SCRUTINIZING AND PRACTICING THE IMPACT OF DATA SCIENCE IN HEALTHCARE SECTOR

Thesis Submitted for the Award of the Degree of

DOCTOR OF PHILOSOPHY

in

COMPUTER SCIENCE AND ENGINEERING

By

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LOVELY PROFESSIONAL UNIVERSITY, PUNJAB

2025

DECLARATION

I, hereby declare that the presented work in the thesis entitled **“Scrutinizing and Practicing the Impact of Data Science in Healthcare Sector"** in fulfillment of the degree of **Doctor of Philosophy (Ph. D.)** is the outcome of research work carried out by me under the supervision of Dr. Parminder Singh, working as Professor, in the School of Computer Science and Engineering, Lovely Professional University, Punjab, India. In keeping with general practice of reporting scientific observations, due acknowledgements have been made whenever work described here has been based on findings of other investigator. This work has not been submitted in part or full to any other University or Institute for the award of any degree.

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CERTIFICATE

This is to certify that the work reported in the Ph. D. thesis entitled **Scrutinizing and Practicing the Impact of Data Science in Healthcare Sector** submitted in fulfillment of the requirement for the award of degree of **Doctor of Philosophy (Ph.D.)** in the School of Computer Science and Engineering, Lovely Professional University, is a research work carried out by Richa Jain, 41800136, is bonafide record of her original work carried out under my supervision and that no part of thesis has been submitted for any other degree, diploma or equivalent course.

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ABSTRACT

The increasing complexity of healthcare systems and the exponential growth of medical data necessitate advanced analytical methods for improving disease prediction, diagnosis, and treatment outcomes. This thesis explores machine learning and deep learning techniques applied to healthcare analytics, specifically focusing on lung cancer prediction. It addresses gaps in traditional healthcare analytics through sophisticated data mining techniques, optimized classification algorithms, and the integration of emerging technologies like the Internet of Medical Things.

Data mining techniques have emerged as pivotal tools in processing vast healthcare datasets. The thesis discusses the significance of these techniques in disease prediction, patient care improvement, and resource optimization. By employing algorithms that can detect patterns and trends within complex datasets, healthcare providers can make more informed decisions, leading to better patient care. The importance of data mining techniques is highlighted, showcasing their effectiveness in disease prediction and resource optimization while addressing challenges like data privacy and high dimensionality.

Subsequently, the study dicusses the applications of machine learning and deep learning methodologies, presenting real-world implementations that demonstrate improved diagnostic accuracy. The research underscores the limitations of traditional analytics methods and articulates the need for robust models in multi-disease prediction and lung cancer detection.

The primary objectives of this thesis include improving disease detection capabilities, enhancing prediction accuracy, and optimizing resource utilization, particularly concerning lung cancer and multi-disease diagnosis. The proposed work includes a comprehensive methodology for developing machine learning models, featuring comparative analyses of various classifiers and demonstrating significant improvements in diagnostic accuracy. The proposed framework utilizes ensemble learning techniques to enhance predictive accuracy. Hyperparameter tuning and optimization strategies, such as grid search, are employed to refine model performance. The results demonstrate a significant improvement in diagnostic accuracy compared to traditional methods, with the Multilayer Perceptron (MLP) and Logistic Regression models achieving accuracy rates of 93.65% and 93.54%, respectively.

The advantages of utilizing deep learning models for lung cancer detection and multi-disease classification are highlighted. The research employs various architectures, including DenseNet201, VGG16, VGG19, MobileNet and EfficientNet, refined through transfer learning. The integration of ensemble reinforcement learning techniques further enhances model robustness and reliability. Deep learning implementations showcase architectures refined through transfer learning, achieving a diagnostic accuracy of 99.40%. The findings validate the efficacy of the proposed frameworks and their transformative potential in healthcare.

The research highlights the necessity for scalable machine learning frameworks that improve model generalization while addressing ethical concerns in healthcare data analytics. Future research directions are proposed, emphasizing the need for robust validation across diverse datasets and the integration of emerging technologies such as IoMT to facilitate real-time monitoring and personalized medicine.

This thesis serves as a significant contribution to the field of healthcare analytics, providing valuable insights into the application of advanced analytical techniques for improving disease prediction, diagnosis, and overall patient care. The findings underline the critical importance of leveraging data mining, machine learning, and deep learning methodologies to navigate the complexities of healthcare data and enhance clinical outcomes.

ACKNOWLEDGEMENTS

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Richa Jain

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LIST OF ABBREVIATIONS

AI	Artificial Intelligence
ANN	Artificial Neural Network
AUC	Area Under the Curve
CAD	Computer-Aided Diagnosis
CKD	Chronic Kidney Disease
CNN	Convolutional Neural Network
CNN-UDRP	CNN-based Uni- modal Disease Risk Prediction
CRM	Customer Relationship Management
CT	Computed Tomography
CXR	Chest X-Ray
DL	Deep Learning
EHR	Electronic Health Records
FN	False Negative
FP	False Positive
GANs	Generative Adversarial Network
GBM	Gradient Boosting Machines
GNB	Gaussian Naive Bayes
HIPAA	Health Insurance Portability and Accountability Act
IoMT	Internet of Medical Things
IoT	Internet of Things

KNN	K-Nearest Neighbor
ML	Machine Learning
MLP	Multilayer Perceptron
NIH	National Institutes of Health
POMDP	Partially-Observed Markov Decision Proces
RL	Reinforcement Learning
RNNs	Recurrent Neural Network
SCH	Soonchunhyang University Hospital
SMO	Sequential Minimal Optimization
SMOTE	Synthetic Minority over-sampling Technique
SVM	Support Vector Machine
TN	True Negative
TP	True Positive

CHAPTER 1

INTRODUCTION

The healthcare sector is undergoing a remarkable transformation driven by the proliferation of digital technologies and the integration of advanced data analytics techniques. With the rapid advancement of medical technologies, the volume of healthcare data has surged exponentially, leading to the emergence of big data in healthcare. This phenomenon presents both challenges and opportunities for healthcare providers, researchers, and policymakers alike [1, 2]. The ability to effectively mine and analyze this vast amount of data has the potential to revolutionize healthcare delivery, enhance patient outcomes, and reduce costs [3]. The following sections discuss the role of data mining algorithms in healthcare, the evaluation of ML classifiers for disease prediction, and innovative approaches to lung cancer detection, showcasing the critical need for research and development in this domain.

1.1 Overview of Human Lung Anatomy

The lung is the most vital organ in the human respiratory system. The lungs are organs in the chest that resemble sponges and are an essential part of the breathing system. To make room for the heart, the left lung is smaller, having only two lobes, whereas the right lung has three lobes. Air enters the body through the mouth or nose, travels through each bronchus and the trachea, and then enters the lungs. The lungs are a couple of sponge-shaped organs that resemble cones. Inhaled air provides the lungs with a full supply of oxygen. As oxygen travels to the body's other organs, lung tissue transfers it to the blood. When cells take in oxygen, they release carbon dioxide. Carbon dioxide is returned to the lungs by the bloodstream and is expelled from the body while breathing out. Figure 1.1 [4] shows the lung's anatomical structure. The other main components of the lung areas besides atmospheric air are pulmonary arteries and bronchi. The two lungs (left and right) form the regions of the lung. In the left lung, an additional fissure, the oblique fissure further divides the lung into upper and lower lobes. The geometry of the human thoracic airway can be understood as a binary tree structure. The left and right main bronchi branch from the base of the trachea or tracheal tree to enter the left and right sides of the lung. The main bronchus consists of five lobar bronchi, two left bronchi, and three right bronchi, respectively, entering each lobe of the lung. The segmental bronchial tree (8–10 per lung region) branches from the lobar bronchi. Although the distribution of the bronchi is random, the branches of the pulmonary arteries follow the bronchi in parallel.

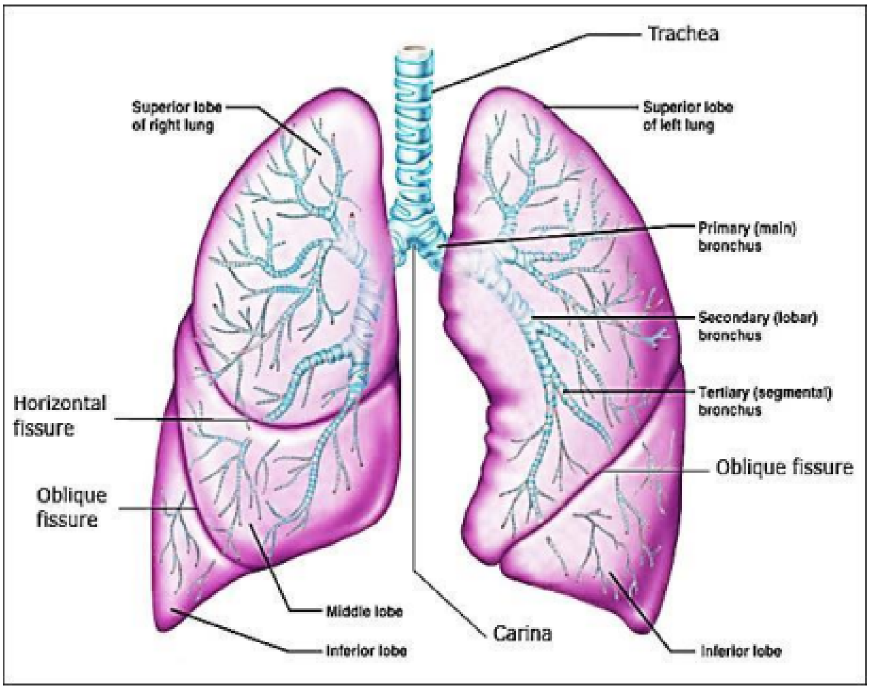

Figure 1.1: Structure of Human Lung

1.1.1 Overview of Lung Cancer

The World Health Organization reports that in 2022, there were 2.5 million new instances of lung cancer, accounting for 12.4% of all the new cancer cases, and deaths were 1.8 million, accounting for 18.7% of the total cancer fatalities [5]. A quick diagnosis, appropriate treatment, or discovery are critical to the patient's health. The treatment plan and prognosis for the patient are usually dictated by the stage at which the illness is identified. Early disease detection is therefore crucial to patients' chances of recovery. Computer-Aided Diagnosis (CAD) technology can greatly aid the diagnosis of lung cancer.

There are two primary types of lung tumors.

- Malignant
- Benign

Malignant tumors are cancerous, develop uncontrollably, invade adjacent tissues, and spread to other parts of the body, whereas benign tumors are not cancerous, develop slowly, and don't spread or invade other tissues.

1.1.2 Lung Cancer Detection

Early detection of lung cancer is instrumental in enhancing patient survival rates. The conventional techniques used in detecting lung cancer involve imaging procedures like chest X-rays, CT scans, and PET scans, which are used to detect suspicious masses in the lungs. These are often followed by biopsy procedures, where tissue samples are examined for malignancy. More recently, advanced technologies have come out as powerful tools for lung cancer detection, providing automated and highly accurate diagnostic support [6]. These AI-driven methods, including convolutional neural networks (CNN), can analyze medical images to detect lung nodules and classify cancerous and non-cancerous tissues, often outperforming traditional techniques in terms of speed and accuracy. Early detection through such automated systems can lead to improved outcomes, enabling timely interventions. Figure 1.2 shows each phase in the cancer detection process.

Raw data often contains noise, missing values, or irrelevant features. Preprocessing involves handling these issues to ensure high-quality data. Relevant features from the

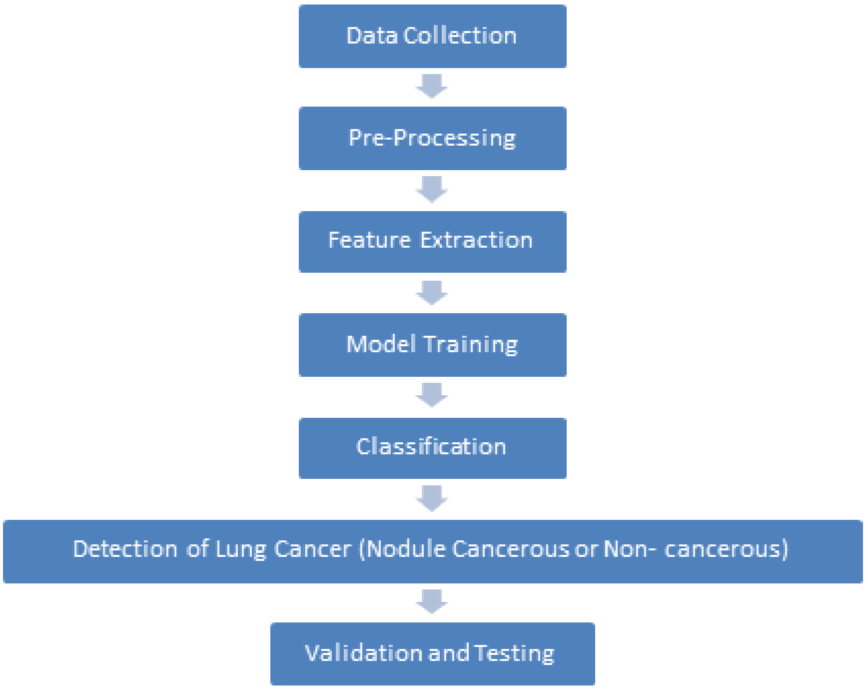

Figure 1.2: Steps Involved in Detecting Lung Cancer

dataset such as texture, shape, and intensity of lung nodules are extracted using image processing techniques or DL models [7]. Machine Learning (ML) or Deep Learning (DL) Algorithms are used to train on the extracted features to classify whether a lung nodule is malignant or benign. Data mining techniques like k-fold cross-validation are employed to evaluate the model's performance [8].

1.2 Overview of Healthcare Data Analytics

Healthcare data analytics represents a significant advancement in the ability of healthcare providers to utilize data for improved patient outcomes and operational efficiency. As the healthcare sector transitions to a more data-driven approach, understanding the types and sources of healthcare data becomes crucial. The role of data analytics extends beyond mere data collection; it encompasses sophisticated techniques that transform raw data into meaningful insights that can drive clinical decisions, enhance patient care, and optimize healthcare delivery systems.

Healthcare data encompasses a broad range of information generated through various processes within the healthcare ecosystem. This data can originate from numerous sources, including electronic health records (EHR), medical imaging systems, wearables, laboratory results, and patient surveys [9]. As healthcare becomes increasingly digitized, the volume and variety of data generated continue to expand rapidly, leading to what is commonly referred to as big data in healthcare [10].

Big data in healthcare can be defined by the "three Vs": volume, variety, and velocity. The volume of healthcare data is immense, with millions of patients generating countless data points through their interactions with healthcare providers. The variety of data types is extensive [11]. Finally, the velocity of data refers to the speed at which data is generated and analyzed, necessitating real-time analytics capabilities.

The effective analysis of healthcare data can lead to numerous benefits, including enhanced patient safety, reduced costs, improved operational efficiency, and better decision-making. Data analytics enables healthcare organizations to identify trends, make predictions, and develop targeted interventions, ultimately improving patient outcomes.

1.2.1 Importance of Data Mining in Healthcare

Data mining is the practice of using a variety of analytical approaches to huge databases in order to find patterns, trends, and insightful information. In the context of healthcare, data mining serves as a powerful tool for extracting meaningful information from EHRs, clinical databases, and other healthcare-related data sources. As the healthcare industry increasingly adopts digital technologies, data mining plays a pivotal role in transforming raw data into actionable insights that can improve patient care and streamline operational efficiency.

The digitalization of healthcare has resulted in the accumulation of data, often unstructured and heterogeneous, which presents a significant challenge for healthcare professionals. Data mining algorithms facilitate the extraction of valuable information from these complex datasets, allowing for improved decision-making, resource allocation, and personalized treatment plans. Furthermore, the use of data mining techniques enables healthcare organizations to identify trends, monitor disease outbreaks, and evaluate the effectiveness of interventions, ultimately enhancing the overall quality of care.

Data mining involves a series of processes that transform raw data into valuable information. Each of these techniques serves distinct purposes in healthcare analytics:

- **Clustering** identifies groups of similar patients or conditions, allowing for targeted interventions and personalized care.

- **Classification** assigns patients to predefined categories based on their health data, facilitating early diagnosis and treatment decisions.
- **Regression** analyzes the relationships between variables, helping healthcare professionals understand how different factors impact health outcomes.
- **Association rule mining** uncovers hidden relationships between variables, which can be crucial for identifying patterns in disease progression.

The significance of data mining techniques in healthcare cannot be overstated. As healthcare systems face mounting pressures to improve patient care while controlling costs, data mining provides actionable insights that can lead to informed decision-making and effective interventions.

Applications of Data Mining in Healthcare

The applications of data mining in healthcare are diverse and extensive. One of the most prominent applications is in predictive medicine, where data mining algorithms are used to forecast disease outbreaks, predict patient outcomes, and identify high-risk patients. By analyzing historical data, healthcare providers can implement proactive measures to mitigate risks, allocate resources efficiently, and improve patient safety.

Another critical application of data mining is in customer relationship management (CRM) within healthcare organizations. By leveraging patient data, healthcare providers can enhance their understanding of patient preferences and behaviors, leading to improved patient engagement and satisfaction [12]. Data mining techniques can also be used to identify trends in patient feedback, enabling organizations to address concerns and improve service delivery.

Moreover, data mining plays a vital role in fraud detection and prevention within the healthcare system. By analyzing billing patterns, data mining algorithms can identify anomalies and flag potential fraudulent activities. This application is particularly crucial in combating healthcare fraud, which costs the industry billions of dollars annually.

In addition to these applications, data mining is instrumental in monitoring healthcare quality and evaluating the efficiency of various therapies. By analyzing treatment

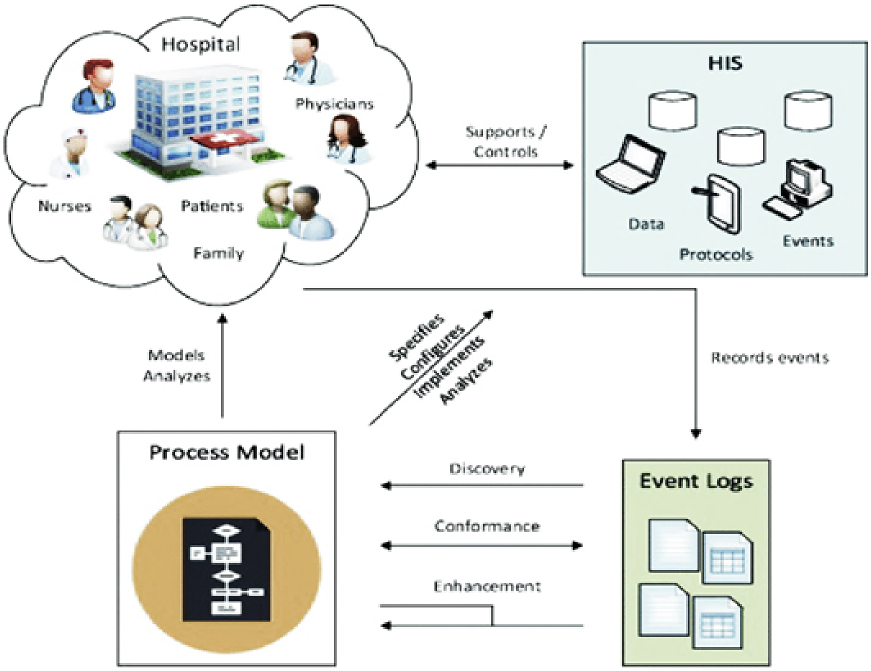

Figure 1.3: Healthcare Mining Analysis

outcomes [13, 14] as per Figure 1.3, healthcare providers can determine the effectiveness of different interventions.

Challenges in Data Mining

While data mining offers significant advantages in healthcare, it is essential to address several challenges and considerations. These include data privacy and security concerns, data problems are good and experts are needed to analyze and interpret data patterns.

1. **Data Privacy and Security** The increasing use of data mining methods [15] has raised concerns about patient privacy and data security. Healthcare organizations have a legal obligation to comply with Health Insurance Portability and Accountability Act (HIPAA) rules and safeguard patient data. The proper governance of data and the use of encryption mechanisms are essential to implement effective safeguards for patient data.

2. **Data Quality** Data mining techniques generally yield better results when samples are taken from high-quality data [16]. Faulty conclusions can lead to incorrect data, which are not consistent and not complete, making the decision-making

process difficult. This can include prescriptive levels to enhance data cleaning and preprocessing.

3. **Skilled Professionals** The proper implementation of data mining techniques requires trained personnel with backgrounds in data analytics, statistics, and medicine [17]. Data mining, as a powerful approach to analyzing and leveraging data, can contribute significantly to the advancement of healthcare by transforming the contemporary nature of patient care and providing insights for enhancing operational efficiencies.

4. **Lack of Explainability** ML and DL models, particularly deep neural networks, tend to be "black boxes" in that they provide predictions without revealing how they reached them. Because of this lack of transparency, it is hard for clinicians to trust or defend the model's decision in a clinical context [18].

5. **Bias and Fairness** AI models trained on unbalanced data can perform poorly for certain populations, leading to unequal treatment. These kinds of biases may worsen already existing health inequities.

6. **Generalizability and Validation** Models that perform well in controlled environments may fail in real clinical settings. To ensure consistent performance, AI systems need thorough testing and validation across diverse real-world scenarios.

1.3 Machine Learning and Deep Learning in Healthcare

The integration of ML and DL techniques into healthcare has transformed the landscape of disease prediction and diagnosis. As vast amounts of healthcare data continue to grow, the need for sophisticated analytical methods becomes increasingly important. ML is a form of artificial intelligence (AI) that generates algorithms capable of learning from data samples and making predictions based on them. A subset of neural networks with several layers used to examine intricate patterns in huge datasets is called deep learning. It has found its best applications in image and speech recognition tasks. In healthcare, these techniques are applied to predict diseases, detect anomalies, and support medical decision-making, ultimately leading to improved patient outcomes.

1.3.1 Machine Learning for Disease Prediction

ML encompasses a range of algorithms designed to analyze data, learn from it, and make predictions. Figure 1.4 represents various different approaches in machine learning. Common techniques used in healthcare include:

- **Supervised Learning:** This method uses labeled datasets, to train algorithms. This group includes algorithms such as random forests, logistic regression, decision trees, and SVM.

- **Unsupervised Learning:** When the algorithm has to find patterns or groupings within the data samples and the data is unlabeled, this method is employed. To find hidden links, methods like association rule mining and clustering are frequently used.

- **Reinforcement Learning:** This technique involves training algorithms through trial and error, with rewards given for successful outcomes. While less common in healthcare, it has applications in optimizing treatment plans and patient management.

1.3.2 Deep Learning for Disease Prediction

Deep learning is built on top of neural networks which are computing systems that are modeled loosely after human brain architecture. More specifically, these neural networks have multiple layers which modify the input samples through processes. The following are key DL methods applied to medicine:

- **Convolutional Neural Networks (CNNs):** CNNs are a type of deep neural network that is often used to analyze visual images and are particularly good at processing medical images like MRIs, X-rays, and CT scans. They automatically discover what features should be engaged from images of different diseases to correctly identify those illnesses.

