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Lung Cancer Prediction Using Machine Learning: A Comparative Analysis of KNN, SVM, Random Forest, and Logistic Regression

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Abstract: *Among the major issues of cancer-associated fatalities universally is lung cancer, and survival rates are heavily reliant on prompt and precise diagnosis. Conventional diagnostic techniques, while effective, frequently miss early-stage lung cancer detection. By examining intricate patterns in medical data, machine learning offers a reassuring method for enhancing the prediction of lung cancer. However, the algorithm and optimization strategies employed determine how successful machine learning models are. This study explores the comparative evaluation of four machine learning approaches for the prediction of lung cancer: Random Forest, Logistic Regression, K-Nearest Neighbors (KNN), and Support Vector Machine (SVM). To improve model performance, the Kaggle dataset was preprocessed, encoded, and put through feature selection procedures. Hyperparameter tuning was used to refine model parameters acceptable to upsurge accuracy still more. Key performance pointers counting accuracy, precision, recall, and F1-score were accustomed to evaluate the models. The findings demonstrate with an accuracy of 90%, the Logistic Regression method performed best, with other models exhibiting varied degrees of performance. The outcome of this work highlights the significance of model assortment and parameter optimization, as well as the promise of machine learning in the prediction of lung cancer. Future research could explore deep learning approaches and integrate additional patient data to enhance predictive performance. Ultimately, leveraging machine learning for lung cancer diagnosis could lead to earlier detection, better persevering consequences, and a significant decrease in death rates.*

Keywords*:* Lung cancer, Machine learning, Random Forest, Logistic Regression, Hyperparameter tuning

I. INTRODUCTION

The lungs are essential respiratory organs in charge of gas exchange, particularly the elimination of carbon dioxide and the absorption of oxygen, which sustains cellular metabolism in the human body [1]. Lung cancer, a malignant proliferation of lung tissue, remains one of the most lethal diseases worldwide, with increasing mortality linked to smoking, air pollution, and exposure to carcinogens. The disease often progresses silently in early stages, manifesting symptoms such as chronic cough, hemoptysis, chest pain, and fatigue only when it has advanced [2].Machine Learning (ML) is asubset of artificial intelligence permitselectronic devicesto absorb from data without the need for explicit programming [3]. It has found transformative applications across domains, from personalized recommendation systems to medical diagnostics. In healthcare, ML has proven especially promising in analyzing high-dimensional datasets and extracting non-trivial patterns for predictive modelling [4].

For illness classification tasks, including cancer prediction, machine learning techniques together with K-Nearest Neighbors (KNN), Support Vector Machines (SVM), Random Forest Classifier (RFC), and Logistic Regression (LR)

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have been used. Every method presents different compromises between interpretability, computational effectiveness, and performance in categorization.

1. **KNN** is a straightforward and flexible method that classifies new data points according to the common vote of the adjacent neighbors in feature space [4] [5].
2. **SVM** looks for the best hyperplane to separate classes, demonstrating high accuracy in jobs involving binary categorization, including identifying instances that are malignant and those that are not [6].
3. A variety of decision trees are built using Random Forest, an ensemble learning approach, to increase resilience and reduce overfitting [7].
4. A sigmoid function is employed in logistic regression to represent the probability of a binary outcome and is favored for its interpretability in clinical settings [8].

Despite the success of these models, challenges persist, such as obtaining high-quality annotated datasets, tuning hyperparameters, addressing model overfitting, and deploying models in clinical workflows [8]. This study conducts a comparative analysis of KNN, SVM, RFC, and LR using publicly available lung cancer datasets to assess their predictive performance through system of measurement like exactness, correctness, precision, recall, and F1-score.
With the intention to improve data-driven decision and improve patient results, the ultimate objective is to assess the viability and clinical usefulness of machine learning techniques in early lung cancer detection.

