.95 | 95 | 90 |
| Multimodal methods | 0.96 | 95 | 90 |
| XAI techniques | 0.92 | 90 | 85 |
| Clinical risk assessment | 0.80 | 80 | 75 |
| 3D CNNs | 0.96 | 95 | 90 |
| Transformers | 0.95 | 95 | 90 |
| U-Net | 0.94 | 95 | 90 |
| GNNs | 0.93 | 90 | 85 |
| 1D CNNs | 0.88 | 85 | 80 |
| Multi-architecture models | 0.98 | 97 | 92 |

**Table 6.** Tools for lung cancer against specific aspects

| Tool Name | Type | Input Data | Prediction Method |
|---|---|---|---|
| Lung-RADS | Assessment system for risk | Images (CT scan) | Categorization |
| NLST risk prediction tool | Calculator for risk | Smoking history, demographics | Statistical model |
| PLCOm2012 | Prediction model for risk | Smoking history, demographics | Logistic Regression |
| Brock University model | Prediction model for risk | Demographics and CT scans | Logistic Regression |
| Deep learning models | Prediction using AI | Clinical data, MRI/CT images | Convolutional Neural Networks (CNNs) |
| LCP model | Prediction model for risk | Smoking history, demographics | Machine learning (e.g., Random Forest) |
| Computer-Aided Diagnosis (CAD) | Diagnostic aid | Images (CT scan) | Image processing algorithms |
| Multi-model approach | Prediction model for risk | Multi-type inputs | Deep learning techniques and AI |

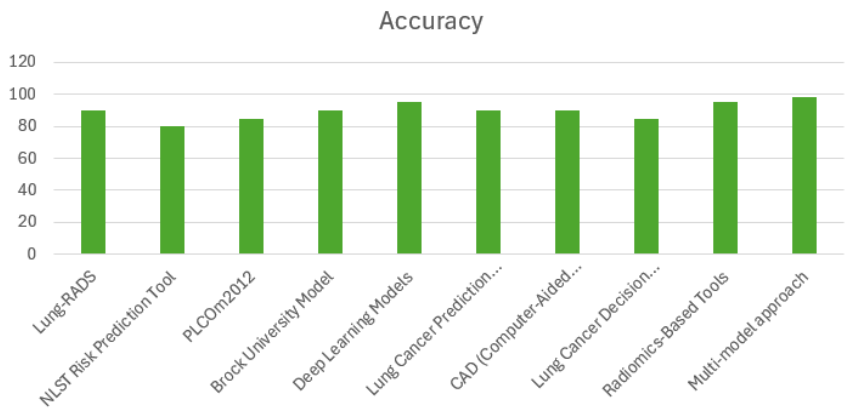


**Figure 4.** Accuracy of the tools considered

**Table 7.** Accuracies of tools against our proposed approach

| Tool Name | Accuracy | Evaluation Metric | Observation |
|---|---|---|---|
| Lung-RADS | 90 | Sensitivity, specificity | High specificity but lower sensitivity for small nodules |
| NLST risk prediction tool | 80 | Area Under Curve (AUC) | Based on demographic and smoking history |
| PLCOm2012 | 85 | AUC | Validated in multiple cohorts for 6-year lung cancer risk prediction |
| Brock University model | 90 | AUC | Strong performance in predicting malignancy based on nodule characteristics |
| Deep learning models | 95 | AUC, sensitivity, specificity | High accuracy in research settings, but dependent on training data |
| LCP model | 90 | AUC | Incorporates genetic and environmental factors, still under research |
| CAD | 90 | Sensitivity, specificity | Assists radiologists; accuracy depends on nodule size and image |

| | | | |
|---|---|---|---|
| | | | quality |
| Lung cancer decision support tools | 85 | AUC | Rule-based systems, accuracy varies with input data quality |
| Radiomics-based tools | 95 | AUC, sensitivity, specificity | High accuracy in research, but requires high-quality imaging data |
| Multi-model approach | 98 | AUC, sensitivity, specificity | Ensures the highest accuracy due to multiple types of input |

### 4.4 Analysis of statistical tests

The statistical significance of the proposed model against traditional, ML, and DL for only image type models was tested using DeLong's method and observed over p-value, based on Table 4, and are listed in Table 8. The p-value is increased for a multi-architecture model.

**Table 8.** P-values against the considered models

| Method | AUC | CI | P-Value |
|---|---|---|---|
| Traditional | 0.85 | 0.82 – 0.88 | < 0.001 |
| ML | 0.90 | 0.87 – 0.92 | < 0.001 |
| DL (image) | 0.95 | 0.93 – 0.96 | 0.004 |
| Proposed | 0.98 | 0.97 – 0.99 | < 0.05 |

## 5. CONCLUSION

To overcome delayed decision-making, insufficient handling of multiple modalities, and limited performance, there is a need to detect lung cancer with better performance and accuracy. The input data sources are categorized into imaging, genomics, and clinical data. In this process, data preprocessing is applied, features are extracted using feature extraction, then a 3D CNN is applied for imaging analysis, Transformers for genomics interpretation, and RNN+LSTM is used for temporal clinical data. The significant features are extracted and combined for better evaluation of lung cancer risk. The activities in the construction of 3D CNN, Transformer, and RNN+LSTM involve modal training, hyperparameter fine-tuning, and modal evaluation are demonstrated in PS1, PS2, PS3, and PS4. The predictions are more accurate due to a combination of important features, for instance, such as smoking history, nodule size, and EGFR mutations. The effectiveness of the hybrid method and UI tool of the proposed method is determined as better than other models. In the future, the work might extend to different populations and look for a lightweight interface for easy classification. It also expects expanding the model to incorporate additional biomarkers like proteomics and radiogenomics, with federated learning for multi-institutional privacy-preserving training.

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