- **Recurrent Neural Networks (RNNs):** These are designed to process sequences and so is well-suited for time series analysis as well. They analyze data of patients monitoring and predict the disease progress in upcoming times.

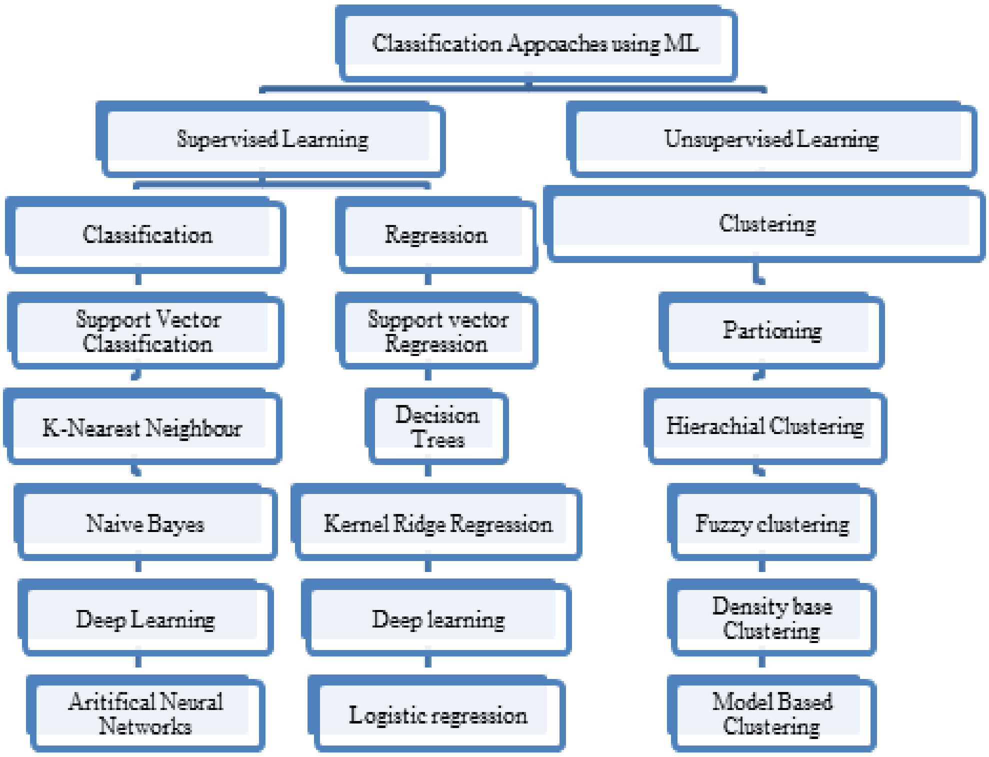

Figure 1.4: Classification of Machine Learning Techniques.

- **Generative Adversarial Networks (GANs):** GANs have two distinct neural networks, which are a generator and a discriminator, and are trained in a way that they compete with each other. They have been helpful in data augmentation, particularly in medical imaging, where we often have small datasets to train models.

1.4 Motivation for Research

In recent years, the healthcare industry has witnessed a significant surge in the generation and availability of data, driven largely by advancements in technology and the digitization of medical records. Despite the tremendous potential of this data, existing healthcare analytics techniques have not fully capitalized on it, leading to various research gaps and limitations in traditional methods.This section highlights the motivations for pursuing innovative solutions, and the anticipated benefits of adopting advanced ML and DL models to enhance healthcare outcomes.

1.4.1 Motivations for Exploring Advanced Machine Learning and Deep Learning Models

The limitations of traditional healthcare analytics techniques underscore the need for advanced ML and DL models. By addressing existing research gaps, these innovative approaches promise to enhance predictive accuracy, operational efficiency, and patient care.

1. **Enhancing Predictive Accuracy:** One of the main motivations for using ML and DL models is to improve the accuracy of disease diagnosis and treatment outcomes. Researchers aim to create models with greater predictive power by leveraging advanced algorithms that can analyze large amounts of data.

   For instance, deep learning techniques, particularly CNNs, have shown remarkable success in analyzing medical images. These models can learn hierarchical features from images, allowing them to achieve higher accuracy rates in diagnosing conditions such as cancer or cardiovascular diseases compared to traditional image analysis methods.

2. **Improving Efficiency in Healthcare Delivery:** In addition to enhancing predictive accuracy, advanced ML and DL models can significantly improve the efficiency of healthcare delivery. The ability to process large datasets quickly and make real-time predictions allows healthcare providers to streamline operations and optimize resource allocation.

   For example, machine learning algorithms can analyze patient data to identify trends in hospital admissions, enabling hospitals to allocate resources more effectively. Forecast models predict patient numbers, allowing healthcare organizations to adjust staffing levels and reduce patient wait times.

3. **Facilitating Personalized Medicine:** As healthcare shifts towards personalized medicine, advanced machine learning and deep learning models play a pivotal role in tailoring treatment plans to individual patients. By analyzing genetic, clinical, and lifestyle data, these models can help healthcare providers identify the most effective treatments for each patient.

For instance, ML techniques have been successfully applied to predict responses to cancer therapies based on a patient's genetic makeup. By leveraging patient-specific data, healthcare providers can design targeted treatment plans, minimizing adverse effects and enhancing treatment efficacy.

4. **Addressing the Challenge of Data Complexity:** The complexity of medical records poses a major challenge to traditional diagnostic procedures. Advanced ML and DL are specifically designed to address this challenge. For example, DL models can extract relevant features from raw data, reducing the need for manual selection and enabling data analysis. Images, text, and data structures, among many others.

1.4.2 Research Gaps in Existing Healthcare Analytics Techniques

Despite the advancements in healthcare analytics, several research gaps remain that warrant exploration. Identifying and addressing these gaps can lead to more effective machine learning and deep learning applications in healthcare.

1. **Limited Generalizability of Models:** Many existing models are trained on specific datasets, which may not be representative of broader patient populations. This limitation can affect the generalizability of models when applied to new populations or settings. There is a need for research that focuses on developing models capable of adapting to diverse populations and contexts.

2. **Insufficient Data Integration:** Healthcare data often resides in silos, with different systems and formats hindering comprehensive analysis. Integrating data from multiple sources—such as EHRs, wearable devices, and genomics—poses a significant challenge.

3. **Interpretability and Trust:** As ML and DL models become more complex, the issue of interpretability becomes increasingly important. Future research should focus on developing interpretive models to gain insight into decision-making processes.

1.5 Research Objectives

The overarching aim of this research is to explore and enhance the use of data mining techniques, ML, and DL algorithms in the healthcare sector. Through a detailed analysis of various methodologies and their applications, this study seeks to contribute to the improvement of patient care, disease prediction, and treatment strategies. The following objectives outline the specific goals to be accomplished through this research:

1. To study data mining techniques used by healthcare organizations to build inferences concerning patient health.
2. To implement procedures to precisely recognize diseases via examining symptoms and other relevant medical factors.
3. To build a consumer focused integrated model in relevance with evaluation parameters intended to provide the right care and right living pathway.
4. To perform predictive analysis of Respiratory diseases so that individual patients can be better treated.

1.6 Thesis Contribution

The thesis contribution is mentioned as per the following:

- *To study data mining techniques used by healthcare organizations to build inferences concerning patient health.*
    1. A thorough literature review has been conducted to identify existing data mining methods that are currently in use within the healthcare domain.
    2. The review highlights the advantages and limitations of different methods, providing a comprehensive understanding of their applicability in different healthcare scenarios.
    3. Assess the impact of data mining on patient care, focusing on predictive analytics and decision support systems.
- *To implement procedures to precisely recognize diseases via examining symptoms and other relevant medical factors.*

    1. Compared nine machine learning classifiers based on multiple evaluation metrics.The top-performing classifiers were selected for further optimization and integration into the final ensemble model.
    2. Evaluated classification models using accuracy, recall, precision,and F1-score to ensure effective disease identification.

- *To build a consumer-focused integrated model in relevance with evaluation parameters intended to provide the right care and right living pathway.*
    1. Designed a comprehensive framework using data mining and machine learning to deliver personalized care plans based on patient-specific information.
    2. To enhance feature extraction integrated K-Means clustering with fuzzy logic, leading to improved model performance evaluated through metrics such as precision, accuracy, recall,and F1-score.
    3. Implemented a voting classifier ensemble with majority voting to combine predictions from multiple models, and further enhanced predictive power through grid search-based hyperparameter tuning.
- *To perform predictive analysis of Respiratory diseases so that individual patients can be better treated.*
    1. Integrated model was introduced using DenseNet201, EfficientNet B7, VGG16, MobileNet, and VGG19 to accurately predict lung cancer using a multiclass dataset.
    2. The Elastic Transformation augmentation approach was applied to the dataset with significant class disparity.
    3. The performance of the model was assessed against the individual model.
    4. An Ensemble Reinforcement Learning framework was proposed to continuously enhance prediction accuracy and reliability.

The objectives outlined above represent a comprehensive framework for the proposed research work in healthcare analysis. By studying data mining techniques, implementing accurate disease recognition procedures, developing a consumer-focused integrated model, and performing predictive analyses of respiratory diseases, this research aims to advance the application of data science in healthcare sets. Through these efforts, the study aspires to contribute to the enhancement of patient care, the optimization of treatment strategies, and the overall improvement of healthcare systems.

1.7 Thesis Organization

The thesis is structured to provide a comprehensive overview of the role of machine learning and deep learning in healthcare analytics, with a particular focus on lung cancer detection and multi-disease prediction. The organization of the thesis is designed to guide the reader through a logical progression of research objectives, methodologies, and findings, highlighting the significance of each chapter in contributing to the overall aim of improving healthcare outcomes through advanced data mining techniques. The structure of the thesis and its dependencies are shown in Figure 1.5.

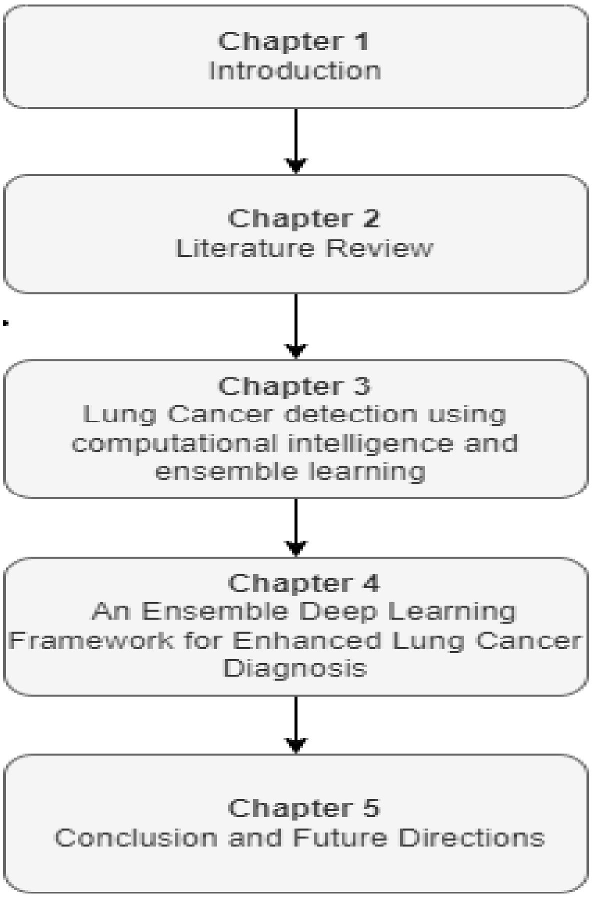

Figure 1.5: Chapter Wise Thesis Organization

Chapter 2 provided an extensive review of existing research in healthcare analytics and compares various data mining algorithms, highlighting their strengths and weaknesses in healthcare applications. Chapter 3 detailed the methodologies employed in the research, specifically focusing on machine learning techniques for disease prediction. Chapter 4 presented the research methodology used for developing deep learning models, including preprocessing techniques, architecture selection, and data augmentation strategies. It emphasized the role of ensemble techniques in improving diagnostic accuracy. Chapter 5 encapsulates the key findings of the research, emphasizing the contributions made to healthcare analytics and also explored future research directions. In detail, the organization of the thesis is as follows:

- Chapter 2 provides an extensive review of existing research in healthcare analytics. It also compares various data mining algorithms, highlighting their strengths and weaknesses in healthcare applications. This chapter is partially derived from:

  - ∗ **Richa Jain,** Devendran V., “Data Mining Algorithms in Healthcare: An Extensive Review”, *Fifth International Conference on I-SMAC (IoT in Social, Mobile, Analytics and Cloud) (I-SMAC)* (Published), 2021. (Scopus)

- – Chapter 3 presents an innovative approach therapy prototype that optimizes resource use through computational intelligence. We proposed a novel IOMT-based framework that is consumer-focused, designed to enhance patient care, integrating Logistic Regression, MLP Classifier, Gaussian NB, and intelligent feature selection using K-Means and Fuzzy Logic. Ensemble learning with a voting classifier and hyperparameter tuning further improves performance. This chapter is derived from:

  - ∗ **Richa Jain,** Parminder Singh, Mohamed Abdelkader, and Wadii Boulila, “Efficient lung cancer detection using computational intelligence and ensemble learning”, *PloS one* (Published), 2024. (Scopus, SCIE 2.9 IF)
  - ∗ **Richa Jain,** V. Devendran, and Parminder Singh, “Evaluation of Machine Learning Classifiers for Multiple Disease Prediction.”, *Computer Science Engineering and Emerging Technologies: Proceedings of ICCS* (Published), 2024.

- – Chapter 4 introduces a new framework that combines deep learning with RL to improve the accuracy of CT scans for lung cancer diagnosis. This chapter is derived from:

  - ∗ **Richa Jain,** Parminder Singh, and Avinash Kaur, “An Ensemble Reinforcement Learning-Assisted Deep Learning Framework for Enhanced Lung Cancer Diagnosis”, *Swarm and Evolutionary Computation* (Published), 2024. (Scopus, SCIE 8.2 IF)

- – Chapter 5 presents the conclusion of the thesis finding and introduces the possible future directions.

CHAPTER 2

LITERATURE REVIEW

Lung cancer remains a significant public health challenge, being one of the leading causes of cancer-related deaths worldwide. To improve patient outcomes and survival rates, lung cancer must be detected early and diagnosed accurately. Recent developments in DL and ML methods have demonstrated enormous promise for transforming the healthcare industry, especially in the diagnosis and treatment of illnesses like lung cancer. By leveraging the power of ML algorithms and deep learning models, researchers and clinicians can analyze vast amounts of medical data, such as imaging scans, genetic profiles, and patient records, to develop innovative and accurate tools for early detection, prognosis, and personalized treatment of lung cancer. This literature aims to explore the application of machine learning, deep learning, and reinforcement learning in the context of cancer prediction, highlighting the potential benefits, challenges, and future directions in utilizing these technologies to combat this deadly disease.[1] *[19].*

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[1] This chapter is partially derived from:

R. Jain and D. V, "Data Mining Algorithms in Healthcare: An Extensive Review," 2021 Fifth International Conference on I-SMAC (IoT in Social, Mobile, Analytics and Cloud) (I-SMAC), Palladam, India, 2021, pp. 728-733, doi: 10.1109/I-SMAC52330.2021.9640747.

2.1 Machine Learning in Healthcare

Over the past few decades, data mining—a potent method for gleaning important information from massive datasets—has seen substantial development, especially in the healthcare industry. As the volume of healthcare data has exponentially increased due to advancements in technology and digitalization, the need for sophisticated data mining methods has become paramount. This section provides an overview of data mining applications in healthcare, tracing the development from early rule-based systems to the modern ML and DL methods employed today.

ML provides creative ways to enhance patient outcomes, optimize treatment plans, and expedite clinical procedures. By harnessing the power of advanced algorithms and computational models, ML enables healthcare professionals to analyze vast amounts of complex data, identify patterns, and make more accurate predictions in diagnosis, treatment planning, and disease management. In the context of lung cancer, ML techniques have shown great promise in enhancing early detection, predicting patient prognosis, and personalizing treatment regimens. The integration of machine learning in healthcare holds the potential to revolutionize medical research and practice.

Shamrat et al. [17] explored the use of ML for predicting breast diseases, including cancer. Algorithms like SVM, KNN,logistic regression, decision trees, random forest, and naive Bayes were evaluated. The SVM model demonstrated the best performance, with an accuracy of 97.07% in breast disease prediction.

Ed-daoudy et al. [20] presented a real-time health prediction system using big data technologies. By applying a distributed machine learning model via Spark streaming and Kafka, it transformed the standard decision tree (C4.5) into a scalable and efficient version for processing streaming data. The system predicted health status from various disease sources, sends alerts to caregivers, and stores results in a distributed database for further analytics. Performance evaluation shows Spark's decision tree outperforms traditional tools like Weka in terms of throughput and execution time, demonstrating its ability to handle real-time, large-scale medical data effective

Vinitha, S et al. [9] The proposed system provided machine learning algorithms for predicting disease occurrences in high-risk communities, using real-life hospital data. To handle incomplete data, a latent factor model was used to reconstruct missing information. Experiments focused on cerebral infarction, utilizing both structured and unstructured hospital data. Machine Learning Decision Tree and MapReduce algorithms were applied, marking one of the few works to address both data types in medical big data analytics. The system outperformed the CNN-based Unimodal Disease Risk Prediction (CNN-UDRP) algorithm in terms of convergence speed and prediction accuracy, achieving 94.8%.

Revathy et al. [21] studied the performance of algorithms such as SVM,Random Forest, decision tree, and Naive Bayes on chronic kidney disease(CKD)dataset.

V. Mounika et al. [22] used ML algorithms to predict type-2 diabetes based on various risk factors. The algorithms tested included logistic regression, and random forest. The LR model achieved the highest accuracy of 97% in predicting type-2 diabetes.

Dahiwade. D et al. [23] proposed a system that predicted general diseases based on patient symptoms using K-Nearest Neighbor (KNN) and CNN algorithms. It used a symptom dataset and considered patient habits and checkup details for accuracy. CNN achieved an accuracy of 84.5%, outperforming KNN, which also required more time and memory than CNN.

Reddy et al. [24] used the Cleveland Heart data, ten learning machines classified by Bayesian, functional, lazy, meta, rule, and tree clustering were trained to predict heart disease risk. Classifications were tested using the full set of methods and optimized methods from our measured behavior, using 10-fold cross-validation. Hyperparameter tuning was performed on the IBk classifier by adjusting the number of nearest neighbors. The sequential minimal optimization (SMO) classifier achieved 85.14% accuracy.

Bharathy S et al. [25] primarily used multi-stage classification, including data enhancement and segmentation. Segmentation was performed using thresholding, marker-controlled watershed, and binary classifiers. Various algorithms like Random Forest, Support Vector Machine (SVM),Logistic Regression, KNN, Decision Tree, and Naïve Bayes were used for training the dataset, with Random Forest achieving the highest performance.

Mohan K. et al. [26] developed an accurate learning model for early lung cancer prediction using different populations and treatment regimens. Different ML techniques were used. The Random Forest model outperformed the others, achieving an accuracy of 90.32%.

Modak C. et al. [27] aimed to develop machine learning algorithms to assist physicians in determining the appropriate diagnosis level for lung cancer patients, reducing unnecessary treatment and costs. XGBoost achieved the highest accuracy of 95.92%, followed by Random Forest (93.32%), Decision Tree (91.50%), Naïve Bayes (90.32%), and Logistic Regression (57.41%).

2.2 Deep Learning in Healthcare

Deep learning has emerged as a transformative force in the field of healthcare, particularly in the area of disease prediction. This section delves into the role of deep learning models in disease prediction, emphasizing their unique strengths and applications.

Deep learning is a branch of machine learning that uses neural networks with multiple layers (hence the term "deep") to analyze large datasets. These networks are designed to recognize and extract features from raw data, allowing them to perform complex tasks like image recognition, natural language processing, etc.In healthcare, deep learning has proven particularly effective in handling unstructured data, which comprises a significant portion of the information generated in clinical settings.

C.Wang et al. [28] investigated CT images from 1,222 patients across three medical institutions. The pathological labels were categorized into 2, 3, and 8 classifications. A modified ResNet-34 deep learning network, combined with radiomics strategies, was used for the classification task. The deep radiomics algorithm achieved an internal accuracy of 0.8776 for the 2-category classification and 0.8061 for the 3-category classification, while the AUC for the 8-category classification ranged from 0.739 to 0.940. Additionally, the prognostic model achieved a C-index of 0.892.

Seyrek, E. C. et al. [29] conducted a comparative analysis of various activation functions and optimizers. Six robustness enhancements (LReLU, Mish, PReLU, ReLU, Swish, and Sigmoid) and four smoothing enhancements (Adam, Adamax, Nadam and RMSProp) were tested on CNN models using two datasets Indian Pines and WHU-. The results show that the CNN model using the Adamax optimizer and Mish optimization function achieves the highest accuracy with 98.32% accuracy for Indian Pines dataset and 97.54% accuracy for WHU Hi HongHu dataset.

Sungyeup Kim et al. [30] proposed a deep learning method utilizing transfer learning to classify lung diseases in chest X-ray (CXR) images. Experiments were conducted on three classes (normal, pneumonia, and pneumothorax) using the U.S. National Institutes of Health (NIH) dataset, yielding validation results of loss = 0.6933, accuracy = 82.15%. Additional experiments on the Cheonan Soonchunhyang University Hospital (SCH) dataset, which included four classes (normal, pneumonia, pneumothorax, and tuberculosis), achieved validation results of loss = 0.7658, accuracy = 82.20%.

Alshmrani, G. M., et al. [31] proposed a deep learning architecture for multi-class classification of different diseases. A pre-trained VGG19 model was utilized, followed by three CNN blocks for feature extraction and classification. Results showed that the VGG19 + CNN model achieved 96.48% accuracy, significantly enhancing diagnostic efficiency for healthcare practitioners.

Tan, Mingxing et al. [32] proposed a scaling method that uniformly scaled all dimensions of depth, width, and resolution using a compound coefficient. This method was applied to MobileNets and ResNet, enhancing their scalability. Additionally, a baseline network was designed through neural architecture search, resulting in the EfficientNet family. EfficientNet-B7 achieved 84.3% top-1 accuracy on ImageNet, being 8.4x smaller and 6.1x faster than prior ConvNets. It also transferred well to datasets like CIFAR-100 (91.7%) and Flowers (98.8%), using significantly fewer parameters.

Shandilya et al. [33] aimed to develop a CAD method to classify histopathological images of lung tissues. Multi-scale processing was applied for image feature extraction. Seven pre-trained CNN models were compared for lung cancer classification. After hyper-tuning various factors, ResNet 101 achieved the highest accuracy at 98.67%.

R. Pandian et al. [34] aimed to detect abnormal lung tissue growth using a highly accurate detection tool. It analyzed lung images from healthy and malignant individuals, developing databases for various CT scan views (axial, coronal, sagittal). Neural networks based on image texture were used to classify normal and malignant tissues. CNN and GoogleNet deep learning algorithms were proposed to improve detection, utilizing the VGG-16 architecture. The method achieved a precision of 98% in detecting and classifying lung cancer.