A. The Lungs' Anatomy and Function

The thoracic cavity contains the lungs, which are spongy, cone-shaped organs. Because of the heart's restriction of space, the left lung has two lobes while the right has three [1]. They perform gas exchange approximately 12–20 times per minute, a process crucial to sustaining life. Protective mechanisms such as nasal hairs, mucus lining the airways, and the sweeping motion of cilia work collectively to filter airborne pollutants [1].

B. Lung Cancer: Overview and Classification

Lung cancer arises from epithelial cells and is separatedinto two keyclasses: small cell lung cancer (SCLC) and non-small cell lung cancer (NSCLC). NSCLC, which comprises big cell carcinoma, squamous cell carcinoma, and adenocarcinoma, makes up around 85% of cases. More aggressive, SCLC grows and spreads quickly, and is usually presented as restricted or vast [2][9].
Major risk factors include tobacco use (accounting for ~90% of cases), secondhand smoke, occupational exposure (e.g., asbestos, arsenic), air pollution, genetic predisposition, and emerging risks like vaping [2][10]. Notably, early-stage lung cancer often lacks symptoms, making early detection critical to improving survival, which remains around 19% overall [2].

C. Predictive Analytics in Medical Diagnosis

Using both historical and current data, predictive analytics makes predictions about the future outcomes using statistical models, ML, and AI [11]. In oncology, predictive modelling can identify patients at high risk, guide diagnostic testing, and inform personalized treatment strategies.

D. Machine Learning Paradigms

ML algorithms are categorized into four main paradigms:

1. **Supervised Learning:** Uses labelled data to train classifiers (e.g., SVM, decision trees, KNN, LR) for tasks like cancer diagnosis [12].
2. **Unsupervised Learning:** Uses methods like dimensionality reduction and clustering to find patterns in unlabeled data [13].
3. **Semi-Supervised Learning:** To increase learning efficiency, a small labeled dataset is combined with a larger unlabelled sample [14].
4. **Reinforcement Learning:** Involves learning optimal actions through feedback mechanisms, commonly used in robotics and adaptive systems [12].

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E. Review of Related Works

[14] sought to weigh the efficiency of diverse old-fashioned machine learning methods for example SVM, Decision Trees, and Random Forests in identifying lung cancer through clinical data analysis. The researchers made use of a dataset containing patient demographics, clinical characteristics, and histopathological information. They utilized a methodical strategy for selecting features in order to improve the algorithms' effectiveness. The research included thorough testing and verification to confirm the accuracy of the findings. SVM outperformed other algorithms with an accuracy of 92% and a sensitivity of 90%, suggesting its superior effectiveness. The Study highlighted the significant of selecting the right features to enhance model performance, indicating that thorough data preprocessing can greatly influence the findings from machine learning in the healthcare field.

[15] [25] examined how Convolutional Neural Networks (CNNs) can be applied to determine lung cancer in radiological pictures for example CT scans and chest X-rays. The research included teaching a model for deep learning that uses a vast collection of labeled pictorial data, enabling the CNN to grasp complex patterns linked to lung cancer. The researchers evaluated how well the CNN performed compared to conventional diagnostic techniques, demonstrating the possiblility of using deep learning to imaging in medicine. With an astounding 97% accuracy rate, the CNN algorithm far outperformed traditional methods. The writers emphasized that deep learning methods have the capacity to automate image analysis, lessening the workload for radiologists and enhancing diagnostic precision. This research represented a major progress in the application of AI in medical imaging, indicating that deep learning has the capacity to completely transform lung cancer detection.

Liu and associates investigated the efficiency of CNNs and other deep learning models in contrast to conventional machine learning algorithms aimed at identifying lung cancer in CT scans [16], [17]. The scientists used a dataset containing different lung cancer cases for a thorough assessment of model performance. Different CNN architectures were tested to find the best configuration for this particular task, with an emphasis on maximizing both efficiency and precision of the model. The findings revealedthat CNN models consistently performed better than traditional algorithms, achieving a 95% correct rate. The research emphasized the benefits of deep learning in capturing intricate features from imaging data that traditional methods frequently overlook. The researchers determined that deep learning could greatly improve the ability to diagnose lung cancer in radiology.