Al-Yasriy et al. [35] introduced a computer-aided system for detecting lung cancer using a convolutional neural network with the AlexNet architecture. The model achieved 93.55% accuracy, with a sensitivity of 95.71% and specificity of 95%.

Priya and Bharathi [36] proposed a deep learning model that combines SE-ResNeXt-50 and CNN to improve lung cancer classification using CT images. The model leverages advanced feature extraction, QDHE-based preprocessing, and data augmentation, achieving 99.15% accuracy and high performance across metrics. Notable advantages include precise classification, robust generalization, and enhanced feature learning. However, drawbacks involve high computational demand and limited clinical validation, potentially affecting its real-world applicability.

Vadala et al. [37] proposed SpiLenet, a deep learning-based hybrid framework that integrates SpinalNet and LeNet for lung cancer detection and severity classification using CT scans. The model employs advanced pre-processing, DRINet for segmentation, and a fuzzy logic layer for improved decision-making. Key advantages include high detection accuracy 92.10%, effective segmentation, and reduced computational overhead. However, limitations involve reliance on large annotated datasets and the absence of clinical deployment, which could restrict its practical implementation.

Yagappan et al. [38] introduced a hybrid framework, T-RGB, combining attention-based CNNs, Vision Transformers, and a novel Gooseneck Barnacle Optimization algorithm for enhanced lung cancer classification. The model effectively captures critical spatial features using attention-enhanced convolution layers and classifies them through a Vision Transformer, which excels at modeling global dependencies in medical images. GBO is employed for efficient hyperparameter tuning, accelerating convergence and boosting performance. The model was tested on histopathological and CT scan datasets, achieving 99.61% accuracy. Its strengths include innovative integration of transformer architecture, biologically inspired optimization, and strong generalization across datasets. However, weaknesses include reliance on high computational resources, lack of clinical validation, and limited explainability in real-world deployment of AI in healthcare.

Table 2.1 explains the comparative analysis of various machine learning and deep learning techniques for the cancer prediction used in the literature. Findings from the existing research include: dataset used, the techniques/methodology applied, and major findings which leads the researchers to solve existing problems.

Table 2.1: Summary of the Relevant Literature on Machine Learning and Deep Learning Methods.

Author and Year	**Technique Used**	**Dataset**	**Observations**
Nageswaran S, et al. [39] (2022)	Artificial Neural Network (ANN), KNN, and RF	Dataset of 83 CT pictures from 70 individual patients.	ANN outperformed other machine learning techniques in accuracy for lung cancer detection.

V. Durga Prasad Jasti, et al. [40] (2022)	Geometric mean filter, AlexNet, Relief algorithm, KNN, LS-SVM, NB, and Random Forest	MIAS database of 322 mammograms from 161 patients.	LS-SVM achieved the highest accuracy, while KNN exhibited superior sensitivity and specificity for breast disease detection.
Wang J, et al. [28] (2021)	Chest CT imaging with MPP and mixed infections of MPP and streptococcal pneumonia (SP)	Pediatric chest CT scans from the MPP group	CT scans reveal differences between MPP and MPP+SP co-infections, with more lung abnormalities in the MPP group.
C. Anil Kumar, et al. [41] (2022)	SVM for lung cancer prediction	UCI Lung Cancer dataset with 32 instances and 57 features	SVM classifier, especially with SMOTE resampling, showed superior accuracy, precision, recall, and F1-score.
Dritsas, E.; Trigka, M. [42] (2022)	Naive Bayes, Bayesian Network, Stochastic Gradient Descent, SVM, Logistic Regression, ANN, KNN, Decision Trees, Random Forest, Rotation Forest, RepTree, and AdaBoostM1	Dataset of 309 participants and 15 features	Rotation Forest (RotF) model outperformed others with an accuracy of 97.1%.
Vani Rajasekar, et al. [43] (2023)	Inception V3, CNN, CNN GD, Resnet-50, VGG-16, and VGG-19	Dataset comprising CT and histopathological images	CNN GD model achieved the highest accuracy of 97.86%.
Deepapriya, et al. [44] (2023)	MSD-NET deep learning model	Chest X-rays and CT scans	MSD-NET demonstrated superior performance compared to other models.

Hanaoka, J., et al. [45] (2021)	Dynamic Perfusion Digital Radiography, Pulmonary Perfusion Scintigraphy, and Spirometry	52 individuals included, specific dataset details not disclosed	Dynamic perfusion digital radiography effectively matched with scintigraphy and spirometry for post-surgical risk predictions.
KMA Alheeti et al. [46] (2024)	Transfer learning models for deep learning classification.	Chest CT-Scan dataset used for analysis.Focused on CT scan images for lung cancer detection.	MobileNetV2 achieved highest accuracy of 98%.SVM model achieved overall accuracy of 89%.

2.3 Ensemble Learning and Reinforcement Learning in Healthcare

The advent of machine learning in healthcare has led to significant advancements in diagnostic accuracy and patient care. Among the various approaches used in this domain, ensemble learning and reinforcement learning have emerged as powerful techniques that enhance the performance of predictive models. Ensemble learning is a machine learning paradigm that combines multiple models to improve predictive performance compared to individual models. By aggregating the predictions of various classifiers, ensemble methods can reduce variance, bias, and improve accuracy. Common ensemble techniques include Bagging (Bootstrap Aggregating), Boosting, and Stacking, each employing different strategies to combine the strengths of individual models.

Reinforcement learning (RL)is an ML method in which an agent gradually learns to make decisions via its environment interaction. In the form of feedback, it receives of its behavior but learn to act in a way to maximize a goal in the presence strategies over time. RL has also been successful in many other applications, such as the healthcare domain, from where it can be used to optimize decision-making processes. This section reviews the integration of ensemble learning and reinforcement learning in healthcare applications, emphasizing their contributions to improving diagnostic accuracy, robustness, and overall healthcare delivery.

2.3.1 Techniques of Ensemble Learning

1. **Bagging:** Bagging is an ensemble method where many models are trained independently on different subsets of the data. Typically, this subset is created by bootstrapping-sampling with replacement.

   Application in Healthcare: Bagging techniques, such as Random Forests, have been widely used in healthcare for disease prediction tasks. For instance, Random Forests have been employed to predict the onset of diabetes by aggregating the predictions of numerous decision trees, leading to improved accuracy and reduced overfitting compared to single decision trees.

2. **Boosting:** Boosting is another ensemble method that combines weak learners sequentially, where each new model is trained to correct the errors of the preceding ones. This process emphasizes misclassified instances, allowing the ensemble to focus on challenging cases.

   Application in Healthcare: Gradient Boosting Machines (GBM) and AdaBoost are common boosting techniques used in healthcare. For example, GBM has been effectively applied in predicting cardiovascular disease risk by improving classification accuracy through iterative training, which accounts for previously misclassified cases.

3. **Stacking:** Stacking involves training multiple models and combining their predictions using a meta learner (usually a simple model) that uses the results of the base models as input.

   Application in Healthcare: Stacking has been utilized in complex diagnostic tasks where different models provide unique strengths. For instance, a combination of neural networks and traditional classifiers can enhance lung cancer prediction accuracy, leveraging the strengths of both deep learning and statistical methods.

2.3.2 Overview of Reinforcement Learning

Reinforcement learning is an ML technique in which an agent learns to make decisions by interacting with its environment. It receives feedback in the form of rewards or punishments based on its behavior, which allows it to learn better strategies over time. Reinforcement learning holds promise in a variety of applications, including healthcare, where it can facilitate decision-making processes.

Applications of Reinforcement Learning in Healthcare

1. **Treatment Recommendations:** RL has been applied to develop personalized treatment recommendations for patients based on their individual responses to previous treatments. For instance, RL algorithms can analyze patient data to recommend optimal medication dosages or therapies, considering both short-term and long-term health outcomes.

   Case Study: A study utilized reinforcement learning to personalize treatment for chronic conditions such as diabetes. By leveraging patient data on glucose levels and treatment responses, the RL model optimized insulin administration, resulting in improved glycemic control and patient satisfaction.

2. **Resource Allocation:** RL can be employed to optimize resource allocation in healthcare systems, particularly in emergency departments or intensive care units. RL algorithms can dynamically adjust staffing, equipment usage, and patient assignments to maximize efficiency and minimize waiting times.

   Case Study: In a hospital setting, an RL approach was used to manage bed assignments. The model adapted to changing patient inflows and resource availability, significantly improving bed utilization rates and reducing patient wait times.

3. **Personalized Health Interventions:** RL enables the design of personalized health interventions by continuously learning from patient interactions. For instance, an RL framework can recommend lifestyle changes or monitoring strategies based on real-time health data, adjusting its recommendations as the patient's condition evolves.

> **Case Study:** A study explored the use of RL to provide personalized health coaching for weight management. By analyzing data on dietary habits, physical activity, and weight changes, the RL agent provided tailored recommendations, resulting in more effective weight loss outcomes for participants.

Xiao, Yawen et al. [47] proposed a deep learning-based ensemble method, combining outputs from five different classifiers trained on gene expression data. Differential gene expression analysis provided the most informative genes, which were input into the classifiers. The ensemble method, improved cancer prediction accuracy compared to single classifiers or majority voting methods.

Khalid El Asnaoui [48] evaluated single and ensemble learning models for classifying pneumonia. The ensemble models were fine-tuned versions of Inception-ResNetV2, ResNet50, and MobileNetV2. A new dataset of 6,087 chest X-ray images was compiled for comprehensive testing. Among single models, InceptionResNetV2 achieved a 93.52% F1 score. The ensemble of ResNet50, MobileNetV2, and InceptionResNetV2 outperformed other configurations, reaching an F1 score of 94.84%.

Talukder Md. Alamin et al. [49] introduced a hybrid ensemble feature extraction model to identify lung and colon cancer effectively. It combined deep feature extraction, ensemble learning, and high-performance filtering on the LC25000 histopathological lung and colon datasets. The results of the study show that this approach provides better results than existing models.

Yang J. et al. [50] presented an imbalance classifier centered on RL for training on highly imbalanced datasets, applicable to multi-class cases. Our approach was to combine dueling and double-deep Q-learning architectures with a custom reward function and episode-training process to support our multi-class imbalanced data. The framework, which used clinical case studies for testing purposes, yielded better results than existing imbalanced learning methods, leading to more balanced classification and leading to a substantial advance in predicting the minority class.

Wang L. et al. [51] proposed a Supervised Reinforcement Learning with Recurrent Neural Network framework, integrating supervised reinforcement learning with an RNN to effectively manage complex relationships among medications, diseases, and patient characteristics. The SRL-RNN utilized an off-policy actor-critic structure, where the "actor" adjusted its prescription decisions based on both indicator and evaluation signals to ensure optimal treatment and reduced mortality. RNN was employed to address the Partially-Observed Markov Decision Process (POMDP) challenges, handling real-world cases with incomplete data. Experiments on the MIMIC-3 dataset demonstrated that SRL-RNN could decrease estimated mortality and improve the accuracy of prescriptions in alignment with doctors' decisions.

Ausawalaithong, W et al. [52] investigated DenseNet-121, a 121-layer CNN, with a transfer learning approach to classify lung cancer using chest X-ray images. The model was pre-trained on a lung nodule dataset to address limited data availability, followed by training on the lung cancer dataset.

Ansari et al. [53] proposed a hybrid SVMVGGNet-16 model that combines deep learning (VGGNet-16) and machine learning (SVM) to classify lung cancer into four types (ADC, LCC, SCC, and Normal) using CT images. The model achieved high accuracy (96.72%) and AUC (96.87%), benefiting from precise feature extraction and strong classification synergy. Its notable merits include multi-class capability, robust preprocessing, and excellent performance across multiple metrics. However, key drawbacks involve dependence on a single dataset, limited modality coverage, and lack of clinical validation, which restrict generalizability.

G.Liang [54] presented a DL framework combined with segmentation and cross-correlation algorithms for the diagnosis of pneumonia in children. To address overfitting and degradation in deep models, residual structures were used, while dilated convolutions helped preserve feature space information as model depth increased. Transfer learning with pre-trained parameters mitigated the impact of limited data and structured noise. The method achieved good results, effectively handling low-resolution images and occlusions in children's chest X-rays, showing improvement over previous methods.

Vignesh Kumaran et al. [55] proposed an intelligent ensemble framework for lung cancer classification using CT images, combining models like VGG19, ResNet152V2, and EfficientNet with a fuzzy logic-based SALLC-NeT system. The model achieved high accuracy upto 96.69% across various subtypes, demonstrating improved early-stage nodule detection and reduced diagnostic errors. Strengths include robust ensemble modeling, enhanced feature extraction using fuzzy inference, and multi-dataset validation. However, limitations involve high computational complexity and a lack of explainability and real-world clinical validation, which may hinder direct clinical deployment.

Table 2.2 explains the comparative analysis of various ensemble learning and reinforcement learning techniques for the cancer prediction used in the the literature. Findings from the existing research include: dataset used, the techniques/methodology applied, and major findings which leads the researchers to solve existing problems.

Table 2.2: Summary of the Relevant Literature on Ensemble Learning and Reinforcement Learning.

Citation	**Dataset**	**Technique Used**	**Observations**
SP Venkatesh et al. [56] (2022)	Surveillance, Epidemiology and End Results (SEER) dataset used.	Ensemble methods in machine learning evaluated Bagging, Adaboost, K-Nearest Neighbours, Decision Tree, Neural Networks	Results affirm that ensemble methods are powerful tools for enhancing the accuracy of lung cancer survival predictions, emphasizing the need for careful data preprocessing and the potential for improved patient management in clinical settings
U Subashchandrabose et al. [57] (2023)	Kaggle cancer dataset.	Ensemble Federated Learning for multi-order lung cancer classification. Combines multiple models with distributed data for privacy.	Ensemble Federated Learning improves accuracy and generalization and achieved 89.63% accuracy in lung cancer classification.

J Zhou et al. [58] (2023)	1075 lung nodules with preoperative thin-section CT scans less than or equal to 30 mm and greater than or equal to 4 mm nodules.	Ensemble multi-view 3D convolutional neural network (EMV-3D-CNN) model is used to analyze preoperative thin-section CT scans for risk stratification	EMV-3D-CNN model achieves 91.3% diagnosis performance and outperforms doctors with 77.6% accuracy in risk stratification.
M Mamun et al. [59] (2022)	Survey dataset of 309 people with lung cancer. The dataset includes various health-related attributes.	Ensemble techniques: XGBoost, LightGBM, Bagging, AdaBoost. Oversampling SMOTE method for dataset enhancement.	XGBoost achieved 94.42% accuracy in predictions. Ensemble techniques improved lung cancer prediction accuracy.
D Hu et al. [60] (2022)	Real clinical dataset of 1848 postoperative NSCLC patients.	Ensemble learning with active sampling (ELAS) method. Active sampling queries informative samples for classifier training.	ELAS achieved 0.736 AUROC and 0.453 AUPRC values. Significant improvements over SVM, AdaBoost, and other methods.
MI Faisal et al. [61] (2018)	Benchmark dataset obtained from UCI repository.	Evaluated classifiers: SVM, C4.5, Multi-Layer Perceptron, Neural Network, Naive Bayes. Compared with ensembles: Random Forest and Majority Voting	Gradient-boosted Tree achieved 90% accuracy in predictions.

Y Wang et al. [62] (2024)	National Lung Screening Trial dataset used.	Optimal stopping approach using Snell envelope. Model-free deep reinforcement learning for diagnosis decisions.	EarlyStop-RL enhances lung cancer risk assessment and diagnosis. Surpasses Lung-RADS and Brock model performance in evaluations.
S Luo [63] (2023)	LIDC-IDRI dataset used.	LLC-QE model combines ensemble and reinforcement learning. Pre-training with Artificial Bee Colony algorithm utilized.	LLC-QE model achieves F measure of 89.8%. Reinforcement learning improves the classification of underrepresented classes.
J Balajee et al. [64] (2023)	Clinical data, MRI images, and X-rays utilized.	Adaptive Reinforcement Learning Model (ARLM) implemented. Deep transfer learning and feature extraction techniques used.	ARLM achieved 92% accuracy in lung cancer detection. False negative rate reduced with adaptive learning approach.
SK Shah et al. [65] (2024)	CT scans of individuals diagnosed with lung cancer stages	Deep learning with pre-trained CNN architectures for classification. Elastic transformation and data augmentation for preprocessing.	Achieved 98.19% accuracy using weighted CNN ensemble.
A Choudhary et al. [66] (2024)	Polymorphisms data of five XRCC1 SNPs.	Machine learning-based ensemble approach utilized for prediction. Input includes XRCC1 SNPs and smoking status data.	Ensemble model predicts lung cancer risk with 85% accuracy. The model outperforms individual models in evaluation parameters.

2.4 Summary

The existing literature on healthcare data analytics reveals significant gaps, particularly concerning high false-positive rates, limitations in model generalization, and the need for real-time decision-making frameworks. Addressing these challenges is crucial for enhancing the effectiveness of disease prediction models and improving patient outcomes in healthcare.

This thesis aims to fill these gaps by exploring advanced techniques that reduce false-positive rates, enhance model generalization, and develop real-time decision-making frameworks. By doing so, the research seeks to contribute to the growing body of knowledge in healthcare analytics and facilitate the integration of data-driven approaches into clinical practice. The findings from this thesis will not only advance the field of healthcare analytics but also ultimately enhance the quality of care provided to patients.

CHAPTER 3

LUNG CANCER DETECTION USING COMPUTATIONAL INTELLIGENCE AND ENSEMBLE LEARNING

Lung cancer emerges as a major factor in cancer-related fatalities in the current generation, and it is predicted to continue having a long-term impact. Detecting symptoms early becomes crucial for effective treatment, underscoring innovative therapy's necessity. In this chapter, we present an innovative approach therapy prototype that optimizes resource use through computational intelligence. We propose a novel IOMT based framework that is consumer-focused, designed to enhance patient care, integrating Logistic Regression, MLP Classifier, Gaussian NB, and intelligent feature selection using K-Means and Fuzzy Logic. Ensemble learning with a voting classifier and hyperparameter tuning further improves performance. The proposed model's performance is demonstrated through comparative analysis with existing NB, J48, and SVM approaches, achieving a 98.50% accuracy rate. This chapter highlights the potential of computational intelligence *and IoMT in developing efficient, cost-effective lung cancer therapies.*[1] *[68]*

3.1 Introduction

Machine learning (ML) has emerged as a cornerstone technology in healthcare analysis, providing innovative solutions to enhance diagnostic accuracy, predict patient outcomes, and improve overall healthcare delivery. The increasing availability of vast amounts of healthcare data—ranging from electronic health records (EHRs) to medical imaging—has necessitated the adoption of sophisticated analytical techniques. Lung cancer is a life-threatening disease that significantly impacts individuals and communities worldwide, leading to severe respiratory complications and a high mortality rate. Early detection is crucial in improving survival rates, making the identification of lung nodules—a potential precursor to lung cancer—a priority in medical diagnostics. With the increasing prevalence of lung nodules, the need for advanced techniques such as CAD systems has become more urgent. These systems, which leverage the power of Computed Tomography (CT) scans, utilize sophisticated X-ray technology to capture images from multiple angles.

Early detection of lung cancer is crucial so that effective treatment can be provided to improve the survival rate. Wheezing is the commonly observed symptom of lung-related cancer, which needs special care because of the reason of many individuals who have lung cancer also suffer from a chronic obstructive respiratory disorder, which is the primary cause of coughing. The characteristics behind the cough disease change, which is a critical pulmonary syndrome. Additionally, expectorating, discomfort in the chest, shortness of breathing process, anorexia, weight loss, fever, and bloody sputum are all signs as well as symptoms of lung cancer [69–71].

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[1] This chapter is derived from:

Richa Jain, Parminder Singh, Mohamed Abdelkader, and Wadii Boulila."Efficient lung cancer detection using computational intelligence and ensemble learning." PloS one 19.9 (2024): e0310882. (`https://doi.org/10.1371/journal.pone.0310882`) [67]. Jain, Richa, V. Devendran, and Parminder Singh. "Evaluation of Machine Learning Classifiers for Multiple Disease Prediction." Computer Science Engineering and Emerging Technologies: Proceedings of ICCS 2022 (2024): 401.

The conventional diagnostic methods, like X-rays and CT scans, provide detailed images but rely heavily on the expertise of radiologists, leading to potential delays and errors in diagnosis [72–74]. Furthermore, many patients with lung cancer also suffer from chronic obstructive respiratory disorders, which can mask or complicate the diagnosis.

ML techniques and AI approaches are crucial in the healthcare industry. One of the most important applications in healthcare is predictive modeling, which includes developing mathematical models that can predict future outcomes based on existing data [75]. Predictive modeling, for example, can be used to identify individuals who are more likely to develop a particular disease or condition, enabling medical professionals to intervene sooner and treat or prevent the ailment more successfully. Predictive modeling can also be used to improve drug adherence and treatment plans, improving patient outcomes and saving healthcare costs. A variety of laws should be established like in [76, 77] to assess and promote the real-world evolution of software utilities based on AI/ML for the initial presumption and recognition of disease due to the broad application of AI/ML in multiple health disorders' prediction.

In particular, ML techniques have proved their potential in several healthcare applications [78–82]. Recently, attempts at analyses have also been made to predict different diseases beyond hypertension and diabetes using language models of symptoms [83]. The one that elaborates on how the machine learning domain expanded to include not only the image-based data analysis of skin lesions [84] but also the prediction and management of physiological conditions were further extending an application scope within healthcare [85].

In this chapter, many classifiers are compared and analyzed to create a highly sensitive and discrimination-capable model. The benchmark indicators include accuracy, recall, precision, F-Score, and Area Under the Curve (AUC), each crucial component of the diagnostic jigsaw. The proposed method assessments are embellished with AUC ROC curves, which improve the visual comprehension of our models' effectiveness. In this ever-changing environment, research keeps pace with computational intelligence, where cutting-edge methods like Python scripted Intelligent Feature Selection, Logistic Regression, MLP Classifier, Gaussian NB Classifier, and a unified Voting Classifier ensemble combine to improve the accuracy of early detection. Computational intelligence and ensemble learning both have their key roles in lung cancer detection, mainly in comparison to techniques developed earlier. Computational intelligence involves using algorithms such as Logistic Regression, MLP Classifier, and Gaussian NB Classifier to improve the analysis of complex datasets, hence greatly improving diagnostic accuracy. Ensemble learning improves this further through methods such as Voting Classifier by fusing several models to avoid false positives. Hyperparameter modification, carried out by diligent grid search, improves model performance further, portending a future in which lung cancer prediction is characterized by accuracy, early action, and lives saved.

3.1.1 Major Contributions

This chapter presents an advanced machine learning-based approach for lung cancer prediction, with the following key contributions:

1. Cloud-Based IoMT Framework for Remote Lung Cancer Monitoring.
   Challenge: Remote monitoring and management of lung cancer patients require an efficient and scalable framework for data handling. **Contribution:** We propose a cloud-based Internet of Medical Things (IoMT) framework that facilitates remote patient care by enabling effective data collection, analysis, and seamless sharing with physicians, thereby improving treatment outcomes.
2. Feature Selection Using K-Means and Fuzzy Logic.
   Challenge: Extracting relevant features from complex lung cancer datasets for accurate prediction is challenging. **Contribution:** We developed a model utilizing Logistic Regression, MLP classifier, and Gaussian NB classifier. To enhance feature extraction, we integrated K-Means clustering with fuzzy logic, leading to improved model performance evaluated through metrics such as accuracy, recall, precision, and F1-score.
3. Performance Comparison of Machine Learning Classifiers
   Challenge: Selecting the most effective classifiers from a broad range of

options for accurate disease prediction.**Contribution:**The study compared nine machine learning classifiers, including Random Forest, Naive Bayes, Logistic Regression, MLP, and others, based on multiple evaluation metrics. From this analysis, the top-performing classifiers—Logistic Regression, MLP, and Gaussian Naive Bayes—were selected for further optimization and integration into the final ensemble model.

4. Ensemble Learning Through Voting Classifier

   Challenge: Single-model predictions often suffer from limitations in accuracy and robustness. **Contribution:** We implemented a voting classifier ensemble with majority voting to combine predictions from multiple models, and further enhanced predictive power through grid search-based hyperparameter tuning.

5. Better Performance Through Experimental Validation

   Challenge: Existing techniques for lung cancer prediction often lack sufficient accuracy and efficiency. **Contribution:** Experimental results demonstrated that our proposed system outperformed existing methods, validating its superior performance and potential for real-world application attaining a remarkable 98.50% accuracy rate.

This chapter is organized as follows: Section 3.2 describes the relevant existing work. The proposed methodology is discussed in Section 3.3. The Proposed Consumer-Focused Integrated Framework for Lung Cancer Diagnosis is highlighted in Section 3.4. The experimental setup is discussed in Section 3.5. In Section 3.6, the results of the suggested work are thoroughly detailed and the conclusion is summarized in Section 3.7.

3.2 Related Work

Numerous studies have explored machine learning models for improving lung cancer detection accuracy.In this section, we go over the crucial contributions of the researchers in predicting diseases using machine learning models. Nageswaran et al. [39] used machine learning methods and mainly image processing technologies to demonstrate precise classification and anticipation of lung tumors.

Gathering photographs was the first step. 83 CT scan images from 70 separate individuals were incorporated into the experimental investigation as the dataset. When processing digital images, the geometric mean filter was employed. Due to this, picture sharpness was improved. The k-mean method was used for the segmentation of photos. After that, machine learning-assisted organizing techniques were applied. It was identified that the ANN architecture is more successful in the prognosis of lung carcinoma.

Durga V. et al. [40] enveloped a data-driven process and image processing method mainly based on evolutionary techniques for sorting and uncovering breast cancer. To contribute to the segmentation and pinpointing of skin-related chaos, this paradigm integrated image optimization and trait extraction methods. The exponential mean image filter was put into practice to improve the resolution of the scan images. AlexNet was used to extract the features. An algorithm known as relief was used to pick attributes. The proposed architecture used methods such as KNN and Nave Bayes to categorize illness conditions and their identification. Next, data from MIAS was gathered for scientific research. After that, the analysis by using images to accurately diagnose cancer of the breast proved beneficial for the suggested method. Halder and Kumar [86] proposed a unique active learning approach employing a rough-fuzzy classifier (ALRFC) for categorizing cancer disease samples by using gene expression data. The suggested method can deal with overlapping, indiscernibility, and ambiguity of gene expression data. The recommended algorithm was tested using different available illness datasets. The experimental findings for cancer prediction are superior to other cutting-edge methods. The primary purpose of the recommended strategy by Wang J et al. [28] was to investigate the CT results of pediatric suffered patients who have MPP as well as MP. It is quite frequent, and pediatric respiratory doctors should do crucial studies on treating this type of mixed pneumonia disorder.

Kumar et al. [41] discussed the current causes of lung cancer and the usage of ML algorithms, paying particular emphasis to their respective advantages and disadvantages. Instead of referring to several articles, this one allowed the researchers to swiftly scan the pertinent literature. Dritsas and Trigka [42] developed effective models to detect patients who are at high risk of developing lung tumors or cancer and must be treated sooner to avoid long-life consequences. The Rotation Forest was the main approach of the article. In further detail, the trials' assessment revealed that the suggested model outperformed others with high F-measure, precision, recall, and accuracy.

Deepapriya et al. [44] tested several models using a chest X-ray or a CT-scanned image to identify a specific condition. The goal was to determine which deep learning methods best predicted lung illness. Various performance criteria, including accuracy, recall, precision, and Jaccard index, were used to assess the method's effectiveness. Doyle et al. [87] described the primary diagnosis characteristics of NTMLD patients in the primary care wards and to see if machine learning might be used to recognize NTMLD patients who have not yet received a diagnosis. The UK's electronic-based medical records primary care database, IQVIA Medical Research Data (a Cegedim Database), was used. Patients with NTMLD were located between 2003 and 2017 based on records of their NTMLD treatment plan or main or secondary care diagnoses. At least one of these traits was added to the control population.112 784 control subjects and 741 NTMLD patients were chosen. For NTMLD patients, COPD and bronchial disorder were the most prevalent pre-existing diagnoses, along with penicillin, macrolides, and inhaled corticosteroids. With an AUC of 0.94, machine learning significantly increased the identification of NTMLD patients compared to random testing. In 2016, it was predicted that there were 9 to 16 diagnosed and unrecognized instances of NTMLD for every 100,000 people. The findings of this study suggest that there may be a sizable number of unconfirmed instances of NTMLD in the UK, supporting the viability of computational learning practiced to primary health data to screen for unverified NTMLD patients.

Almarzouki et al. [88] greatly lessen the perplexity of real-time monitoring and data collecting operations for a healthcare practitioner, resulting in better healthcare management. Raising awareness can aid in the development of important dangers and regulating measures. Along with aiding in mitigating strokes, it also detects high-risk variables. In the coming years, the EEG-based brain-computer interface will have a bright future in preventing DALY. Thakur et al. [89] created several techniques based on gene expression. DNA is transformed into Ribose

Nucleic Acid (RNA), which is then transported into proteins through gene expression. This protein can be used for many things, such as creating new cells, treating cancer, and even creating hybrid species. Some gene malformations are also passed along to the next generation since genes transport genetic information from generation to generation. Consequently, it's necessary to find the malformation. To predict malignant and non-cancerous genes using gene expression data, there are several strategies present in the literature. This is a significant breakthrough in diagnosing the illness and providing a prognosis. Ricciuti et al. [90] aimed to ascertain if alterations in the levels of circulating tumor DNA following the start of first-line pembrolizumab treatment in NSCLC would allow early response expectation before radiological evaluation. Plasma patient samples were analyzed by next-generation sequencing employing improved tagged amplicon and coding sections from 36 genes. The outcomes were linked with an early AF. To determine if real-time blood flow radiography may be used to evaluate pulmonary microcirculation scintigraphy in comparison to predict early post-operative lung function and problems, Hanaoka et al. [45] conducted the study. Spirometer and dynamic perfusion digital radiography were done before, as well as one and three months following radical lung cancer resection. The same cases were then used to validate correlation coefficients between blood flow ratios. The relationship between projected values derived from the blood flow ratio and measured taken values was examined for all patients with dynamic perfusion digital radiography.

Lakshmanaprabu, S. K., et al. [91] proposed a new method for the automated diagnosis of lung cancer using CT images. The features have been extracted from the CT lung images through deep transformation and dimensionality reduction. Then, the optimized ODNN has been reached using M-GSA sensitivity, specificity, and accuracy declared as 96.2%, 94.2%, and 94.56%, respectively. This kind of automation can help screen for lung cancer effectively and reliably, allowing radiologists to raise the rate of early detection to improve survival. Althubiti, Sara A., et al. [92] introduced an effective approach for automated lung cancer diagnosis on CT scans. The median filter was the best filter to be applied to medical CT images, which gave better results than the Gaussian, 2D convolution, and mean filters. The preprocessed image was optimized by two optimization algorithms, such as fuzzy c-means and k-means clustering, and later compared. From the two, fuzzy c-means had 98% accuracy. Features of a texture were extracted using the Gray Level Co-occurrence Matrix (GLCM), and three classification algorithms were compared. The best one from this selection was gradient boosting with 90.9% accuracy.

3.3 Research Methodology

The suggested method's flow diagram, shown in Fig 3.1, includes the following steps:

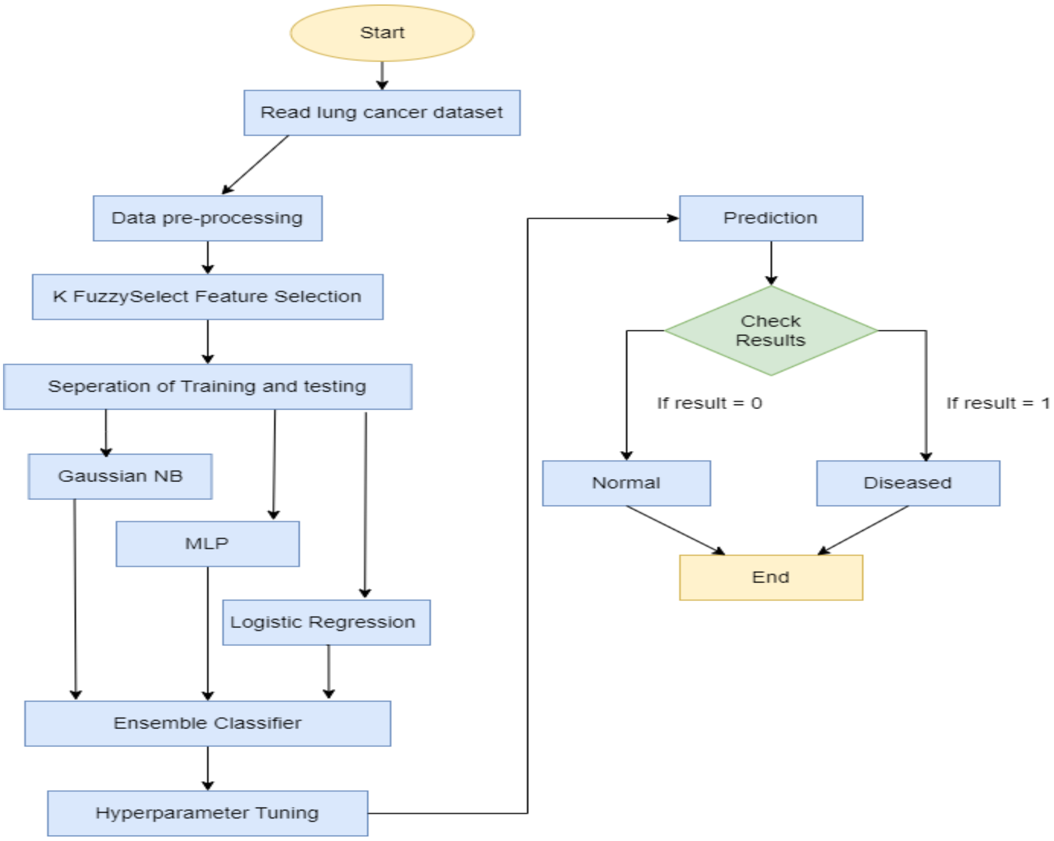

Figure 3.1: Flow Diagram of the Proposed Methodology.

3.3.1 Data Acquisition

The University of California, Irvine provided the dataset used for this study [93]. The dataset is housed in the Lung Cancer repository, which indicates the database in which the dataset is stored. The UCI lung cancer dataset is a well-known dataset widely used for benchmarking various machine learning algorithms. It serves as the basis of our analysis and consists of 32 instances referred to as individual samples in the dataset. In addition to this, the dataset has 56 characteristics. These refer to the attributes or variables that describe each instance. The dataset comprises many features, including age, gender, alcohol use, genetic risk, chronic lung disease, balanced diet, obesity, smoking, passive smoking, chest pain, blood cough, weight loss, shortness of breath, difficulty swallowing, snoring, and others. [94] Moreover, the dataset contains a single class attribute used in machine learning and data analysis tasks. The class attribute is used to predict or classify the network output.

3.3.2 Data Pre-processing

In the data pre-processing phase of our study, we imported the lung cancer dataset into Python utilizing the Pandas module. This initial step facilitated data accessibility for subsequent processing steps. To ensure data quality and relevance, we conducted gap-filling and removing irrelevant data. Handling missing values effectively and eliminating superfluous information were essential to maintain the dataset's integrity and suitability for analysis; Hence, the missing values were dropped. Furthermore, the Synthetic Minority over-sampling Technique (SMOTE) was employed to mitigate any possible class imbalance in the dataset. This technique allowed us to balance the representation of different classes, a crucial consideration in many classification tasks, particularly when dealing with imbalanced datasets. Moreover, to augment our dataset and expand its diversity, we employed synthetic data augmentation technique. These techniques leveraged random functions to generate additional data points, enhancing the dataset's richness and potentially improving the robustness of our subsequent analyses and machine-learning models. Finally, the normalization is performed using the standardization technique. This approach involves transforming the data with a mean of zero and a standard deviation of one. These comprehensive data pre-processing steps laid the foundation for more accurate and meaningful insights in our research of lung cancer diagnosis.

3.3.3 K-Fuzzy Select Feature Selection Technique

Intelligent feature selection plays a pivotal role in our data analysis process, significantly contributing to the quality and effectiveness of our study. To enhance our attribute extraction efforts, we have incorporated a synergistic approach that combines K-Means clustering with fuzzy logic techniques, which is explained using Algorithm 1 below. K-Means clustering is a well-established unsupervised learning algorithm that excels at identifying natural groupings or clusters within the dataset. We aim to pinpoint cluster data points with common characteristics by applying K-Means. This step is instrumental in uncovering pertinent features within the dataset, as it helps us distinguish relevant patterns and relationships among the variables. We leverage fuzzy logic to refine our feature selection process in tandem with K-Means. Fuzzy logic is particularly valuable in this context because it considers the relevance level associated with each feature. Instead of treating features as strictly binary (relevant or irrelevant), fuzzy logic allows us to assign degrees of relevance, recognizing that some attributes may contribute more significantly to the analysis than others. This nuanced approach to feature selection ultimately increases the attributes' overall discriminating power. Combining K-Means clustering and fuzzy logic makes our feature selection process more sophisticated and data-driven. We identify relevant attributes and consider their varying degrees of importance, resulting in a more precise and robust set of features for our subsequent analysis and modeling. This intelligent feature selection approach enhances the overall quality and depth of insights derived from our study, ultimately advancing our understanding of the underlying factors in our lung cancer diagnosis research.

Explanation of Algorithm Steps:

- **Normalization:** This step standardizes the input dataset X to ensure that all features have a comparable scale. It calculates the mean X_{mean} and standard deviation X_{std} of the dataset and then subtracts the mean from each data point and divides by the standard deviation. By scaling the data, this method yields a mean of 0 and a standard deviation of 1.

Algorithm 1 K-Fuzzy Select: Algorithm for Intelligent Feature Selection via K-Means and Fuzzy Logic

```
Input: Input dataset $X$ of lung disease samples
Output: Optimal attributes $\text{Optimal}_f$
Start
Get dataset $X$
Normalize the dataset $X$ using the equation:
    $$X_n = \frac{X - X_{\text{mean}}}{X_{\text{std}}}$$
    where $X_{\text{mean}} = \frac{1}{n}\sum_{i=1}^{n} X$ and $X_{\text{std}} = \frac{1}{n}\sqrt{\sum(X - X_{\text{mean}})^2}$
Apply k-means clustering technique on dataset $X_n$ and get cluster centers.
Predict the cluster labels for each data point in $X_n$, resulting in $cluster\_labels$
Determine the number of features, $n$, in $X_n$
Initialize $fuzzy\_scores$ as a zero vector of length $n$
for $i \leftarrow$ number of features do
    for $j \leftarrow$ number of clusters do
        Calculate $m_s$ membership value for data in feature $i$ with respect to cluster $j$ using a Gaussian membership function:
            $$X_{\text{mean}}(x; c, X_{\text{std}}) = e^{-\frac{(x-c)^2}{2{X_{\text{std}}}^2}}$$
            where $x$ represents the data point values for the $i$-th feature, $c$ is the cluster center for the $j$-th cluster and the $i$-th feature
        Calculate $f_s$ fuzzy score using $m_s$ membership value and $c$:
            $$f_s[i] = f_s[i] + \left(\sum_{x \in X_i} X_{\text{mean}}(x; c_j, X_{\text{std}})\right) \cdot c_{j,i}$$
            where $X_{\text{mean}}(x; c_j, X_{\text{std}})$ represents the Gaussian membership function for a data point $x$ in feature $i$, with $c_j$ being the center of cluster $j$ for feature $i$
    end
end
Get $\text{Optimal}_f$ optimal attributes by finding indices where $f_s > 0$
End
```

- **K-Means Clustering:** The algorithm applies the K-Means clustering technique to the normalized dataset $X_n\dot{K}$-Means identifies clusters in the data and computes cluster centres $c\dot{E}$ach cluster centre represents a group of similar data points.
- **Feature Loop:** The algorithm enters a loop to evaluate each feature in the dataset. This loop iterates through all features, one at a time i, to determine their importance for feature selection.
- **Cluster Loop:** Within the feature loop, there is another loop that iterates through the clusters j. For each feature, this loop calculates membership values m_s and fuzzy scores f_s for that feature in each cluster.
- **Membership Calculation (m_s):** For each feature i and each cluster j, the algorithm calculates a membership value m_s using fuzzy logic. Fuzzy logic allows for a degree of membership rather than a binary classification. It quantifies how well each data point (feature) belongs to each cluster.
- **Fuzzy Score Calculation (f_s):** After determining the membership values m_s, the algorithm computes a fuzzy score f_s for each feature in each cluster. The fuzzy score takes into account the membership value and the cluster center c. This score reflects the importance or relevance of the feature within that cluster.
- **Optimal Attribute Selection:** After calculating membership values and fuzzy scores for all features in all clusters, the algorithm selects the optimal attributes Optimal_f based on these scores. The selection process aims to identify the features that are most relevant to the clustering results.
- **End:** The algorithm concludes after evaluating all features and clusters.

The *K-Fuzzy Select* algorithm is designed to intelligently select optimal attributes by combining K-Means clustering and fuzzy logic. It assesses the relevance of each feature within different clusters, allowing for a more nuanced and data-driven feature selection process. The resulting *Optimal_f* attributes can be used for subsequent analysis, such as building machine learning models or making data-driven decisions in the context of liver disease diagnosis.

3.3.4 Selection of Machine Learning Classifiers

To assess the effectiveness of several classifiers on the dataset, four different performance evaluation metrics including Accuracy, F1-Score, Recall, and Precision were considered. Figure 3.2 depicts the graphical representation of the comparative analysis of the different performance indicators including accuracy, precision, F1-score, and Recall of the various base algorithms considered for the research. The results show that MLP and Logistic regression in comparison to the other classifiers outperformed better in terms of accuracy and other metrics as well. Since accuracy is an important metric in predicting diseases accurately and which further helps in providing the right care and medication to the patients for their recovery, so more emphasis is given to accuracy. The accuracy achieved through MLP , Logistic Regression and GaussianNB is 93.65% ,93.54 % and 92.65% respectively which is the highest among all other classifiers considered whereas KNN is giving lowest accuracy rate.

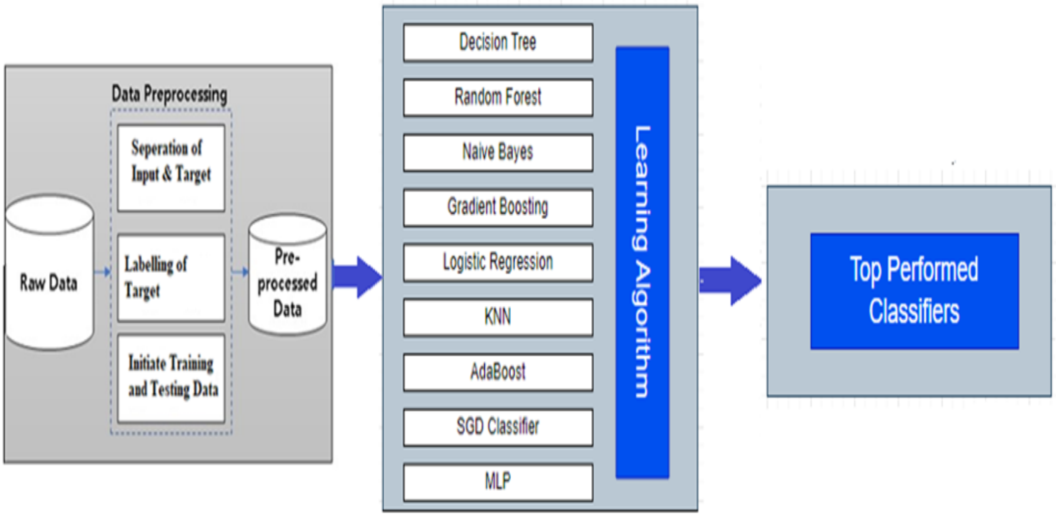

Figure 3.2: Selection of Machine Learning Classifiers.

Selecting the optimal classifier for lung cancer prediction required a comparative analysis of various machine learning models depecited in figure 3.3. Nine machine learning classifiers—Random Forest, Naive Bayes, Logistic Regression, Multilayer Perceptron (MLP), SGD (Stochastic Gradient Descent), KNN, Decision Tree, Gradient Boosting, and Adaboost—were evaluated. Each classifier was assessed based on multiple performance metrics, including accuracy, precision, recall, and F1-score. Logistic Regression, MLP, and Gaussian Naive Bayes (GNB) were identified as the top-performing classifiers. These models demonstrated superior diagnostic accuracy, which led to their selection for further refinement and integration into the final model.

A comparative analysis of nine machine learning classifiers was conducted using multiple evaluation metrics including accuracy, precision, recall, and F1-score. The top-performing models were selected based on consistent high performance across all metrics. This data-driven selection helped ensure that the chosen methods were not only theoretically sound but also practically effective.

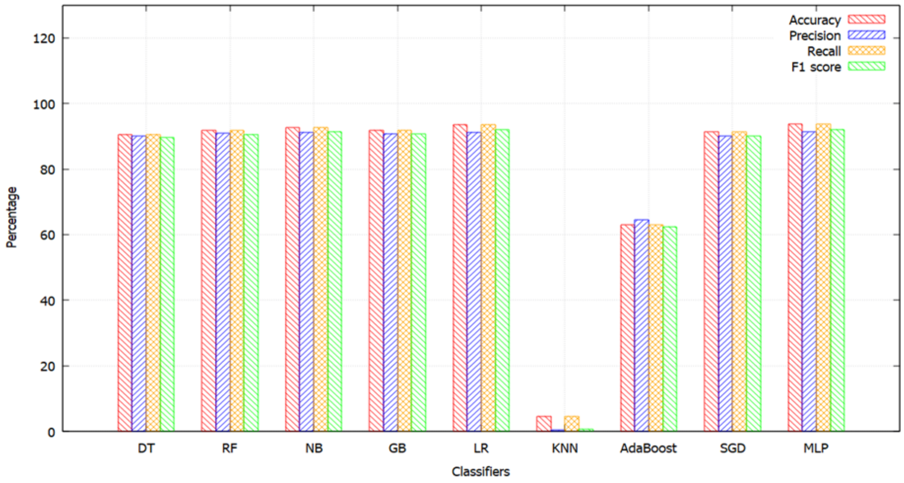

Figure 3.3: Comparision of Machine Learning Classifiers.