Zhang and colleagues carried out a comprehensive analysis of severalmachine learning techniques employing a dataset of people with lung cancer, including Random Forests, K-Nearest Neighbors (KNN), and Logistic Regression [18], [19]. The study aimed to identify the best effective method for identifying lung cancer early using clinical and imaging information. The researchers utilized cross-validation methods to ensure the strength of their results and to prevent overfitting. The study found that Random Forests reached an accuracy rate of 94%, illustrating a solid combination of precision and recall. The researchers determined that ensemble proceduresfor example Random Forests are highly successful in medical diagnosis because of their ability to handle complex datasets andavoid overfitting, rendering them applicable for practical use in detecting lung cancer.

Table 1 summarizes key studies on lung cancer prediction, highlighting their methodological strengths such as high accuracy, effective use of CNNs, EHR integration, transfer learning, and radiomics-based approaches. However, it also notes common weaknesses, including limited datasets, dependency on data quality, lack of interpretability, and challenges in generalizing results across domains.

Table 1. Strengths and Weaknesses of the current systems

Study	Strengths	Weaknesses
Ausawalaithong et al. (2019)	High accuracy (93.5%) with CNNs on X-rays	Limited dataset, black-box interpretability [20]
Yeh et al. (2020)	Uses EHR for early risk prediction (90.2%)	Dependent on EHR quality and completeness [21]

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Islam et al. (2019)	Effective use of transfer learning (95.1%)	May not generalize well to new domains [22]
Li et al. (2020)	Combines radiomics and ML (92.5%)	Limited by radiomics data extraction [23]
Wang et al. (2019)	CNN on CT scans with strong results (94.2%)	Dataset size limits scalability [24]

These findings underscore the growing success of ML, particularly deep learning, in identifying lung cancer from complex clinical and imaging data. However, challenges such as interpretability, generalizability, and integration into clinical workflows remain open research questions.

II. METHODOLOGY

A. Introduction

This chapter presents the methodology for creating an artificial intelligence-based (ML) lung cancer prediction system. Emphasis is placed on the design of the dataset pipeline, preprocessing procedures, classifier architecture, performance evaluation, and tool selection. Ensuring validity and reliability, the section lays the groundwork for replicability and future extension.

B. Proposed System

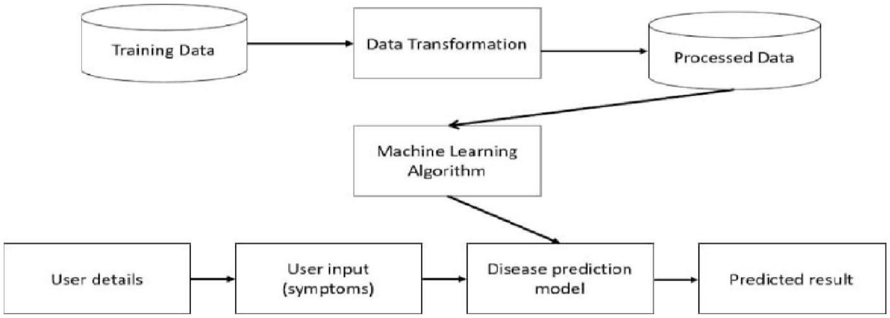

Fig. 1. System Architecture of Lung Disease Prediction

A comparative study is conducted using four supervised classifiers: **Support Vector Machine (SVM)**, **Random Forest Classifier (RFC)**, **K-Nearest Neighbours (KNN)**, and **Logistic Regression (LR)**, to forecast lung cancer risk. Input features include age, smoking habit, air pollution exposure, genetic predisposition, symptoms, and biomarker indicators. Models are trained to classify patients into risk categories: Low, Medium, or High.