3.3.5 Ensemble Voting Classifier

Gaussian Naive Bayes (GNB) Classifier

An effective machine learning method for situations where features have continuous distributions is the GNB classifier. The Gaussian (normal) distribution assumption is included in the GNB method, which builds on the Naive Bayes framework. It uses the Bayes theorem to compute posterior probabilities, as shown by the equation:

$$P(C_k|x) = \frac{P(C_k|x).P(C_k)}{P(x)} \tag{3.1}$$

In equation 3.1, $P(c_k|x)$ stands for the prior class probability, $P(c_k|x)$ for the likelihood of seeing x given class c_k, $P(c_k)$ for the marginal likelihood of observation x, and $P(x)$ for the probability of class c_k given observation x. The feature independence and Gaussian distribution assumptions of GNB make it a trustworthy classification method for continuous data.

Logistic Regression

In the field of machine learning, logistic regression is regarded as a fundamental method that excels at binary classification tasks due to its deceptively straightforward nature. It converts linear combinations into probabilities, denoted: by modeling the association between input characteristics and a binary result using the logistic function.

$$P(y=1|x) = \frac{1}{1+e^{-z}} \tag{3.2}$$

Here, $P(y=1|x)$, where z represents the linear combination of the features and weights, and is the likelihood of the positive class given input x. Logistic regression is a flexible and well-liked classification method since it identifies subtle patterns in data through repeated optimization.

MLP Classifier

The Multilayer Perceptron (MLP) classifier, which is recognized for its capacity to tackle challenging and non-linear classification tasks, is a key component of machine learning. An MLP consists of several layers and functions as a neural network. A weighted sum of inputs processed via an activation function, denoted mathematically as: determines the output of an MLP node.

$$y = \sigma(w.x+b) \tag{3.3}$$

Here, y stands for the node's output, σ for the activation function, w for weights, x for inputs, and b for the bias term. The MLP is a flexible and effective technique for contemporary classification problems because it can capture deep relationships within data through these linked nodes and hidden layers.

Voting Classifier from Ensemble Learning

Due to its ability to improve prediction performance by mixing many models, ensemble learning has emerged as a fundamental component of machine learning. To arrive at a judgment, the Voting Classifier, a well-known ensemble approach, combines the predictions of many classifiers. It uses majority voting for categorization jobs, which is spelled out as follows:

$$y = mode(y_1, y_2, \ldots..y_n) \tag{3.4}$$

Here, y is the final projected class label, but the individual predictions are $y_1, y_2, \ldots, y_n$. The Voting Classifier offers "hard" and "soft" voting algorithms that involve equal collaboration across many models or the averaging of probabilistic predictions for the best possible decision-making.

Our comprehensive classification approach incorporates various machine learning classifiers, including Gaussian NB, MLP, and Logistic Regression. The computational intelligence methods employed, like Gaussian NB, MLP, and Logistic regression, have been explained in the Background section. A Voting Classifier framework, which was synergistically included using Python programming, supports this group of classifiers. The voting classifier is one of the simplest stacking ensemble methods. The Voting Classifier used a soft voting mechanism, where each classifier's prediction is weighted by its confidence level. The ensemble model configured with the respective parameters of the different machine learning classifiers was optimized through GridSearch. The best models taken with this approach capture linear relationships from LR, complex non-linear patterns from MLP, and probabilistic reasoning with independence feature assumptions from GaussianNB. The predictions from these diverse models were aggregated to get a final prediction resulting in increased accuracy than with just a single model. The disease prediction using an ensemble voting classifier and hyperparameter tuning is explained in Algorithm 2.

Algorithm 2 Disease Prediction Using Ensemble Voting Classifier and Hyperparameter Tuning

```
Input: Lung Disease Dataset
Output: Optimized Voting Classifier, Best Hyperparameters, Accuracy Score
1. Get dataset
  2. Preprocess dataset
  3. Apply feature selection using K-Fuzzy Select algorithm
  4. Split dataset into training and testing sets (X_train, Y_train, X_test, Y_test)
  5. Initialize base models for the ensemble:
  GNB ← GaussianNB(), LR ← LogisticRegression(), MLP ← MLPClassifier()
  6. Configure the Voting Classifier with soft voting: voting_clf ← VotingClassifier(estimators=[('LR', LR), ('MLP', MLP), ('GNB', GNB)], voting='soft')
  7. Define the hyperparameter search space:
  H ← { 'LR__C': [0.1, 1, 10], 'MLP__hidden_layer_sizes': [(10,), (50,), (100,)] }
  8. Initialize and configure GridSearchCV:
  GS ← GridSearchCV(estimator=voting_clf, param_grid=H, cv=5, scoring='accuracy')
  9. Perform hyperparameter tuning with GridSearchCV: GS.fit(X_train, Y_train)
  10. Extract the best model and its hyperparameters:
  M* ← GS.best_estimator_, H* ← GS.best_params_
  11. Evaluate M* on the testing set to measure performance: Y_pred ← M*.predict(X_test), P* ← EvaluatePerformance(Y_test, Y_pred)
  12. return M*, H*, P*
```

3.4 Proposed Integrated Framework for Lung Cancer Diagnosis

Internet of Things (IoT) is a computing concept where each device is interconnected through the internet, and one can communicate with others. IoT is widely used in the medical field, where different IoMT devices play significant roles in collecting and sharing patient data across the network. In Fig 3.4, cloud-based IoMT architecture has been designed where data can be collected, shared, and analyzed accordingly. Different use cases of IoMT devices have been mentioned here, where n is the number of local servers connected with a main cloud server. The framework is designed so that patient data can be collected, extracted, analyzed, and shared with physicians so that they can treat their patients more effectively from a remote distance and the right care can be provided to the patients.

Data from m patients are collected through IoMT devices and are shared with the nearest local cloud server. An AI module in the local cloud server is responsible for predicting the classified output. The fetched patient data are extracted and classified in the local cloud server using a defined machine learning algorithm and sent to the Dew servers. The data stored in the dew servers are shared with the main cloud servers and local servers of different health organizations so that doctors, nurses, and patients can access the data. The main cloud server is connected to all the local servers and can exchange information across all the servers.

Different types of IoMT devices are available and used for different applications. Some devices are used in health organizations, and some are portable or wearable to track daily activities and health status. The devices are connected to the internet through a gateway to exchange data through the proper channels. In Fig 3.4, it can be observed that the IoMT devices are directly connected with the respective local servers through the gateway. Once the data is collected from the patient's end, it is sent to the local server through the Internet.

The AI module inside the local server receives the data and preprocesses it initially. The preprocessed data are extracted and classified later using ML algorithms, as explained in the above section.The AI module comes with a predictive output shared with the dew servers and further shared with the main cloud server from the dew servers. Different local servers share the predicted data with the main cloud server, where the main cloud server is connected to hospitals, health research labs, or remote dispensaries.

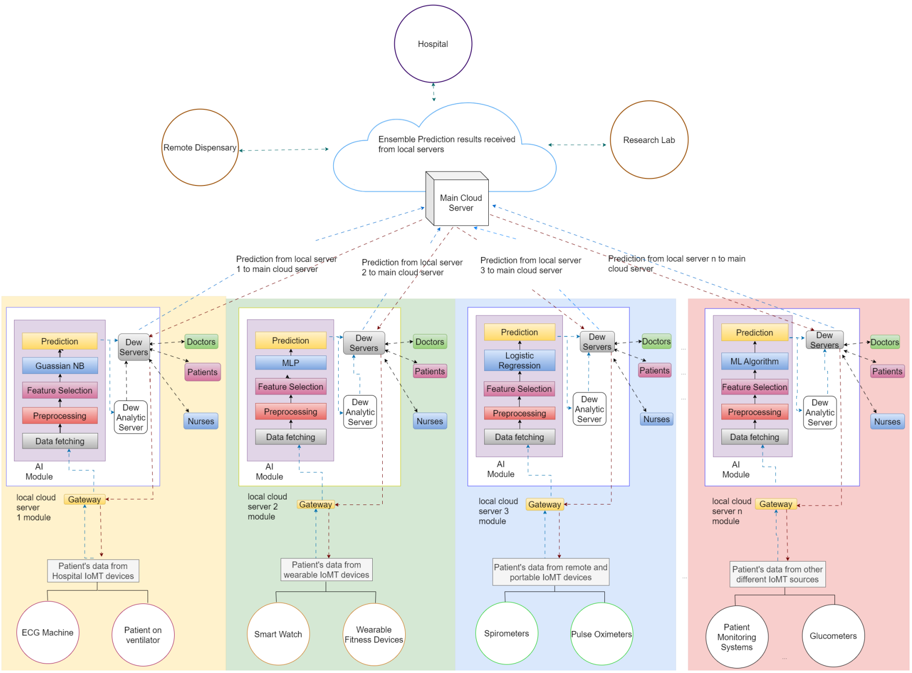

Figure 3.4: Proposed Cloud-Based IoMT Framework.

The local Dew server is represented in Fig 3.5, and different ML algorithms are applied to the dataset. The physicians/health specialists can access the data and share the prescribed feedback with the respective user-ends. The data can be accessed from the local servers so that doctors, nurses, or patients can utilize the stored information anytime.

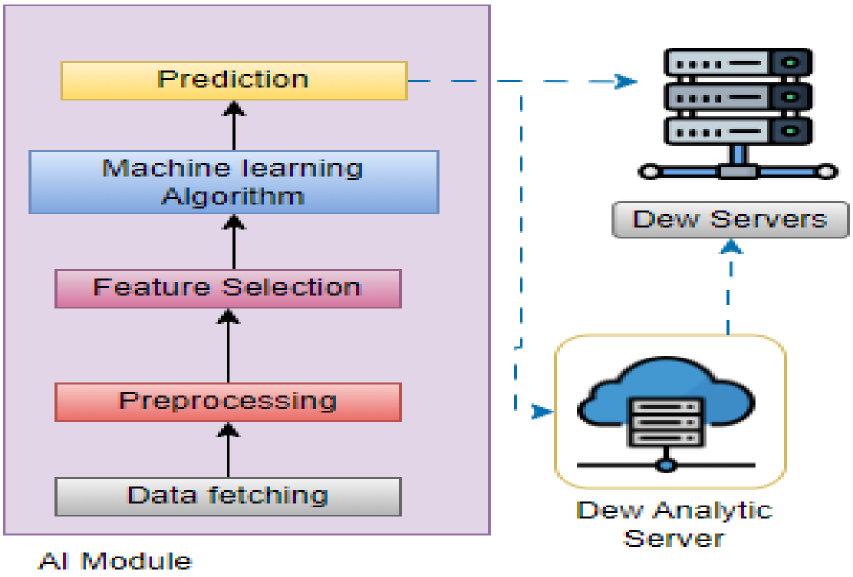

Figure 3.5: Local Cloud Server Module.

With the proposed framework, an intelligent network environment can be designed between users and healthcare professionals so that appropriate treatment can be possible in time from a remote distance. The intelligent AI module can help classify the disease automatically and smartly so that doctors can prescribe medicines and treat them accordingly.

3.5 Experimental Setup

This section contains the experimental analysis and findings of predicting lung disease.

3.5.1 Experimental Setup

Our computational experiments were conducted using Jupyter Notebooks, an open-source web application. Jupyter provides an interactive environment well-suited for exploratory analysis and data visualization. The Jupyter environment was set up with a Python 3 kernel, and experiments were executed on a machine with an Intel Core i5 processor, 16GB RAM, and an NVIDIA GTX 1080 Ti GPU. The Jupyter Notebook interface was accessed via a local server on the host machine, ensuring a consistent and isolated environment for all experimental runs.

3.5.2 Training and Testing Samples

To assess the performance of our machine learning models effectively, we have partitioned the dataset into two distinct subsets: a training sample and a testing sample. This division is a critical step in our study's methodology, ensuring that our models are both trained and evaluated rigorously. Specifically, we have allocated 80% of the dataset to the training sample. This substantial portion serves as the foundation for our machine-learning algorithms. During the training phase, our models learn from this data, capturing underlying patterns, relationships, and trends that are essential for making accurate predictions or classifications related to lung cancer diagnosis. Conversely, the remaining 20% of the dataset is reserved for the testing sample. This sample is an independent and unseen data set that our models have not encountered during their training. By evaluating the models on this test sample, we can gauge their generalization performance—their ability to make accurate predictions on new, unseen data. This division into training and testing samples helps us assess the model's ability to make accurate predictions on real-world, previously unseen cases, a critical measure of its effectiveness.

Table 3.1: Simulation Parameters and Values

Simulation Parameters	**Values**
Training dataset	80%
Testing dataset	20%
Machine learning Models	LR, MLP, Gaussian NB, Ensembled Voting Classifier
Constant c (LR)	0.1 to 10
Hidden layers (MLP)	10 to 100
Best Constant c (LR)	10
Best Hidden Layers (MLP)	50
Hyperparameters Tuning Method	Grid Search Method

3.5.3 Evaluation Parameters

The parameters of evaluation that were considered for the performance evaluation of machine learning models include accuracy, precision, recall, and F-Score [95, 96]. With the contribution of the confusion matrix, these desired metrics were evaluated, consisting of elements: True Positive (TP), True Negative(TN), False Positive(FP), and False Negative (FN). Accuracy measures the proportion of correctly predicted instances, including true positives and negatives, against total instances. Precision looks more at the quality of positive predictions. It is the ratio of true positives to the total predicted as positive. Recall, also known as sensitivity or the true positive rate, measures how well a model can detect all instances of interest. The F1 measure is the harmonic average of both precision and recall, thus balancing between these two measures. The formula for all these metrics is given below:

$$\text{Accuracy} = \frac{TP+TN}{TP+TN+FP+FN} \tag{3.5}$$

$$\text{Precision} = \frac{TP}{TP+FP} \tag{3.6}$$

$$\text{Recall} = \frac{TP}{TP+FN} \tag{3.7}$$

$$\text{F1 Score} = 2 \times \frac{\text{Precision} \times \text{Recall}}{\text{Precision} + \text{Recall}} \tag{3.8}$$

3.6 Results and Discussion

In this section, we report the findings from our thorough examination of classification performance, which considered important parameters, including accuracy, F-score, recall, and precision. We successfully demonstrate the sturdiness of our technique by careful comparison with several existing approaches. Our strategy achieves higher accuracy rates while retaining precision and recall values on par with or beyond those of current techniques. Our inquiry includes a thorough analysis of the components that affect how well our technique performs, revealing potential areas for improvement. These findings highlight the potential of our technique to provide improved accuracy and reliability for classification tasks, placing it as an exciting candidate for practical applications.

Precision, F1-score, Accuracy, and recall were the four key measures we used in our assessment technique mentioned below in Table 3.1, to analyze the effectiveness of our classification model. By calculating the percentage of samples that were properly identified out of all samples, we could determine our model's accuracy. The fraction of samples categorized as genuine positive samples among all samples was also considered while precision was calculated. Recall was computed as the ratio of correctly classified positive samples to all positive samples overall, much like classification. The F-score, a comprehensive performance indicator representing the full power of the model's categorization skills, was constructed using the harmonic mean of accuracy and recall.

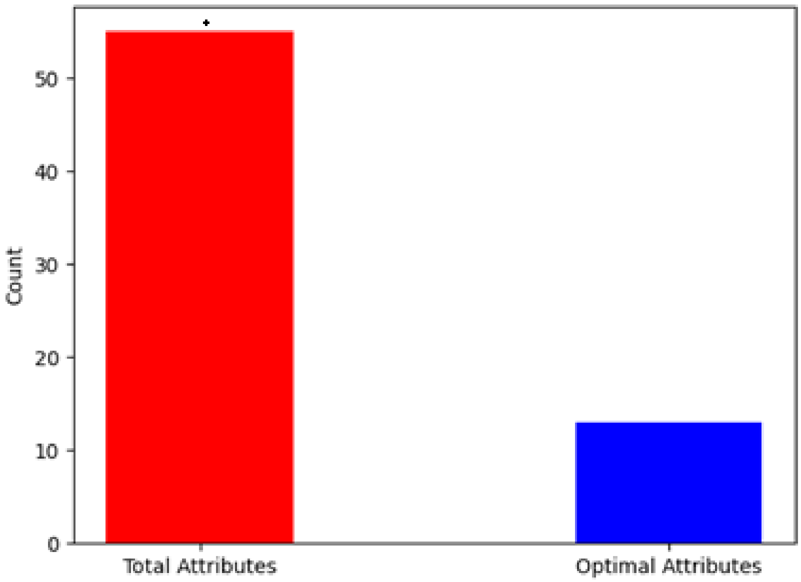

Figure 3.6: Comparison of Attributes.

In Fig 3.6, the red bar in the graphical depiction, which shows a significant variance in the number of characteristics, shows that there are more than 50 different traits. Our ideal attribute count criteria imply that an attribute count of fewer than 15 is represented by the blue bar, which is preferable for best performance, which is in opposition to this finding. Firty six features were reduced to fifteen features using the proposed feature selection technique, which thus saved processing time.

Table 3.2summarizes the values obtained for the validation and test accuracy metrics for different train-test split ratios of the dataset. The highest test accuracy is obtained for the 80:20 train/test split case; the corresponding confusion matrix is presented in Fig 3.7.The total execution time was 38.92 seconds. Within this period, the fuzzy logic-based feature selection process was completed in 0.50 seconds, while the ensemble model training took significantly longer, with a total duration of 35.54 seconds.The confusion matrix comes from its capacity to graphically represent a classification model's performance. This matrix makes it easier to understand how well the model predicts outcomes concerning the labels assigned to each class. The confusion matrix shows 74 true negatives (TN) and 123 true positives (TP) in the context of our particular investigation. Impressive, there have been no false positives (FP) and just 3 false negatives (FN). This astoundingly low percentage of misclassification, especially in predicting the positive class, provides a strong defense of the model's astounding competence and accuracy.

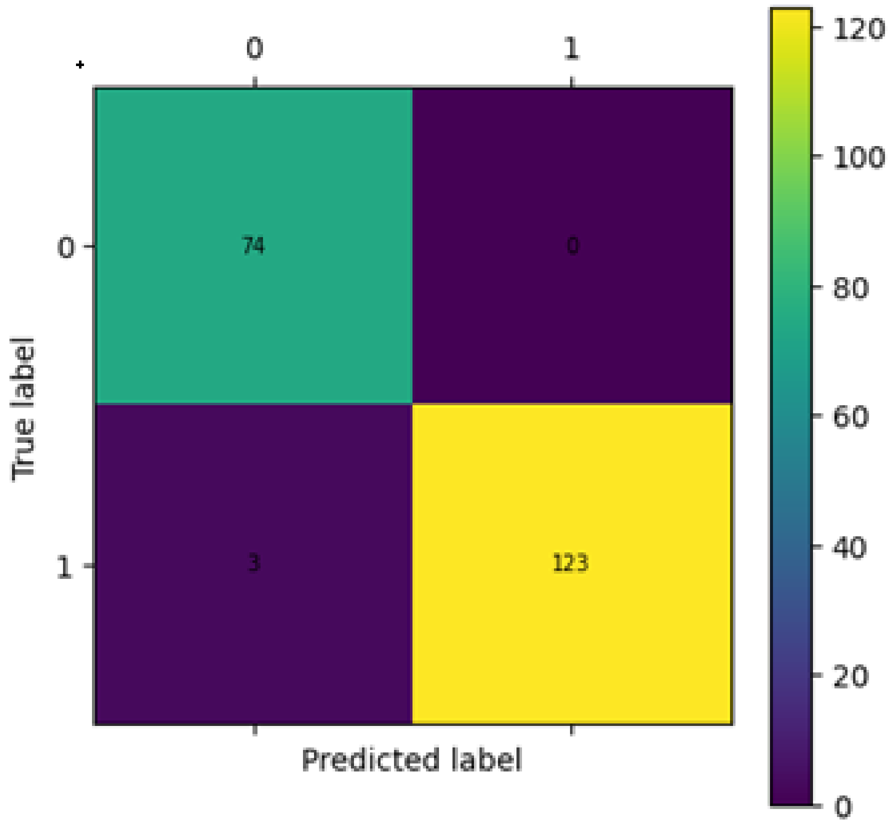

Figure 3.7: Confusion Matrix (20% Data Reserved for Testing).

Table 3.2: Performance of the Model with Different Train/Test Split Ratio

Train/Test Split ratio	Accuracy	Precision	Recall	F1-Score
70:30	0.9792	0.98	0.978	0.978
80:20	0.9850	0.9761	1.00	0.9879

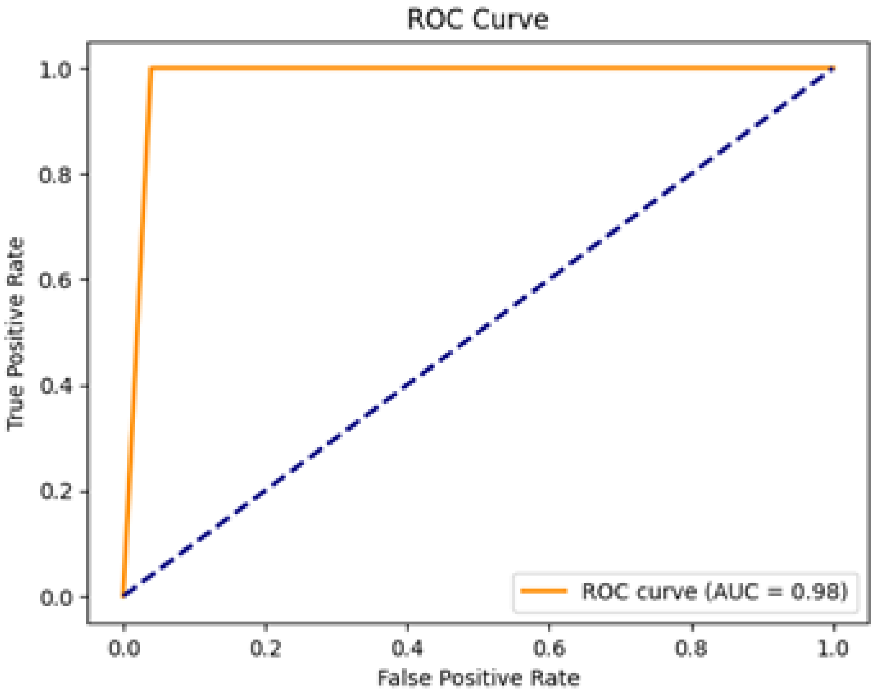

Figure 3.8: Receiver Operating Characteristic (ROC) Curve of AUC.

ROC curve, shown in Fig 3.8, illustrates how the classification model balances its sensitivity and specificity. The orange line shows the ROC curve, and its AUC value of 0.98 denotes exceptional performance.