Prior to model training, data undergoes comprehensive preprocessing: cleaning, imputing, normalization, feature selection, and class balancing. Hyperparameter tuning (e.g., SVM kernel, number of trees for RFC, optimal *k* in KNN) is performed via grid search and k-fold cross-checking. Measures of performance include precision, accuracy, recall, and F1-score.

C. Discussion of Dataset

Dataset Description and Collection

The dataset originates from a publicly available Kaggle repository called "Lung Cancer Risk & Prediction Dataset,"[29] which contains approximately 1,000 records and 25 attributes, including demographics, lifestyle, environmental exposure, symptoms, and a three-level risk target variable (Low, Medium, High).

Features utilized include age, gender, air pollution index, smoking and passive smoking, occupational hazards, genetic risk, chronic respiratory disease history, and clinical symptoms (chest pain, fatigue, weight loss, etc.). The target

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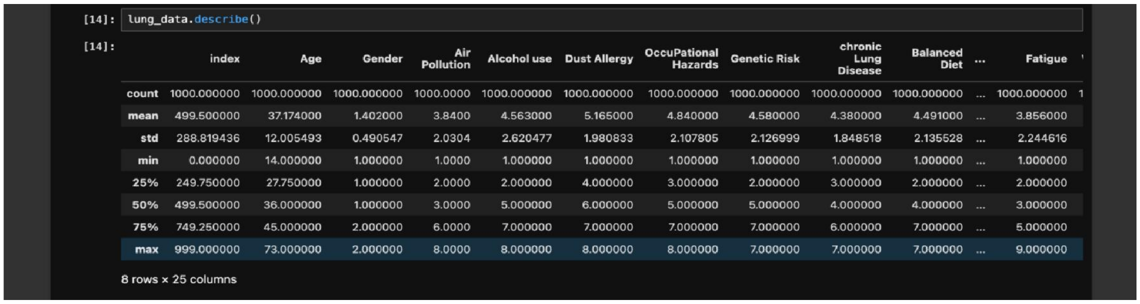
variable indicates lung cancer risk level. Dataset labels and features were extracted in a manner consistent with other published studies.

Table 2: Description of Dataset Features for Lung Cancer Prediction

S/N	Feature	Description
1	Index	Unique ID of records
2	Age	Patient's age
3	Gender	Patient's gender (1 = Male, 2 = Female)
4	Air Pollution	Exposure level to air pollutants (scale of 1–10)
5	Alcohol Use	Frequency of alcohol consumption (scale of 1–10)
6	Dust Allergy	Sensitivity to dust allergens (scale of 1–10)
7	Occupational Hazards	Exposure to hazardous work conditions (scale of 1–10)
8	Genetic Risk	Family history of lung cancer (scale of 1–10)
9	Chronic Lung Disease	Presence of chronic lung diseases (scale of 1–10)
10	Balanced Diet	Quality of diet (scale of 1–10)
11	Overweightness	Obesity level (scale of 1–10)
12	Smoking	Smoking frequency (scale of 1–10)
13	Passive Smoker	Exposure to secondhand smoke (scale of 1–10)
14	Chest Ache	Intensity of chest pain (scale of 1–10)
15	Coughing of Blood	Frequency of coughing up blood (scale of 1–10)
16	Exhaustion	Level of fatigue (scale of 1–10)
17	Weight Loss	Extent of weight loss (scale of 1–10)
18	Shortness of Breath	Severity of breathlessness (scale of 1–10)
19	Gasping	Intensity of wheezing (scale of 1–10)
20	Swallowing Difficulty	Difficulty in swallowing (scale of 1–10)
21	Clubbing of Finger Nails	Changes in nail appearance (scale of 1–10)
22	Frequent Cold	Frequency of catching colds (scale of 1–10)
23	Dry Cough	Severity of dry cough (scale of 1–10)
24	Snoring	Frequency of snoring (scale of 1–10)
25	Level	Target variable (Low, Medium, High – indicating lung cancer risk)

Figure 3 shows the statistical summary of a lung cancer dataset, containing the lowest, quartiles, maximum, count, mean, and standard deviation values for every aspect. Figure 4 indicates that the dataset has no missing values, as all features show a count of zero null entries.



```
[14]: lung_data.describe()
```

```
[14]:
                                                   Air                                       OccuPational                    chronic     Balanced
             index          Age       Gender    Pollution   Alcohol use   Dust Allergy      Hazards     Genetic Risk        Lung         Diet   ...      Fatigue  '
                                                                                                                          Disease
count  1000.000000  1000.000000  1000.000000  1000.0000  1000.000000  1000.000000  1000.000000  1000.000000  1000.000000  1000.000000  ...  1000.000000  1
 mean   499.500000    37.174000     1.402000     3.8400     4.563000     5.165000     4.840000     4.580000     4.380000     4.491000  ...     3.856000
  std   288.819436    12.005493     0.490547     2.0304     2.620477     1.980833     2.107805     2.126999     1.848518     2.135528  ...     2.244616
  min     0.000000    14.000000     1.000000     1.0000     1.000000     1.000000     1.000000     1.000000     1.000000     1.000000  ...     1.000000
  25%   249.750000    27.750000     1.000000     2.0000     2.000000     4.000000     3.000000     2.000000     3.000000     2.000000  ...     2.000000
  50%   499.500000    36.000000     1.000000     3.0000     5.000000     6.000000     5.000000     5.000000     4.000000     4.000000  ...     3.000000
  75%   749.250000    45.000000     2.000000     6.0000     7.000000     7.000000     7.000000     7.000000     6.000000     7.000000  ...     5.000000
  max   999.000000    73.000000     2.000000     8.0000     8.000000     8.000000     8.000000     7.000000     7.000000     7.000000  ...     9.000000

8 rows × 25 columns
```

Fig. 3. Describing the dataset

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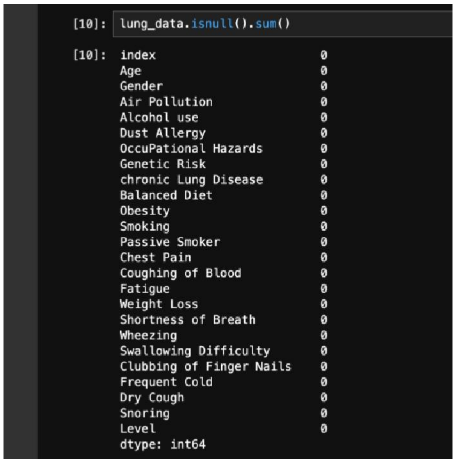

```
[10]: lung_data.isnull().sum()

[10]: index                        0
      Age                          0
      Gender                       0
      Air Pollution                0
      Alcohol use                  0
      Dust Allergy                 0
      OccuPational Hazards         0
      Genetic Risk                 0
      chronic Lung Disease         0
      Balanced Diet                0
      Obesity                      0
      Smoking                      0
      Passive Smoker               0
      Chest Pain                   0
      Coughing of Blood            0
      Fatigue                      0
      Weight Loss                  0
      Shortness of Breath          0
      Wheezing                     0
      Swallowing Difficulty        0
      Clubbing of Finger Nails     0
      Frequent Cold                0
      Dry Cough                    0
      Snoring                      0
      Level                        0
      dtype: int64
```

D. Data Pre-processing

- **Data Cleaning:** Missing or invalid entries were handled via imputation or removal as appropriate.
- **Standardization:** Feature scaling was performed using scikit-learn's StandardScaler, ensuring zero mean and unit variance.
- **Feature Selection:** Key predictors were identified using scikit-learn's SelectKBest with chi-squared scoring to reduce dimensionality and enhance interpretability.
- **In order to discourse class Imbalance: The** Synthetic Minority Over-Sampling Technique (SMOTE) remained applied via the imbalanced-learn package to balance class distribution and prevent bias toward majority classes.
- **Train-Test Split:** Using scikit-learn's train_test_split function, the cleaned dataset was separated into subgroups for training (80%) and testing (20%).