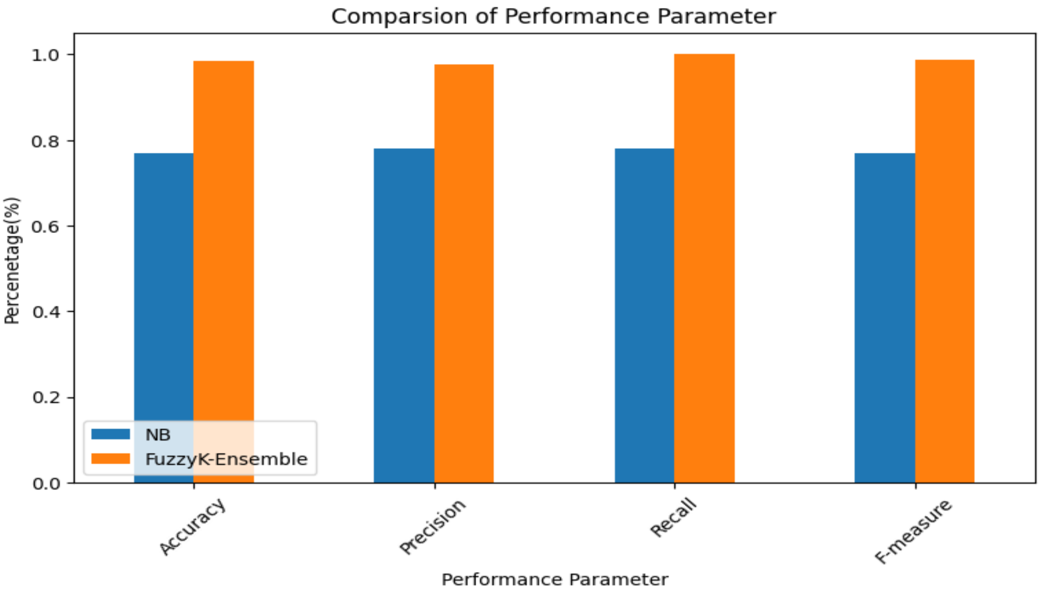

Figure 3.9: Comparison of Fuzzy K-Ensemble Performance Parameters with NB Classifier.

Clear differences in the performance measures are visible in Fig 3.9 when contrasting the classification results of Naive Bayes (NB) and Fuzzy K-Ensemble techniques. The NB method's recall, accuracy, and precision are 0.77, 0.78, and 0.77, respectively. These results demonstrate the higher classification skills of the Fuzzy K-Ensemble method, demonstrating its potential for increased precision and accuracy in real-world applications.

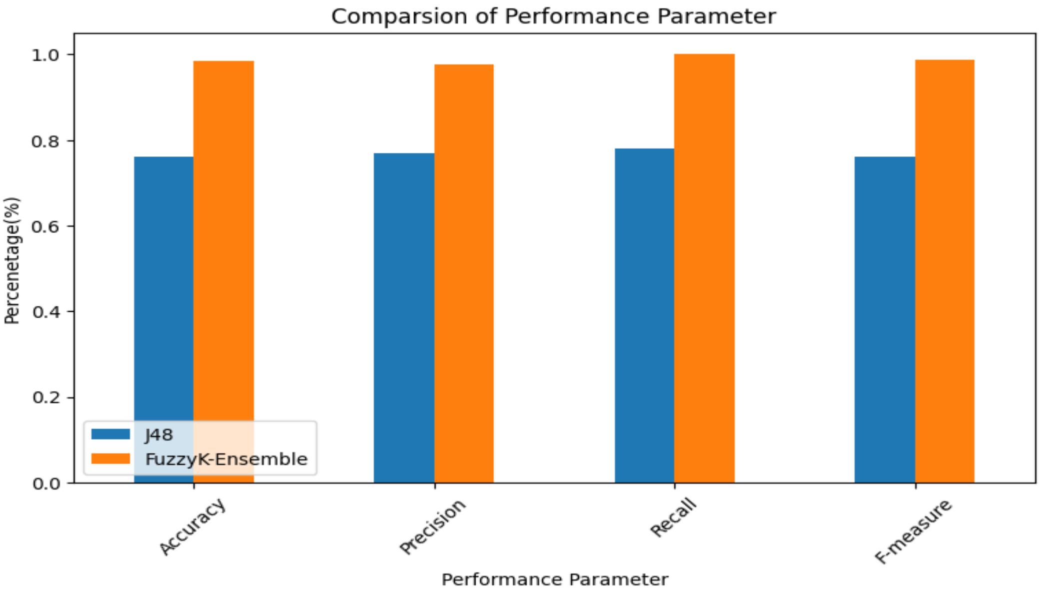

Figure 3.10: Comparison of Fuzzy K-Ensemble Performance Parameters with J48 Classifier.

Different performance patterns can be seen in Fig 3.10 when contrasting the J48 and Fuzzy K-Ensemble classification techniques. J48 yields an accuracy of 0.76, recall of 0.78, precision of 0.77, and F-measure of 0.76. Conversely, Fuzzy K-Ensemble consistently outperforms the other models, achieving 0.9850 accuracy, 0.9761 precision, 1.00 recall, and 0.9879 significant F-measure.

There are noticeable performance patterns when comparing the SVM (Support Vector Machine) and Fuzzy K-Ensemble classification techniques as depicted in Fig 3.11. The Fuzzy K-Ensemble consistently outperforms the SVM technique in all four of these measures, with values of 0.9850 for accuracy, 0.9761 for precision, 1.00 for recall, and a noteworthy 0.9879 for F-measure. The SVM strategy results in an accuracy, precision, recall, and F-measure of 0.81 and 0.82. These results highlight the Fuzzy K-Ensemble's strong accuracy performance.

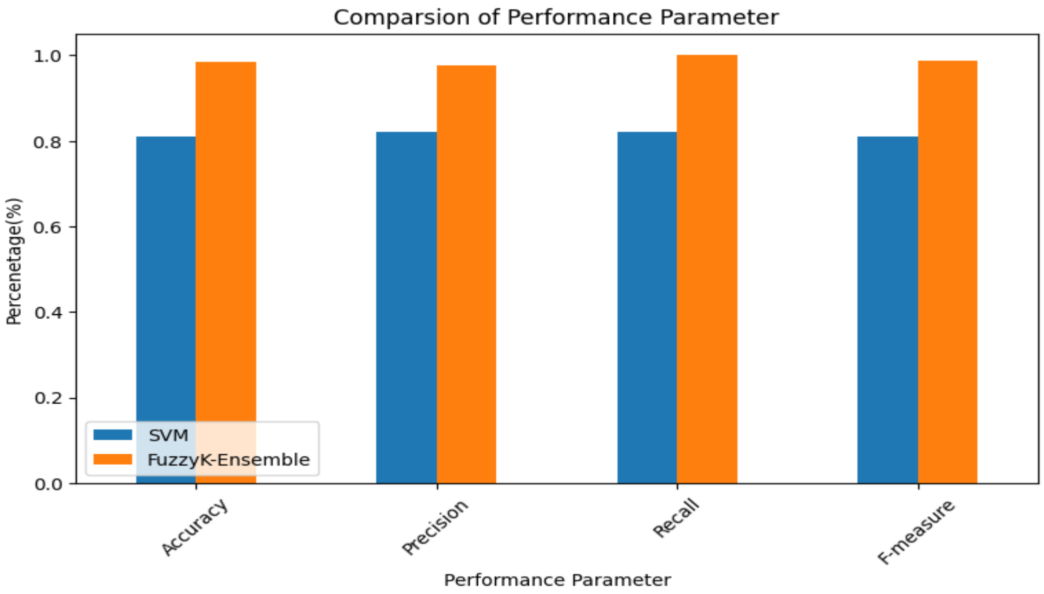

Figure 3.11: Comparison of Fuzzy K-Ensemble Performance Parameters with SVM Classifier.

Table 4.9 compares the performance of four different machine learning models—NB, J48, SVM, and our proposed model across four parameters: Accuracy, Precision, Recall, and F-measure.

Table 3.3: Comparison of NB, J48, SVM with FuzzyK-Ensemble

Parameters	**NB**	**J48**	**SVM**	**FuzzyK-Ensemble**
Accuracy	0.77	0.76	0.81	0.9850
Precision	0.78	0.77	0.82	0.9761
Recall	0.78	0.78	0.82	1.00
F-measure	0.77	0.76	0.81	0.9879

The paired t-test is the statistical method for comparing two related groups. This research has used it to compare the performance metrics of baseline machine learning models and the proposed model over accuracy, precision, recall, and F1-score with J48, SVM, and NB. The results of the paired t-test are shown in Table 3.4. Paired t-test results indicate that the proposed model performs significantly better for all metrics under investigation than the baseline models represented by J48, SVM, and NB. Indeed, all the p-values are very small and below the common threshold of 0.05. This will provide very strong evidence to prove that the improvements observed are statistically significant and not due to random chance. Therefore, the proposed model is likely to be a superior choice that will offer a more reliable and accurate prediction.

Table 3.4: Paired t-test Results for Performance Metrics.

Metric	**p-value**
Accuracy	0.0055
Precision	0.0060
Recall	0.0048
F1-Score	0.0055

The comparison of accuracy results between previous studies and the suggested model presents a clear progression in developing and refining machine learning methods for a specific task. This progression is illustrated in Table 3.5 through the incremental improvements in accuracy percentages, culminating in the suggested model's superior performance.

Table 3.5: Comparison Results of Accuracy Between Previous Studies and Suggested Model

Authors Name	**Methods used**	**Accuracy (%)**
Gultepe Y. [94]	KNN, NB, DT	83
Faisal et al. [97]	Majority voting ensemble model	90
Patra R. [98]	RBF classifier	81.25
Khashei M et al. [99]	DIMLP	94.43
Our Work	Fuzzy K-Ensemble	98.50

The limitation of the model is that it was tested only on lung cancer; however, its generalizability needs to be tested for other types of cancers also. There are no defined measures of the model's performance concerning accuracy, precision, recall, and F1 score against other cancer types. Different cancers have different characteristics and genetic profiles. A model trained using lung cancer data may not effectively capture the relevant features to predict other cancers.

3.7 Summary

The increasing prevalence of chronic diseases, particularly lung cancer, poses significant challenges to healthcare systems globally. As a leading cause of cancer-related deaths, lung cancer necessitates innovative approaches to enhance early detection and improve patient outcomes. In light of this pressing need, this chapter presents a comprehensive study focused on leveraging machine learning algorithms for the detection of lung cancer and the prediction of multiple diseases. The proposed work integrates computational intelligence, ensemble learning, and rigorous evaluation methodologies to develop robust predictive models that can be applied in clinical settings.

To sum up, the fact that lung cancer is a primary cause of cancer-related death highlights the urgent need for novel approaches. This research capitalizes on recent computational intelligence advancements to establish an environmentally conscious prototype for lung cancer treatment, offering optimized resource utilization and potential time and cost savings. Intelligent Feature Selection, Logistic Regression, MLP Classifier, Gaussian NB Classifier, and Voting Classifier ensemble methods, all implemented using Python, collectively enhance early detection accuracy. Hyperparameter tuning through grid search further refines the model. Comparative analysis against existing methods substantiates the proposed model's superior performance, attaining a remarkable 98.50% accuracy rate. These findings highlight the transformative potential of computational intelligence in advancing effective lung cancer diagnosis and treatment paradigms.

CHAPTER 4

AN ENSEMBLE DEEP LEARNING FRAMEWORK FOR ENHANCED LUNG CANCER DIAGNOSIS

This chapter presents a novel framework that combines deep learning with integrated reinforcement learning to improve the accuracy of lung cancer diagnosis from CT scans. To address the issue of class imbalance, we apply elastic transformation and data augmentation techniques to enhance model generalization. For multi-class classification of lung tumors, five pre-trained convolutional neural network architectures—DenseNet201, EfficientNetB7, VGG16, MobileNet, and VGG19—are employed, with each model refined through transfer learning. To further improve performance, we introduce a weighted average ensemble model, "DEV-MV," combined with grid search hyperparameter optimization, achieving an impressive diagnostic accuracy of 99.40%. The integration of ensemble reinforcement learning contributes to enhanced robustness and reliability in predictions. This approach represents a significant advancement in automated lung cancer detection, offering a highly accurate and scalable solution for early diag-

nosis.[1]

4.1 Introduction

Lung tumor continues to be one of the most important causes of health disorders and the greatest causes of death from cancer in the world. It refers to cancer that develops due to the impact of unregulated expansion of abnormal cells in the lungs. This cancer poses a serious health hazard, mostly causing grievous illness and death. The World Health Organization reports that in 2022, there were 2.5 million new instances of lung cancer, accounting for 12.4% of all the new cancer cases, and deaths were 1.8 million, accounting for 18.7% of the total cancer fatalities [5]. Early detection of the diseases can let one have better outcomes, but traditional screening methods, such as CT scans and chest X-rays, are not without their shortcomings.

Recent advances in AI and ML have brought new hope to the potential of deep learning transforming medical diagnostics. Deep learning, a sub-application of ML, utilizes varieties of neural networks arranged in multiple layers to model complex patterns from datasets. It has been effectively used for most of the medical imaging analysis activities, from radiographic tumor detection to classification [101, 102].

In recent years, DL approaches have become increasingly significant for lung tissue cancer diagnosis and prognosis.These include medical image analysis and personalized treatment plans.CNN have also demonstrated remarkable performance in analytical processing of CT scans and X-rays with high accuracy, thereby making techniques of this nature in detecting lung cancer very effective, reducing the false positives and negatives [103, 104].

Some deep learning methods can be trained from large-scale data handling and feature extraction points to achieve a more precise classification of lung cancer

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[1] This chapter is derived from:
Richa Jain, Parminder Singh, and Avinash Kaur. "An Ensemble Reinforcement Learning-Assisted Deep Learning Framework for Enhanced Lung Cancer Diagnosis", Swarm and Evolutionary Computation (Published), 2024, (Scopus, SCIE 8.2 IF) [100].

in test data. These methods are conceived to be invaluable for early lung cancer detection and personalized treatment [104]. However, the poor interpretability of the developed models, along with the problems of unbalanced datasets and limited sample sizes in the case of some diseases, implementation in clinical practice becomes a matter at hand due to data privacy, are only a few of many challenges [104, 105].

4.1.1 Advantages of Deep Learning Over Traditional Methods

The traditional methods for lung cancer detection primarily relied on radiologists' interpretation of CT scans, often using basic image processing techniques. However, these methods have several limitations:

1. **Subjectivity:** Human interpretation is subject to variability; different radiologists may arrive at different conclusions based on the same image.
2. **Time-Consuming:** Manual analysis of images is labor-intensive and can lead to delays in diagnosis.
3. **Inability to Capture Complex Patterns:** Traditional algorithms may struggle to recognize subtle patterns indicative of early-stage tumors, particularly in the presence of noise or artifacts.

In contrast, DL models offer several advantages:

1. **Automated Feature Extraction:** DL algorithms automatically learn relevant features from images without requiring manual intervention. This reduces the risk of human error and biases.
2. **Higher Accuracy:** Studies have shown that deep learning models, especially CNNs, outperform traditional methods in various medical imaging tasks. Their ability to learn complex patterns results in improved diagnostic accuracy.
3. **Efficiency:** DL models can process large volumes of images quickly, facilitating real-time analysis and timely diagnoses.

4.1.2 Motivation for Using Deep Learning

The motivation for selecting deep learning models for lung cancer detection and multi-disease classification stems from several factors:

1. **Need for Improved Diagnostic Accuracy:** The primary motivation behind utilizing deep learning models is the pressing need to enhance diagnostic accuracy in lung cancer detection. Traditional imaging techniques often yield high false-positive and false-negative rates, leading to unnecessary procedures or missed diagnoses. By leveraging deep learning algorithms, which can automatically learn from vast datasets, the aim is to create a model that minimizes errors and provides more reliable results.
2. **Addressing Class Imbalance:** Lung cancer datasets often exhibit class imbalance, where images of cancerous tissues are less frequent than those of healthy tissues. Traditional methods struggle with class imbalance, leading to biased predictions. Deep learning models can incorporate techniques such as elastic transformation to address this imbalance, enhancing the training dataset and ensuring better performance across all classes.
3. **Enhancing Model Generalization:** Deep learning models possess the ability to generalize from training data to unseen data better than traditional methods. This characteristic is crucial in healthcare, where the variability in patient demographics, imaging conditions, and disease presentations can significantly impact model performance. By utilizing data augmentation techniques, the robustness of deep learning models can be improved, enabling them to perform reliably across different scenarios.
4. **Integration of Multi-Modal Data:** Deep learning approaches can seamlessly integrate multiple data types, such as imaging data, clinical records, and demographic information. This capability allows for a more comprehensive assessment of patient health and supports improved decision-making processes. The ability to analyze diverse data sources simultaneously is a significant advantage over traditional methods, which typically focus on single data types.

4.1.3 Major Contributions

The proposed method makes an ensemble and more powerful model that becomes more robust, more reliable, and more diversified in its decision-making. The primary contributions of this research include:

1. DEV-MV model was introduced, integrating DenseNet201, EfficientNet B7, VGG16, MobileNet, and VGG19 to accurately predict lung cancer using a multiclass dataset.
2. The Elastic Transformation augmentation approach was applied to the dataset with significant class disparity to equalize the lung cancer disease classes.
3. The performance of the DEV-MV model was assessed against the individual model, i.e., the CNN model. The result showed that the proposed model performed better than the other individual models.
4. To assess the model's performance in predicting lung cancer from CT scans, the Adam optimizer with a batch size of 16 was employed.
5. An Ensemble Reinforcement Learning framework was proposed to continuously enhance prediction accuracy and reliability.

This chapter is organized as follows: Section 4.2 describes the literature review. Section 4.3describes the proposed methodology used in this study. The experimental results with their discussion is explained in section 4.4, and is concluded in Section 4.5.

4.2 Related Work

Researchers worldwide have made significant advancements in lung cancer prediction. In the study by Rahman et al. [106], the authors classified skin lesions into seven groups using an ensemble algorithm that employs weighted average ensemble learning. This technique has been shown with ample evidence to enhance significantly the accuracy of the concerned classification by ensembling multiple models. The result has improved to an average of 93% for the stupid ensemble model. In their research, Alamin et al. [107] proposed an ensemble-based method to optimize model building, using weight optimization techniques such as Grid Search. Deep learning in medical image-based diagnosis of cancer was applied; Xiaoyan Jiang et al. [108] referred to the study by utilizing deep learning in cancer diagnosis through medical imaging. Also, the authors pointed to the amalgamation of available data augmentation techniques as a way of finding the best strategy in discourse to enhance the precision of the model.

In the work by G.S. Chakraborty et al. [109], a weighted average ensemble approach is followed wherein the given weights were based on priority values obtained from the pre-trained models. The generalized accuracy of the model to 97.25% for binary classification and 94.10% accuracy for multiclass classification purposes. This method can be facilitated to optimize deep models in detecting cancer. Literature shows several past studies that applied deep learning techniques in lung cancer diagnostics. Ahmed Shaffi et al. [110] proposed an optimization cuckoo search with a support vector machine-based classifier for an intelligent lung cancer diagnosis system. The present research showcased the potential of deep learning frameworks for detecting lung cancer in the early stages. The accuracy, specificity, and sensitivity of the system are 92.55%, 93.40%, and 91.70% respectively, demonstrating very good performance measures.

Sher Lyn Tan et al. [111] presented a framework for diagnosing non-small-cell lung tumors using an optimization-driven combination of deep neural networks. Shamrat et al. [112] introduced LungNet22, a deep-learning model specifically designed to enhance the accuracy of lung disease diagnosis through chest X-ray images. Extensive training, data augmentation, and hyperparameter tuning contributed to the model's superior performance. The results showed that LungNet22 outperformed several existing models. The study concluded that LungNet22 is a promising tool for supporting radiologists in the accurate and efficient diagnosis of various lung diseases. In addition, the findings by Thangamani M et al. [113] the optimization was done through grid search, using a weighted convolutional neural framework, and it proved useful in enhancing the prediction of lung cancer. Enlisted altogether, this framework is based on the perspective of deep learning augmented with a weighted average ensemble technique, aided with grid search in configuring the right set of hyperparameters, which could help in deriving lung cancer diagnosis.

Nasser and Naser [114] were able to identify the presence of cancer in lung tissue using an ANN with an accuracy of 96.67%. The approach proposed by Cifci et al. [115], called IPCT not only improved the quality of lung images but increased the diagnosis rate of lung cancer to an approximate accuracy of 98.42%.C. Wang et al. [116] built a deep learning system for accurate prediction of survival and determination of the status of EGFR mutation from CT image subtypes related to lung adenocarcinoma.

S. Kim et al. [117] have used an innovative learning tool for diagnosis through CXR images as a deep learning methodology to enhance the efficiency and accuracy of CAD for lung diseases. The SCH dataset was employed, achieving an accuracy of 82.15% in multi-class classification tasks. M. Alshmrani et al. [118] used CNN and VGG19 in a deep learning architecture to classify different lung diseases into many classes based on CXR pictures. The author proposed that the VGG19 CNN model outperformed existing works in the classification of Lung Cancer, Lung Opacity, TB, Pneumonia, and COVID-19.

Kareem et al. [119] suggested the use of image processing and computer vision techniques in a computer system to detect lung cancer within a dataset. The SVM is employed as the classification strategy to group the instances under one of the three classes: normal, benign, or malignant. Some of the SVM kernels were evaluated with various feature extraction techniques for better results. This yielded an accuracy of 89.88%. Humayun et al. [120] offered a diagnostic tool and employed a deep neural network to drive features for computer-aided diagnosis.

Song. Y. et al. [121] gave a general overview of Ensemble Reinforcement Learning. Ensemble Reinforcement Learning combines several learning models for a variety of applications to improve their performance. He. Xin et al. [122] proposed a new paradigm in STLF using Q-learning to dynamically assign weights to the ensemble members, and it has had a much better prediction accuracy compared to traditional methods. Similarly, in the fault diagnosis of rolling bearings, an ensemble reinforcement method can recognize a fault type effectively under different working conditions, indicating practical engineering benefits [123]. Another contribution is ensemble meta-reinforcement learning for server anomaly detection, which allows for both fast adaptation to changing data distributions and better precision of prediction [124]. Similarly, the ELRL-MD model performed ensemble learning with RL to cope with cardiac imaging data imbalance. It provided better diagnostic performance than traditional approaches for the diagnosis of myocarditis [125].

Point cloud registration is a crucial task in computer science, and has been approached using various methods. In this context, Hangqi Ding, et al., proposed a new technique called sampling-based evolutionary multitasking for point cloud registration. Sampling-based evolutionary multitasking integrates the power of evolutionary computation with multitasking which enables several tasks to be optimized in parallel by exploiting knowledge transfer between them [126]. This approach accelerates convergence as well as sharpens the precision of registration by transferring information across tasks. Another two-level knowledge transfer system has been proposed in order to better improve the robustness of multi-view point cloud registration and handle the complicated datasets better [127, 128].

4.3 Research Methodology

The research methodology employed in this study focuses on the development of a robust framework for lung cancer diagnosis using deep learning and integrated reinforcement learning. The methodology encompasses various stages, including data preprocessing, architecture selection, data augmentation strategies, and model training and evaluation. A workflow diagram in Figure 4.1 illustrates the comprehensive procedure utilized to create and assess our deep learning framework to improve the diagnosis of lung cancer.