E. Model Selection and Training

Each algorithm employed is briefly described below and trained on the preprocessed dataset:

1. **Support Vector Machine (SVM):** Constructs a hyperplane to maximize class separation margin. Kernel and regularization parameters were tuned.
2. **Logistic Regression (LR):** Predicts probabilities via the sigmoid function. Implemented using the 'lbfgs' solver with regularization parameter *C* tuning.
3. Using the Manhattan or Euclidean distance metric, K-Nearest Neighbors (KNN) is a non-parametric classifier it forecasts outcomes by using the majority label among k neighbors. Grid search was used to get the ideal k.
4. Random ForestClassifier (RFC): A bootstrap-aggregated ensemble of decision trees. In tune among the options were min_samples_split, max_depth, and multiple estimators (n_estimators).

F. Hyperparameter Tuning

Each machine learning algorithm's hyperparameters were adjusted to maximize its performance in lung cancer prediction. The specific hyperparameters tuned for each model included:

1. Support Vector Machine (SVM): In order to maximize the model's ability to distinguish between lung cancer risk levels, the regulationconstraint (C) and the kernel type (example., linear, polynomial, RBF) were changed.
2. K-Nearest Neighbors (KNN): To increase the precision of categorizing whereas balancing bias and variance, the number of neighbors (K) and the distance metric (such as Manhattan or Euclidean) were adjusted.
3. Random Forest Classifier: To increase model performance, decrease overfitting, and improve generalization in lung cancer classification, the number of decision trees (n_estimators), maximum tree depth, and minimum number of samples needed for node splitting were tuned.

4. Logistic Regression: To guarantee that the model performed effectively when applied to unknown data, the regularization parameter (C) was adjusted to prevent overfitting.

Hyperparameter tuning's objective was to achieve the highest possible accuracy by tailoring each model to the unique characteristics of lung cancer risk factors. This approach ensured a well-optimized model setup, maximizing predictive performance in lung cancer classification

G. System Design

Figure 2 outlines the sequential workflow of a disease prediction system, starting from entering patient details to validating data, extracting features, and matching values. It then proceeds to classify the data, predict the disease, and finally display the results.

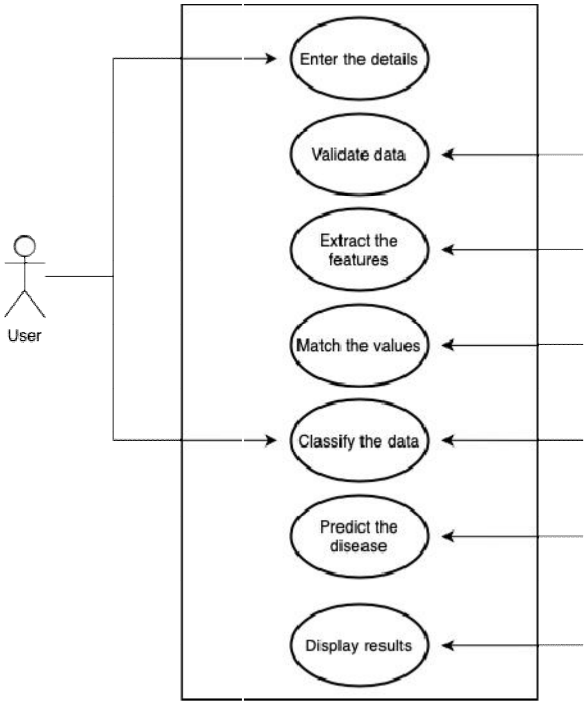

Figure 2. Illustrates the Use Case Diagram, showing user interactions, data input, analytics processing, and output classification.

III. RESULTS AND FINDINGS

A. Result of Model Training

This project trained four machine learning models: Random Forest Classifier, K-Nearest-Neighbors, Support Vector Machine, and Logistic Regression Classifier. An 80-20 dataset split was used to train the logistic regression model. The training data allowed the modelto identify patterns and categorize new occurrencesefficiently. Its prediction skills were measuredby means of a range of performance pointers. The KNN model was trained using 80% of the dataset, with the remaining 20% set aside for testing. The classifier used 3 nearest neighbors and the Minkowski distance (p=2).

Since KNN is a non-parametric model, instead of learning, commits the training data to memory explicit outlines. Predictions were made by assigning new data points to their closest neighbor's predominant class. The SVM model was trained by means of an 80-20 train-examination split with Bagging to improve generalization. It utilized an RBF kernel with C=7 and trained 75 SVM classifiers about various data subsets. The One-vs-Rest strategy handled multi-class classification, and the model's performance was evaluated by means of a confusion matrix and accuracy score on the test set.

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The Random Forest model was trained on a preprocessed dataset, where categorical variables were encoded, and highly correlated features (Pearson > 0.9) were removed. An 80-20 train-test split was used with stratification to maintain class balance. To reduce overfitting, the model was fine-tuned by:

1. Limiting tree depth and number of trees
2. Increasing the minimum samples required for splits and leaf nodes
3. Using fewer features per tree and reducing sample size per tree
4. Applying class weighting to handle class imbalance

A. Performance Evaluation

Table 2: Classification Report Logistic Regression

Class	Precision	Recall	F-1 Score	Support
1	0.92	0.84	0.88	67
2	0.81	0.88	0.84	58
3	0.95	0.96	0.95	95
Overall Accuracy: 0.90	Macro Avg: 0.89	Weighted Avg: 0.90		

Logistic Regression had high accuracy and was particularly effective in predicting class 3. However, it showed slightly lower recall for class 1, which means some high-risk patients may have been misclassified.

K-Nearest Neighbors (KNN): The KNN model attained an accuracy of 0.86, performing best for class 1 with a recall of 0.97, meaning it correctly identified most patients in this category. However, it struggled with class 2, where recall dropped to 0.69, leading to a higher number of false negatives. The weighted F1-score of 0.86 recommends that while the model is fairly balanced, its classification of class 2 could be improved. Table 3 presents precision, recall, F1-score, and support for each class, showing an overall model accuracy of 86%.

Table 3: Classification Report KNN

Class	Precision	Recall	F-1 Score	Support
1	0.83	0.97	0.90	67
2	0.89	0.61	0.78	58
3	0.88	0.91	0.89	75
Overall Accuracy: 0.86	Macro Avg: 0.87	Weighted Avg: 0.86		

KNN was particularly strong in identifying class 1 but struggled with class 2. The high recall for class 1 suggests that KNN can effectively detect early-stage lung cancer cases but may require tuning for better performance across all classes.

Support Vector Machine (SVM): SVM demonstrated an accuracy of 0.88, showing balanced performance across all classes. It performed exceptionally well for class 3, achieving a recall of 1.00, meaning it correctly identified all patients in this category. However, its performance for class 2 was slightly weaker, with a recall of 0.69. The weighted F1-score of 0.88 indicates a well-rounded model. Table 4 presents precision, recall, F1-score, and support for each class, showing an overall model accuracy of 88%.

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Table 4: Classification Report SVM

Class	Precision	Recall	F-1 Score	Support
1	0.94	0.91	0.92	67
2	1.00	0.69	0.82	58
3	0.79	1.00	0.88	75
Overall Accuracy:0.88	Macro Avg: 0.91	Weighted Avg: 0.88		

SVM had a perfect recall for class 3, making it ideal for identifying confirmed lung cancer cases. However, its lower recall for class 2 suggests potential improvements in fine-tuning the model parameters.

Random Forest Classifier: The Random Forest classifier achieved an accuracy of 0.83. It performed best for class 0, with a recall of 1.00, meaning all patients in this category were correctly identified. However, its recall for class 2 was 0.53, indicating a high number of false negatives. The weighted F1-score of 0.82 suggests that while the model is strong in certain areas, it struggles with class 2. Table 5 presents precision, recall, F1-score, and support for each class, showing an overall model accuracy of 83%.