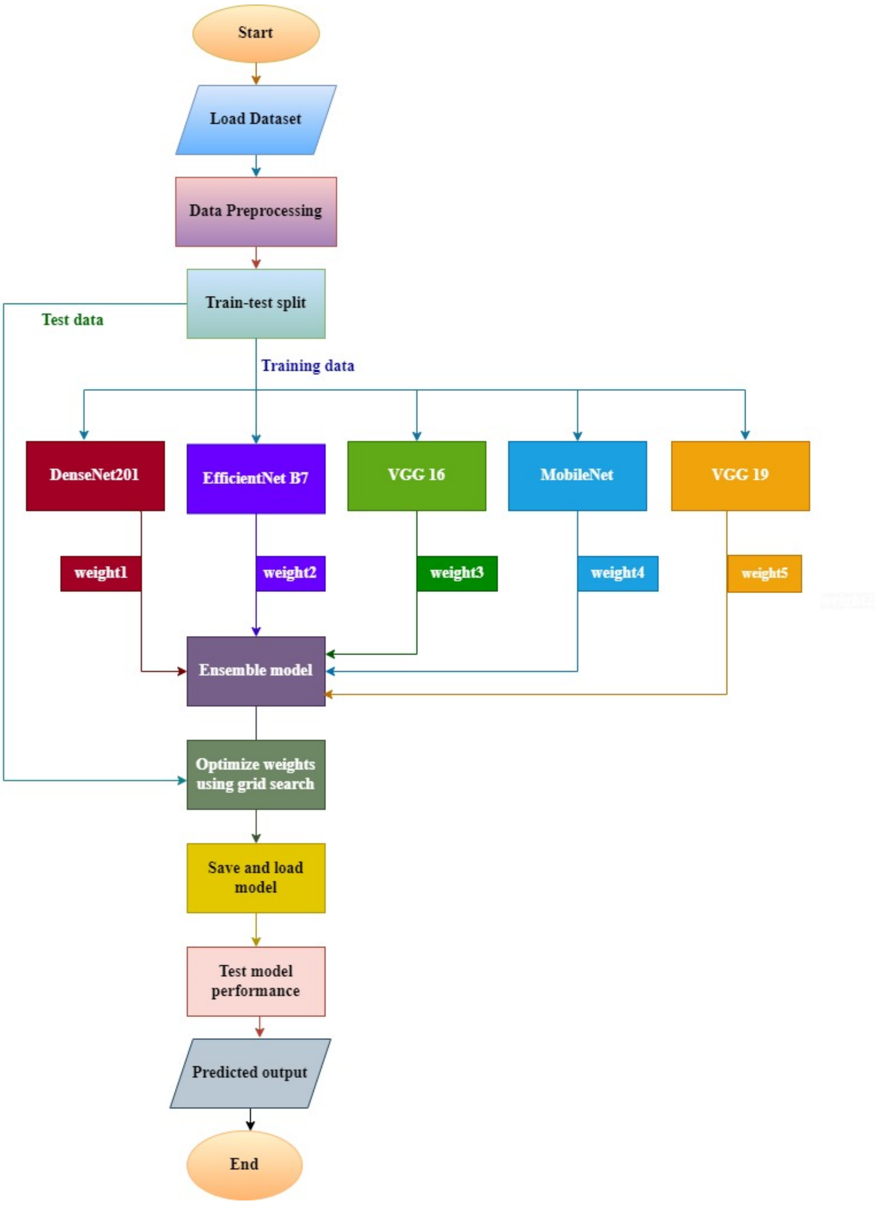


Figure 4.1: Flow Diagram of the Proposed Model.

4.3.1 Dataset

The National Center for Cancer Diseases/Iraq-Oncology Teaching Hospital (IQ-OTH/NCCD) dataset is utilized [129]. It comprises the CT Scan images concerning both healthy individuals and unhealthy patients with lung cancer at different stages gathered from hospitals in the year 2019. The dataset contains 1097 CT scan images of 110 patients involving different categories- benign (120 cases), malignant (561 cases), and normal (416 cases). There are also variations in the size of images ranging from 515 x 515 to 512 x 801. The cases vary in terms of living arrangements, residential areas, gender, age, and level of education. Figure 4.2 depicts the sample data belonging to malignant, benign, and normal cases respectively of the dataset.


Malignant case
Benign case
Normal case

Figure 4.2: Sample Input CT Scan Images at Different Stages of Lung Cancer.

4.3.2 Data Preprocessing

Image preprocessing methods are commonly employed on image samples to enhance classification precision by sharpening and eliminating noise. All the images in the dataset were converted to grayscale, which removed color information and reduced complexity. Then, to guarantee consistency throughout the dataset, the grayscale images were enlarged to a standard image size of 224 by 224 pixels. The images were then subjected to Gaussian blur to improve the quality and minimize noise. Ultimately, the images' pixel values were scaled to a range of 0 to 1 to normalize them. This normalization stage helped in stabilizing and accelerating the model's learning process.

4.3.3 Spliting of Dataset

After preprocessing the dataset was split into 3 different folders namely training, validation, and testing. The first 70% of the data is split into training, the next 15% into validation, and the remaining 15% for testing. Each set contains a randomly selected, well-balanced selection of images from each class. This distribution balances the need to have sufficient training data. It also ensures there is enough validation and test data to provide meaningful insights into performance and generalization.

4.3.4 Data Augmentation

The dataset used has an unequal distribution of the number of images per class. Having imbalanced data can lead to biases in classification. Hence, Data Augmentation using Elastic transformation [130] has been used to augment and balance the classes in the training set to ensure each class has the same number of images. Data augmentation has been performed using the ImageDataGenerator class from the Keras library.

The data generator access the images from the directory and applied a series of random transformations to each image, including rotation, translation, shearing, zooming, and flipping. This allowed the model to generate many different variations of each training image.The transformation is governed by three key parameters: alpha, sigma, and alpha affine.

Alpha controls the intensity of the transformation, dictating the magnitude of pixel displacement. *Sigma* determines the smoothness of the deformation field. *Alpha affine* introduces affine transformations to control the global displacement of the image grid. These parameters enable the production of a range of altered images, which are essential for effectively training the model. It also controls the direction and magnitude of deformations.

Techniques like elastic transformations, introduce controlled variability while preserving the base structure of the images. This will enable the model to generalize more without modifying target class visual characteristics. The values of the parameters alpha, sigma, and alpha affine were chosen based on their effectiveness in prior literature, and we visually supervised the augmented outputs to avoid excessive distortion in images. Thus, the augmentation techniques do not create inappropriate images and or reduce model performance. Instead, they are an enrichment of the dataset diversity which helps in combating class imbalance and enhancing model robustness.

To balance the dataset, the target maximum is determined, which is 392 in our case. For every class, the number of images needed to reach the target maximum is then determined, and the necessary number of modified images is produced by transforming the pre-existing images. By ensuring that every class is fairly represented, this procedure helps the model perform better when generalizing across different samples. Figure 4.3 shows the distribution of classes before and after augmentation.

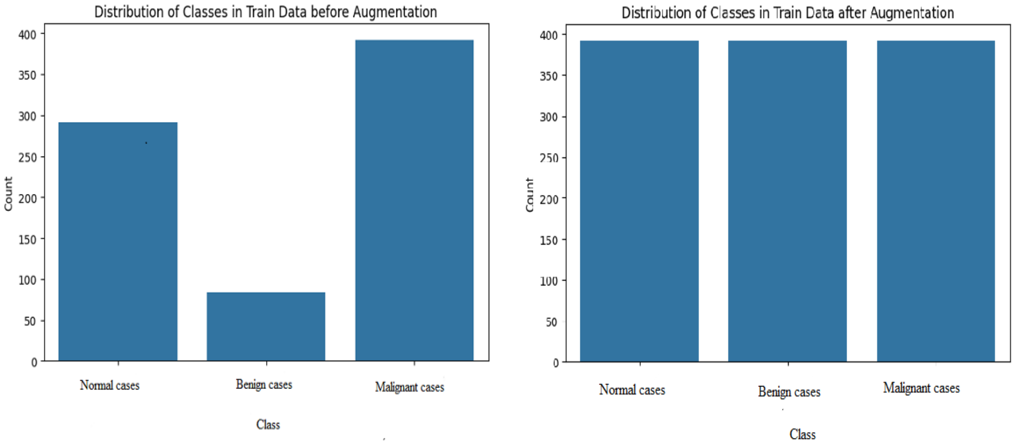


Figure 4.3: Distribution of Classes Before and After Augmentation.

4.3.5 Proposed Weighted Average Ensemble Model

Using a single model can be biased toward the specific aspects of data, and certain critical patterns can be missed. Consequently, different models are integrated to maximize their strengths and minimize their weaknesses [131, 132]. To enhance model performance, making them more accurate, and reliable ensemble methods like weighted average ensembles can be used. The ensemble method improves the overall accuracy by combining the trained model's performances rather than using any single model. In a weighted average ensemble method, predictions from different models are combined and the average of the result is utilized. A weighted average ensemble using Convolutional Neural Networks (CNNs) is a powerful technique in deep learning to improve models' accuracy and robustness. The proposed work combines five CNN models: DenseNet201, EfficientNetB7, VGG16, MobileNetV1, and VGG19. The following subsection orients with the layered architecture of these models.

DenseNet201

Due to its architectural uniqueness, DenseNet201 can perform better feature learning than other CNN architectures. Every layer in a DenseNet201 takes input from all its preceding layers, which helps it in better information flow and at the same time leads to more efficient feature reuse. Each layer of DenseNet201 is directly and feed-forward coupled to every other layer. All dense blocks are divided by transition layers, which consist of a convolution and pooling process, this helps to prevent the deep model from becoming more complex and compresses the feature maps dimensionality. Dense connectivity and transition layers allow for the efficient flow of information and gradients, and thus the DenseNet201 quickly learns relevant features with fewer parameters and computational resources [133].

DenseNet201 was selected for its unique architecture to promote feature reusability through the interconnection of each layer with all the others. This architecture results in the minimum number of parameters with high levels of performance, which is beneficial in applications where efficiency in computing is a concern. Table 4.1 depicts the detailed layer configuration of the DenseNet201 model used in the study.

Table 4.1: DenseNet201 Layer Configuration

Layer	**Output Size**	**Number of Filters**	**Kernel Size**	**Output Shape**	**Parameters**
DenseNet-201 (Functional)	-	-	-	(None, 8, 8, 1920)	18,321,984
Initial Convolution Layer	112x112	64	7x7	(112, 112, 64)	9,472
Max Pooling	56x56	-	3x3	(56, 56, 64)	0
Dense Block 1	56x56	256	-	(56, 56, 256)	94,464
Transition Layer 1	28x28	128	1x1	(28, 28, 128)	32,896
Dense Block 2	28x28	512	-	(28, 28, 512)	367,104
Transition Layer 2	14x14	256	1x1	(14, 14, 256)	131,584
Dense Block 3	14x14	1024	-	(14, 14, 1024)	5,242,880
Transition Layer 3	7x7	512	1x1	(7, 7, 512)	524,800
Dense Block 4	7x7	1920	-	(7, 7, 1920)	12,446,720
Global Average Pooling	1x1	-	-	(None, 1920)	0
Dense Layer 1	1x1	-	-	(None, 128)	245,888
Dropout	1x1	-	-	(None, 128)	0
Dense Layer 2	1x1	-	-	(None, 3)	387

EfficientNetB7

EfficientNet B7 is a much more robust deep learning model concerning both performance and computational efficiency. It has a compound scaling technique specific to scale up network width,depth,and resolution in a balanced way. Thus, EfficientNet B7 is better in terms of precision and efficiency compared to the traditional CNN. This is a baseline of the Neural Architecture Search (NAS)-generated network by using MBConv blocks. Depthwise separable convolutions are applied on Mobile Inverted Bottleneck Convolution (MBConv) blocks. All of these 'convolutions' are augmented in a way that reduces parameters and computational cost with Squeeze-and-Excitation modules. Swish activation and various regularization techniques are applied to enhance the model in terms of performance as well as the robustness of the model [32].

EfficientNet B7 is chosen due to its state of the art performance for balancing between efficiency and accuracy by scaling network dimensions uniformly. In terms of quality, it is considerably higher than many of the traditional methods with a lower computational burden, which makes it an ideal candidate for high-performance applications.Table 4.2 depicts the detailed layer configuration of the EfficientNet B7 model used in the study.

VGG16

The VGG16 is designed by the University of Oxford's Visual Geometry Group. It is a deep CNN with quite a simple and uniform architecture, thus the implementation and extension of this network is quite easy. The architecture consists of 16 layers where parameters are learned: 13 convolutional and also 3 fully connected. Every convolutional layer uses small receptive fields of 3x3 filters applied with a stride of 1 and padding to retain spatial resolution followed by a max-pooling layer using 2x2 filters reducing dimensionality and computational complexity. Since the convolutional layers are organized into blocks, each block consists of a set of convolutional layers followed by a max-pooling layer. This arrangement progressively reduces the spatial dimensions while increasing the depth of the feature maps. The final layer is a softmax classifier that generates the output [134].

Table 4.2: EfficientNet B7 Layer Configuration

Layer (type)	**Output Size**	**Number of Filters**	**Kernel Size**	**Output Shape**	**Parameters**
EfficientNetB7 (Functional)	8x8	-	-	(None, 8, 8, 2560)	64,097,687
Initial Convolution Layer	112x112	64	3x3	(112, 112, 64)	1,792
MBConv Block 1	112x112	32	3x3	(112, 112, 32)	5,888
MBConv Block 2	56x56	32	3x3	(56, 56, 32)	31,168
MBConv Block 3	56x56	48	5x5	(56, 56, 48)	134,304
MBConv Block 4	28x28	48	5x5	(28, 28, 48)	379,776
MBConv Block 5	28x28	80	3x3	(28, 28, 80)	1,240,320
MBConv Block 6	14x14	80	3x3	(14, 14, 80)	3,580,480
MBConv Block 7	14x14	128	3x3	(14, 14, 128)	2,017,152
MBConv Block 8	7x7	128	3x3	(7, 7, 128)	6,015,360
MBConv Block 9	7x7	192	3x3	(7, 7, 192)	10,724,608
MBConv Block 10	7x7	320	3x3	(7, 7, 320)	4,702,080
MBConv Block 11	7x7	1280	1x1	(7, 7, 1280)	1,640,000
Global Average Pooling	1x1	-	-	(None, 2560)	0
Dense Layer 1	1x1	-	-	(None, 128)	327,808
Dropout	1x1	-	-	(None, 128)	0
Dense Layer 2	1x1	-	-	(None, 3)	387

VGG 16 can extract complex hierarchical features pretty well and would also work for an array of Image Classification tasks with decent accuracy due to its consistent architecture and deeper layers. It has been included primarily because of its robust performance across many different domains. Table 4.3 depicts the detailed layer configuration of the VGG16 model used in the study.

MobileNetV1

MoblieNetV1 is a convolutional neural network model crafted for embedded and mobile systems. The novelty is in the use of depth-wise separable convolutions used to break down a standard convolution into spatial convolutions operation, followed by cross-channel convolutions operation. It keeps competitive accuracy and also reduces the model size and computing complexity. It achieves very high efficiency with limited computational resources by concentrating depth-wise convolutions on the spatial correlations in channels and point-wise convolutions to combine information across channels. It also introduces two parameters to set network width in terms of the number of channels and input resolution, giving an option to make the right choices between accuracy and performance subject to deployment constraints. It has a compact structure and efficient architecture that enables the model to run quickly on these devices without sacrificing classification accuracy [135].

Table 4.3: VGG16 Layer Configuration

Layer (type)	**Output Size**	**Number of Filters**	**Kernel Size**	**Output Shape**	**Parameters**
Input Layer	224x224	-	-	(224, 224, 3)	0
Conv2D Layer1	224x224	64	3x3	(224, 224, 64)	1,792
Conv2D Layer2	224x224	64	3x3	(224, 224, 64)	36,928
MaxPooling2D Layer1	112x112	-	2x2	(112, 112, 64)	0
Conv2D Layer3	112x112	128	3x3	(112, 112, 128)	73,856
Conv2D Layer4	112x112	128	3x3	(112, 112, 128)	147,584
MaxPooling2D Layer2	56x56	-	2x2	(56, 56, 128)	0
Conv2D Layer5	56x56	256	3x3	(56, 56, 256)	295,168
Conv2D Layer6	56x56	256	3x3	(56, 56, 256)	590,080
Conv2D Layer7	56x56	256	3x3	(56, 56, 256)	590,080
MaxPooling2D Layer3	28x28	-	2x2	(28, 28, 256)	0
Conv2D Layer8	28x28	512	3x3	(28, 28, 512)	1,180,160
Conv2D Layer9	28x28	512	3x3	(28, 28, 512)	2,359,808
Conv2D Layer10	28x28	512	3x3	(28, 28, 512)	2,359,808
MaxPooling2D Layer4	14x14	-	2x2	(14, 14, 512)	0
Conv2D Layer11	14x14	512	3x3	(14, 14, 512)	2,359,808
Conv2D Layer12	14x14	512	3x3	(14, 14, 512)	2,359,808
Conv2D Layer13	14x14	512	3x3	(14, 14, 512)	2,359,808
MaxPooling2D Layer5	7x7	-	2x2	(7, 7, 512)	0
VGG16 (Functional Layer)	-	-	-	(None, 8, 8, 512)	14,714,688
Global Average Pooling layer	1x1	-	-	(None, 512)	0
Dense Layer 1	1x1	-	-	(None, 128)	65,664
Dropout	1x1	-	-	(None, 128)	0
Dense Layer 2	1x1	-	-	(None, 3)	387

The reason for choosing MobileNet V1 was because it was streamlined architecture, especially designed for mobile and embedded vision applications. It uses depthwise separable convolutions, that could achieve high accuracy while model size and computations demanded are essential for efficient inference. Table 4.4 depicts the detailed layer configuration of the MobileNet model used in the study.

Table 4.4: MobileNetV1 Layer Configuration

Layer	**Output Size**	**Number of Filters**	**Kernel Size**	**Output Shape**	**Parameters**
Input	150,528	-	-	(None, 224, 224, 3)	0
Conv1	401,408	32	3x3	(None, 112, 112, 32)	864
Conv1_BN	401,408	-	-	(None, 112, 112, 32)	128
Conv1_ReLU	401,408	-	-	(None, 112, 112, 32)	0
Conv_dw1	401,408	32	3x3	(None, 112, 112, 32)	288
Conv_pw1	802,816	64	1x1	(None, 112, 112, 64)	2,112
Conv_pw1_BN	802,816	-	-	(None, 112, 112, 64)	256
Conv_pw1_ReLU	802,816	-	-	(None, 112, 112, 64)	0
Conv_dw2	200,704	64	3x3	(None, 56, 56, 64)	576
Conv_pw2	401,408	128	1x1	(None, 56, 56, 128)	8,320
Conv_pw2_BN	401,408	-	-	(None, 56, 56, 128)	512
Conv_pw2_ReLU	401,408	-	-	(None, 56, 56, 128)	0
Conv_dw4	100,352	128	3x3	(None, 28, 28, 128)	1,152
Conv_pw4	200,704	256	1x1	(None, 28, 28, 256)	33,024
Conv_pw4_BN	200,704	-	-	(None, 28, 28, 256)	1,024
Conv_pw4_ReLU	200,704	-	-	(None, 28, 28, 256)	0
Conv_dw6	50,176	256	3x3	(None, 14, 14, 256)	2,304
Conv_pw6	100,352	512	1x1	(None, 14, 14, 512)	131,584
Conv_pw6_BN	100,352	-	-	(None, 14, 14, 512)	2,048
Conv_pw6_ReLU	100,352	-	-	(None, 14, 14, 512)	0
Conv_dw11	25,088	512	3x3	(None, 7, 7, 512)	4,608
Conv_pw11	50,176	1024	1x1	(None, 7, 7, 1024)	525,312
Conv_pw11_BN	50,176	-	-	(None, 7, 7, 1024)	4,096
Conv_pw11_ReLU	50,176	-	-	(None, 7, 7, 1024)	0
GlobalAveragePooling	1024	-	-	(None, 1024)	0
Dense	1000	-	-	(None, 1000)	1,025,000
MobileNetV1	65,536	1024	-	(None, 8, 8, 1024)	3,228,864
GlobalAveragePooling	1024	-	-	(None, 1024)	0
Dense Layer 1	128	-	-	(None, 128)	131,200
Dropout	128	-	-	(None, 128)	0
Dense Layer 2	3	-	-	(None, 3)	387

VGG19

The VGG19 model is created by adding three more convolutional layers to the VGG16 model, which has 19 layers overall with learnable parameters. The convolutional layers are organized into blocks, with each block followed by a max-pooling layer. The final three fully connected layers lead to a softmax layer producing the final class probabilities. It learns subtle features and patterns in the image thus yielding high accuracy. The uniform use of small filters brings along implementation and extensibility [134].

VGG19, provides a deeper network that can capture more complex features. The added layers can improve performance on intricate datasets, justifying its inclusion in our study for comparison with other architectures.Table 4.5 depicts the detailed layer configuration of the VGG16 model used in the study.

Table 4.5: VGG19 Layer Configuration

Layer (type)	**Output Size**	**Number of Filters**	**Kernel Size**	**Output Shape**	**Parameters**
Input Layer	224x224	-	-	(224, 224, 3)	0
Conv2D_1	224x224	64	3x3	(224, 224, 64)	1,792
Conv2D_2	224x224	64	3x3	(224, 224, 64)	36,928
MaxPooling2D_1	112x112	-	2x2	(112, 112, 64)	0
Conv2D_3	112x112	128	3x3	(112, 112, 128)	73,856
Conv2D_4	112x112	128	3x3	(112, 112, 128)	147,584
MaxPooling2D_2	56x56	-	2x2	(56, 56, 128)	0
Conv2D_5	56x56	256	3x3	(56, 56, 256)	295,168
Conv2D_6	56x56	256	3x3	(56, 56, 256)	590,080
Conv2D_7	56x56	256	3x3	(56, 56, 256)	590,080
Conv2D_8	56x56	256	3x3	(56, 56, 256)	590,080
MaxPooling2D_3	28x28	-	2x2	(28, 28, 256)	0
Conv2D_9	28x28	512	3x3	(28, 28, 512)	1,180,160
Conv2D_10	28x28	512	3x3	(28, 28, 512)	2,359,808
Conv2D_11	28x28	512	3x3	(28, 28, 512)	2,359,808
Conv2D_12	28x28	512	3x3	(28, 28, 512)	2,359,808
MaxPooling2D_4	14x14	-	2x2	(14, 14, 512)	0
Conv2D_13	14x14	512	3x3	(14, 14, 512)	2,359,808
Conv2D_14	14x14	512	3x3	(14, 14, 512)	2,359,808
Conv2D_15	14x14	512	3x3	(14, 14, 512)	2,359,808
Conv2D_16	14x14	512	3x3	(14, 14, 512)	2,359,808
MaxPooling2D_5	7x7	-	2x2	(7, 7, 512)	0
VGG19 (Functional layer)	-	-	-	(None, 8, 8, 512)	20,024,384
Global Average Pooling layer	1x1	-	-	(None, 512)	0
Dense Layer 1	1x1	-	-	(None, 128)	65,664
Dropout	1x1	-	-	(None, 128)	0
Dense Layer 2	1x1	-	-	(None, 3)	387

Weighted Average Ensemble with Grid Search (DEV-MV)

An ensemble of predictions by five independent CNN models—DenseNet201, EfficientNet B7, VGG16, MobileNet V1, and VGG19 was prepared to enhance model accuracy. Running every model over the test dataset, obtaining individual predictions, and calculating their respective accuracies were done to get an initial set of weights for models in this preliminary weighted ensemble version.To ensure optimum precision, the best possible combination of weights was found via a grid search. The weighted predictions from every model were summed to obtain the forecasts from the ensembling, and accuracy was calculated. Figure 4.4 illustrates an ensemble learning, where five different deep learning models are combined to enhance the performance of the classification. Every model has a sequence comprising two dense layers with a dropout layer in between. It prevents overfitting by randomly dropping a fraction of the number of units during training.