Table 5: Classification Report Random Forest

Class	Precision	Recall	F-1 Score	Support
1	0.84	1.00	0.91	73
2	0.76	0.97	0.85	61
3	1.00	0.53	0.69	66
Overall Accuracy: 0.83	Macro Avg: 0.87	Weighted Avg: 0.82		

Random Forest was highly effective at predicting class 0 but had lower recall for class 2, meaning it failed to correctly identify a significant number of patients in that category. This suggests that feature selection or additional data balancing techniques may improve its performance.

In summary, Among the models, Logistic Regression achieved the highest accuracy (90%), demonstrating strong overall performance across all lung cancer risk levels. It was particularly effective in predicting class 3 cases, with a high recall and F1-score, making it a reliable choice for identifying lung cancer patients.

SVM performed exceptionally well in detecting advanced lung cancer cases (class 3), achieving a recall of 1.00 for this category. However, it showed lower recall for class 2, indicating that some cases were misclassified.

KNN was most effective in identifying early-stage lung cancer cases (class 1), with a recall of 0.97. However, its performance dropped for class 2, leading to a higher number of false negatives in that category.

Random Forest exhibited strong predictive capabilities for class 0, achieving a perfect recall of 1.00. However, it struggled with class 2, where recall was only 0.53, suggesting a need for further tuning or feature selection to improve its performance.

Overall, Logistic Regression emerged as the best-performing model due to its balanced precision, recall, and high accuracy. SVM and KNN also showed strong predictive abilities, particularly for specific lung cancer stages. Random Forest, while robust, would benefit from hyperparameter tuning and data balancing techniques to enhance its classification performance.

IV. SUMMARY AND CONCLUSION

A. Summary

The paper examined and contrasted the efficiency of four machine learning algorithms in forecasting the peril of lung cancer: Support Vector Machines (SVM), Random Forest Classifier, K-Nearest Neighbours (KNN), and Logistic Regression. The study used a Kaggle dataset and adhered to a methodical approach include acquiring data, preprocessing, choosing features, training the model, adjusting hyperparameters, and assessing performance based on accuracy, precision, recall, and F1-score metrics.

Among the models assessed, Logistic Regression demonstrated the highest accuracy and overall balanced performance, turning it into the most actual algorithm for lung cancer prediction in this study. Each algorithm showed distinct strengths and weaknesses, providing valuable insights into their practical applicability for early lung cancer detection. The paper highlights the promising part of machine learning techniques in supporting clinical decision-making and enhancing diagnostic accuracy for lung cancer patients.

B. Limitations

Despite the encouraging results, this study has limitations. First, the dataset was sourced from Kaggle and may not represent the full spectrum of lung cancer cases across diverse demographics and geographic regions, potentially limiting the generalizability of the findings. Second, the study relied on a limited set of features; important clinical or genetic factors not included could influence model accuracy and robustness. These constraints suggest that real-world application requires further validation and broader feature integration.

C. Future Work

Future research could improve lung cancer prediction by exploring sophisticated methods like deep learning with Artificial Neural Networks (ANNs), which may better capture complex medical data patterns. Expanding datasets to include more diverse populations and additional clinical and genetic features would enhance model generalizability and accuracy. Additionally, including these integrating clinical decision support systems with predictive models with predictive models might enable real-time diagnosis, enabling earlier intervention and improved patient outcomes.

D. Conclusion

In summary, this research shows how machine learning may help with the early diagnosis of lung cancer using accessible medical parameters. Logistic Regression emerged as the best-performing model, highlighting its suitability for classification tasks in lung cancer prediction. While limitations exist, the findings underscore the transformative role artificial intelligence can play in healthcare, providing a foundation for future development of robust, clinically applicable diagnostic tools. With continued research and refinement, machine learning models have the capacity to significantly enhance lung cancer detection and patient care.

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