The outputs from these models were combined using an average weighted ensemble method in which each model is assigned a weight, wi(w1,w2,w3,w4,w5). It was characterized by these weights' contribution in making the final prediction. The weights were tuned by running the grid search algorithm, enabling this ensemble to allow better performance overall.

Algorithm 3 summarizes its stages from fetching a dataset, and then doing all the necessary steps in preprocessing—the extension and normalization of data. After that, it splits data for training and trains five different models: Model1 to Model5. Each model is trained iteratively for the number of epochs specified, where the preprocessed images are augmented and passed to each model to return accuracy scores and validation accuracies. After teaching the models, save and load them for ensemble modeling. Initial weights for each model are set, and predictions from all models are weighted and added together to create an ensemble prediction. It then computes the ensemble accuracy and applies grid search to optimize weights by trying out all different combinations that could maximize accuracy. Finally, the performance of the ensemble model will be evaluated to predict the types of lung cancer using test data, hence ending the process.

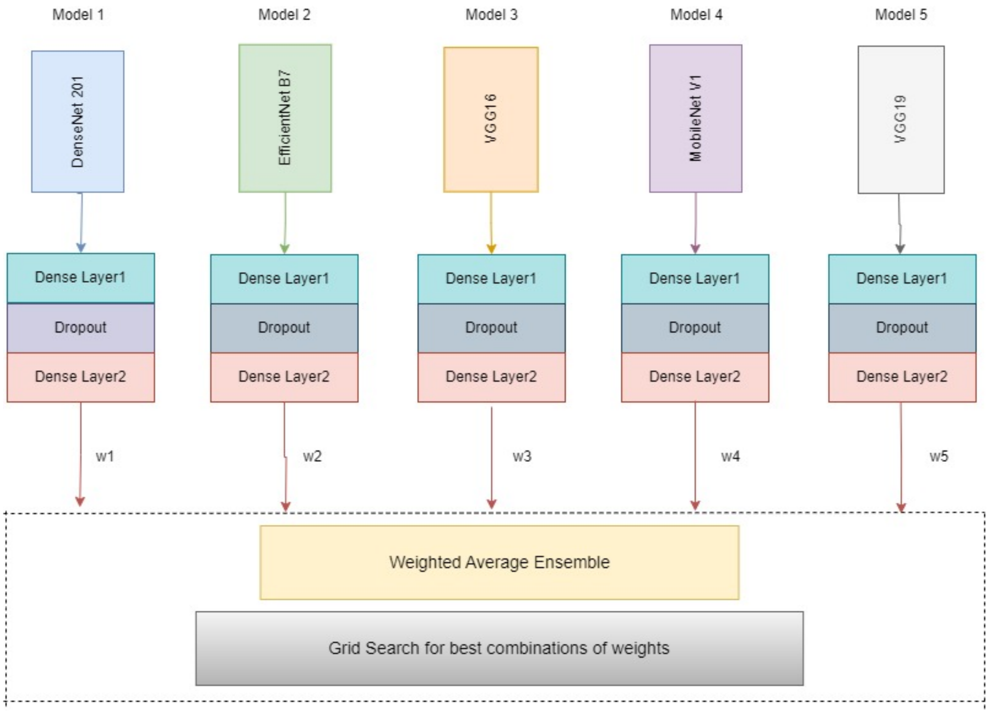


Figure 4.4: DEV-MV Architecture.

Algorithm 4 explains the procedure for training multiple models with early stopping based on validation loss. The training would involve running over each epoch up to maximum epochs. In each epoch, model training and validation are done. In case the validation loss improves, then the algorithm updates best validation loss and resets epochs without improvement to 0. Otherwise, it increments epochs without improvement. If the number of epochs with no improvement reaches or exceeds the patience, training will stop to prevent overfitting. This ensures training will stop when validation loss improvement is no longer seen.The proposed Algorithm 3 and 4 are described below.

Proposed Ensemble Reinforcement Learning Model

Ensemble Reinforcement Learning has emerged as one of the promising approaches towards the integration of both RL and ensemble learning. The figure 4.5 illustrates how ensemble learning and reinforcement learning are combined to improve prediction accuracy and dependability in the healthcare industry. An illustration of data processing and prediction workflow that uses IoMT devices, local servers, deep learning (DL) models, reinforcement learning (RL) agents, and a central cloud server is shown.

Algorithm 3 Proposed Ensemble Approach (DEV-MV) for Lung Cancer Detection

```
Require: CT Scan Images from the dataset      $M$: Models
Ensure: Classification of lung cancer types
Start
Get Dataset
Preprocess Data
Split Data
Define layered architecture of all models $M = \{M_1, M_2, M_3, M_4, M_5\}$
For each model $M_i$ in the set of models $M$:
    – Call Algorithm 4 with model $M_i$ and the Preprocessed dataset.
Save Models
Load Models
Set initial weights $w_1, w_2, w_3, w_4, w_5$
Model Ensembling
Calculate ensemble prediction as:
    $\text{Ensemble\_Prediction} = \sum_{i=1}^{5} w_i \cdot \text{M}_i\_Prediction$
Get Ensemble accuracy
Apply Grid Search to Optimize Weights
Loop through all combinations of weights $w_1, w_2, w_3, w_4, w_5$:
    – Calculate the corresponding weighted ensemble accuracy.
    – If this accuracy is the highest so far, store the ensemble weights.
Evaluate the best ensemble on the test set
End
```

Algorithm 4 Algorithm for Training Multiple CNN Models

```
Input: Model $M_i$, Preprocessed dataset
Output: Trained model $M_i$
Start
Initialize model training parameters:
  Set max_epochs ← 20
  Set patience ← 5
  Set optimizer ← Adam
  Set epochs_without_improvement ← 0
  Set best_val_loss ← ∞
for epoch $i$ ← 1 to max_epochs do
    Train and validate model $M_i$
    if validation loss < best_val_loss then
        Update best_val_loss ← validation loss
        Reset epochs_without_improvement ← 0
    end
    else
        Increment epochs_without_improvement ← epochs_without_improvement + 1
    end
    if epochs_without_improvement ≥ patience then
        Stop training  break
    end
end
End
```

Algorithm 5 describes an ensemble learning framework in healthcare for multiple local servers that employ reinforcement learning to improve deep learning model predictions. These refined predictions are then aggregated in a central cloud server for further processing and decision-making. Data collection begins at various IoMT devices, such as ECG machines and smartwatches, which transmit raw data to the local servers for subsequent processing. Each server preprocesses this data and extracts relevant features, after which they feed it into different DL models, like DenseNet, EfficientNet, MobileNet, etc., to generate the initial predictions.

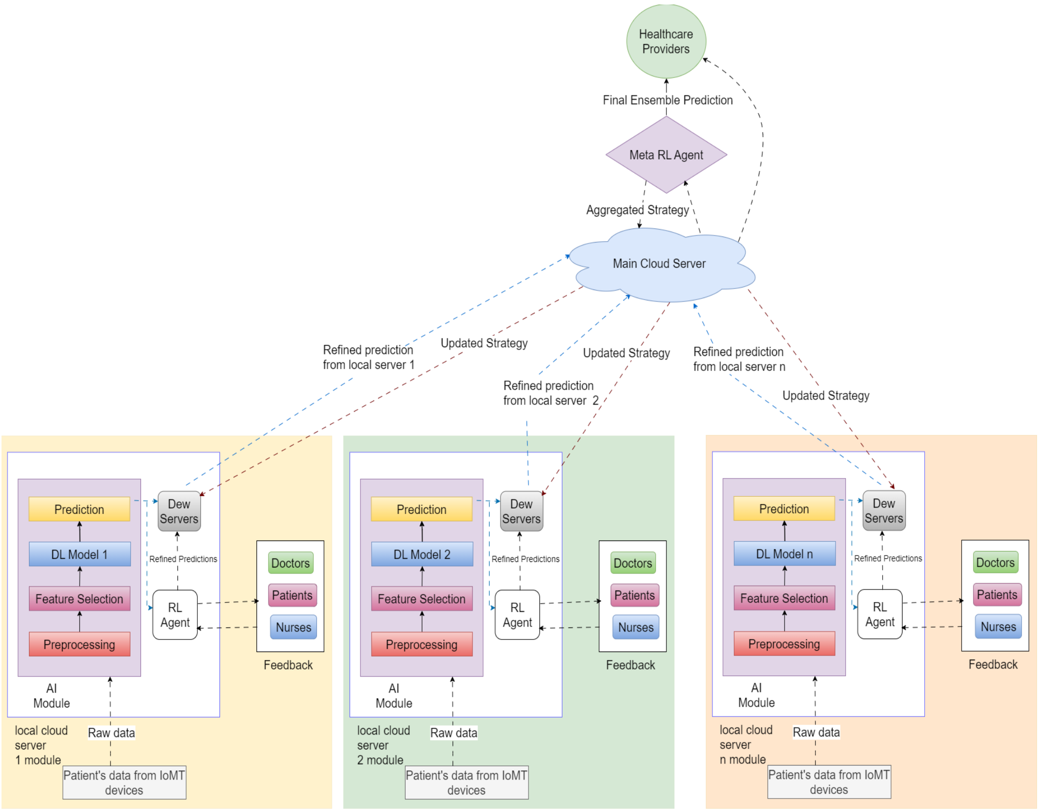


Figure 4.5: Proposed Ensemble Reinforcement Learning Architecture.

Each server at a local level has a reinforcement learning agent that continuously monitors the accuracy of these predictions. In this regard, the agents receive feedback from healthcare professionals—doctors, patients, and nurses—which acts as a reward or penalty signal. The RL agent dynamically adjusts the DL models based on feedback to improve prediction accuracy over time. The process embodies reinforcement ensemble learning, wherein multiple models are adjusted and fitted optimally by reinforcement learning techniques to produce a more robust ensemble prediction.

The key to aggregating all the predictions of the local servers lies with the main cloud server, which connects with a Meta-RL agent. This refines the overall prediction strategy using aggregated feedback and sends updates back to the local servers for further optimization of their models. This iterative, collaborative process ultimately results in a final ensemble prediction that health providers can use for informed decision-making. This model is designed to continuously improve predictive models across a distributed network of servers through real-time feedback and adjustments.

Algorithm 5 Ensemble Learning with Reinforcement Learning in Lung Cancer Diagnosis

```
Input: Patient data $D_1, D_2, \ldots, D_n$ from IoMT devices
Input: Local models $M_1, M_2, \ldots, M_n$
Input: Local RL agents $RL_1, RL_2, \ldots, RL_n$
Input: Main cloud server $CS$
Input: Meta RL agent $MetaRL$
Output: Final ensemble prediction $P_{ensemble}$
Start
Initialize AI module and local RL agents at each local server
for each local server $i \leftarrow 1$ to $n$ do
    Collect patient data $D_i$ from IoMT$_i$
    Preprocess data: $D_i^{'} \leftarrow P_i(D_i)$
    Select relevant features: $F_i^{'} \leftarrow F_i(D_i^{'})$
    Generate local prediction: $P_i^{local} \leftarrow M_i(F_i^{'})$
    Refine local prediction using RL agent: $P_i^{refined} \leftarrow RL_i(P_i^{local})$
    Send refined prediction $P_i^{refined}$ to central cloud server $CS$
end
Aggregate predictions at cloud server: $P_{agg} \leftarrow \frac{1}{n}\sum_{i=1}^{n} P_i^{refined}$
Meta RL agent learns from aggregated predictions: $S_{updated} \leftarrow MetaRL(P_{agg})$
for each local server $i \leftarrow 1$ to $n$ do
    Send updated strategy $S_{updated}$ from cloud server $CS$ to local server $i$
    Update RL agent $RL_i \leftarrow S_{updated}$
end
Generate final ensemble prediction at cloud server: $P_{ensemble} \leftarrow MetaRL(P_{agg})$
Deliver $P_{ensemble}$ to healthcare providers
Collect feedback from healthcare providers, doctors, patients, and nurses
for each local server $i \leftarrow 1$ to $n$ do
    Use feedback to improve RL agents: $RL_i \leftarrow$ Feedback
end
End
```

4.4 Results and Discussion

All the experiments were done on the Colab Pro GPU provided by Google. Every experiment carried out on the multiclass lung cancer dataset is shown in this section. We have used efficient ensemble deep-learning architectures that consumed very few resources. For the study, a learning rate of 0.0001, a batch size of 16, 20 epochs, and a loss function based on categorical cross-entropy were employed. Different optimization algorithms for the training of CNN (Adam, SGD, Adadelta, Adagrad and RMSprop) were used in this study. The experiments with different optimizers revealed the supremacy of Adam over other optimization methods in terms of accuracy as well as convergence rate, hence the suggested ensemble model is trained and tested using Adam optimization.

4.4.1 Results of Individual Deep Learning Models

Experiments were performed using individual fine-tuned deep learning models: DenseNet 201, EfficientNet B7, VGG-16, MobileNet V1, and VGG-19. The particular models were trained and tested using a loss function known as the categorical cross-entropy for benign, malignant, and normal cases, along with various optimizers- Adam (Adaptive Moment Estimation), Adagrad(Adaptive Gradient Descent), Adadelta, SGD (Stochastic Gradient Descent) and RMSprop(Root Mean Square Propagation), for optimizing their performance.

The results presented in table 4.6 show the accuracy comparison of the five different deep learning models using five optimizers. The analysis demonstrated that, when the models were trained using the Adam optimizer, they achieved the highest accuracy compared to the other optimizers. Hence, the Adam optimizer was selected for this work as it outperformed other optimizers. Each of the models applies transfer learning using ImageNet pre-trained weights. Each model adds custom output layers at the top, which include Dense and Global Average Pooling2D layers with Dropout layers to avoid overfitting at a rate of 0.5. The training runs up to 20 epochs and uses early stopping along with ReduceLROnPlateau, which drops learning rates by 0.2 when the validation loss plateaus to fine-tune the learning process.

Table 4.6: Accuracy Comparison of Different Models with Various Optimizers

Model	**Adam (%)**	**SGD (%)**	**Adagrad (%)**	**Adadelta (%)**	**RMSprop (%)**
DenseNet 201	97.59	96.78	95.49	96.89	97.21
EfficientNet B7	95.12	93.88	92.92	94.69	94.83
VGG 16	92.17	90.74	90.67	91.36	92.11
MobileNet V1	93.98	91.71	91.72	92.41	92.96
VGG 19	93.37	92.82	91.93	92.75	93.04

Table 4.7 depicts the performance metrics of individual models. DenseNet201 exhibits the highest performance with an accuracy of 97.59%, a weighted precision, recall, and F1-score of 98.03%, 97.6%, and 97.67% respectively. EfficientNet follows with strong metrics, while VGG16 and VGG19 have lower scores. MobileNet, also has slightly lower values than DenseNet201 and EfficientNet, indicating that DenseNet201 is the most robust among all other models. Figure 4.6 compares the accuracy, f1-score, precision, and recall of each model in terms of performance.

Table 4.7: Performance Metrics of Different Models

Model	**Accuracy (%)**	**Weighted Recall (%)**	**Weighted Precision (%)**	**Weighted F1-Score (%)**
DenseNet 201	97.59	97.60	98.03	97.67
EfficientNet B7	95.12	94.58	94.83	94.45
VGG 16	92.17	92.17	91.92	91.39
MobileNet V1	93.98	94.10	93.60	93.50
VGG 19	93.37	93.00	92.60	92.30

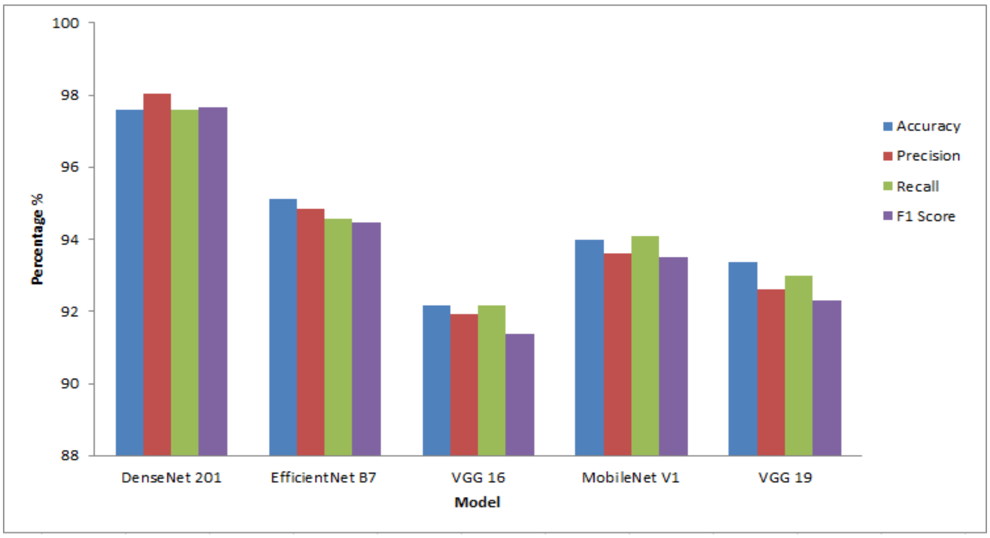
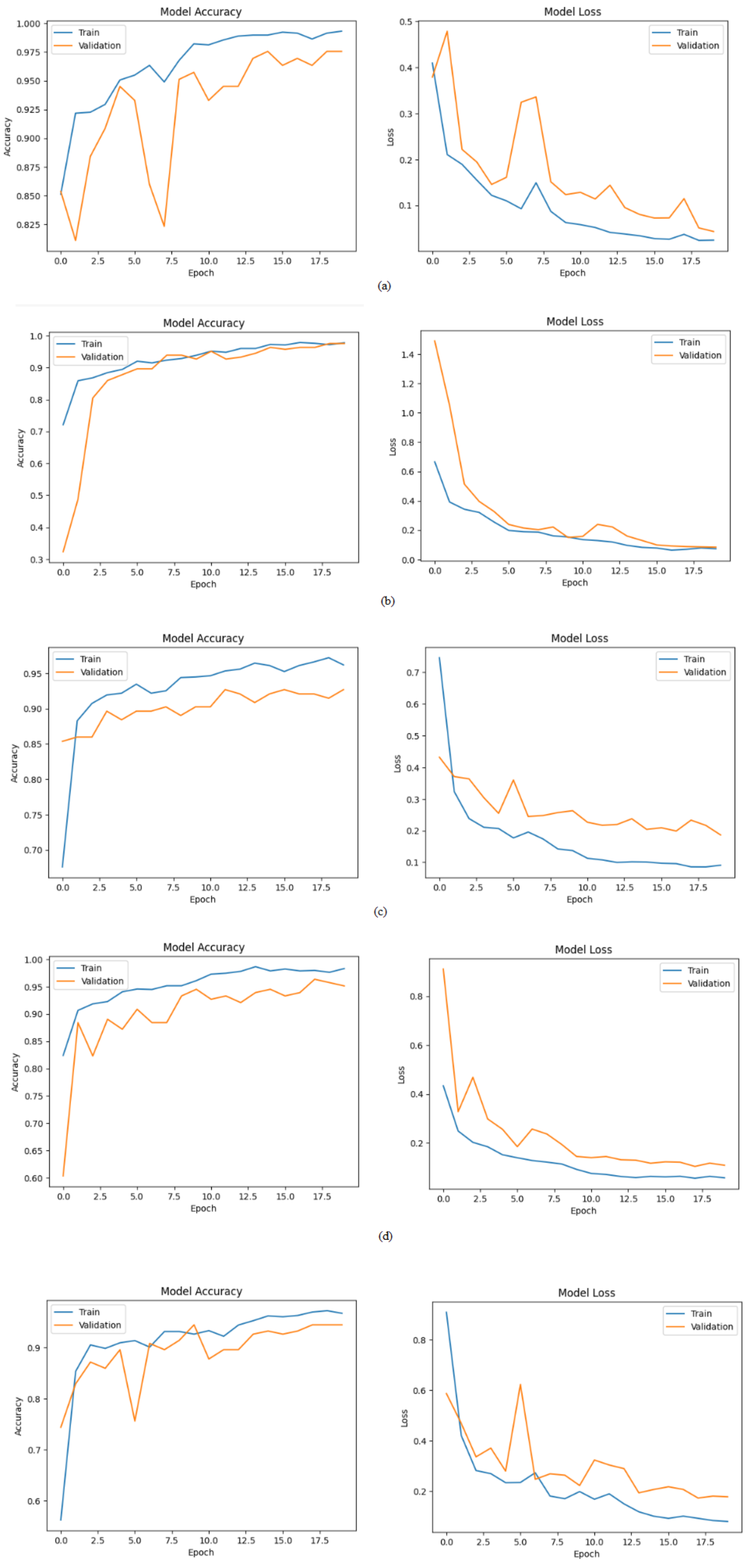


Figure 4.6: Comparison of Performance Metrics of Different Models

Figure 4.7 illustrates the performance metrics for loss and accuracy for various models across 20 epochs of training and validation. The figure 4.7 (a)shows the performance curve of DenseNet 201. As portrayed, the accuracy improved fast in the first 7 epochs and then stabilized at around 0.975 for the train and a bit lower for validation. Also, the loss decreased sharply initially and flattened out, with validation loss showing more fluctuation. The EfficientNet B7 performance curve is represented in figure 4.7 (b) which shows a steady increase, reaching above 0.95 for both training and validation. The loss decreased significantly for training and validation. Figure 4.7 (c) is the performance curve for the VGG 16, which started with an accuracy of around 0.85, increased steadily, and then stabilized at about 0.95. The loss decreased drastically initially and then progressively reduced; validation loss showed more variability. For the MobileNet, the accuracy reached about 0.97 and its validation was about 0.95, also consistent. The loss decreased smoothly for both training and validation as indicated in figure 4.7(d). The performance curve of VGG 19 in figure 4.7(e) shows that the accuracy starts lower but increases rapidly, stabilized around 0.95 for training and slightly less for validation. The loss decreased quickly in the initial epochs and then flattened, with some fluctuations in validation loss. Overall, each model shows an improvement in accuracy and a decrease in loss over the epochs, with some variations in the validation performance.



(a)

(b)

(c)

(d)

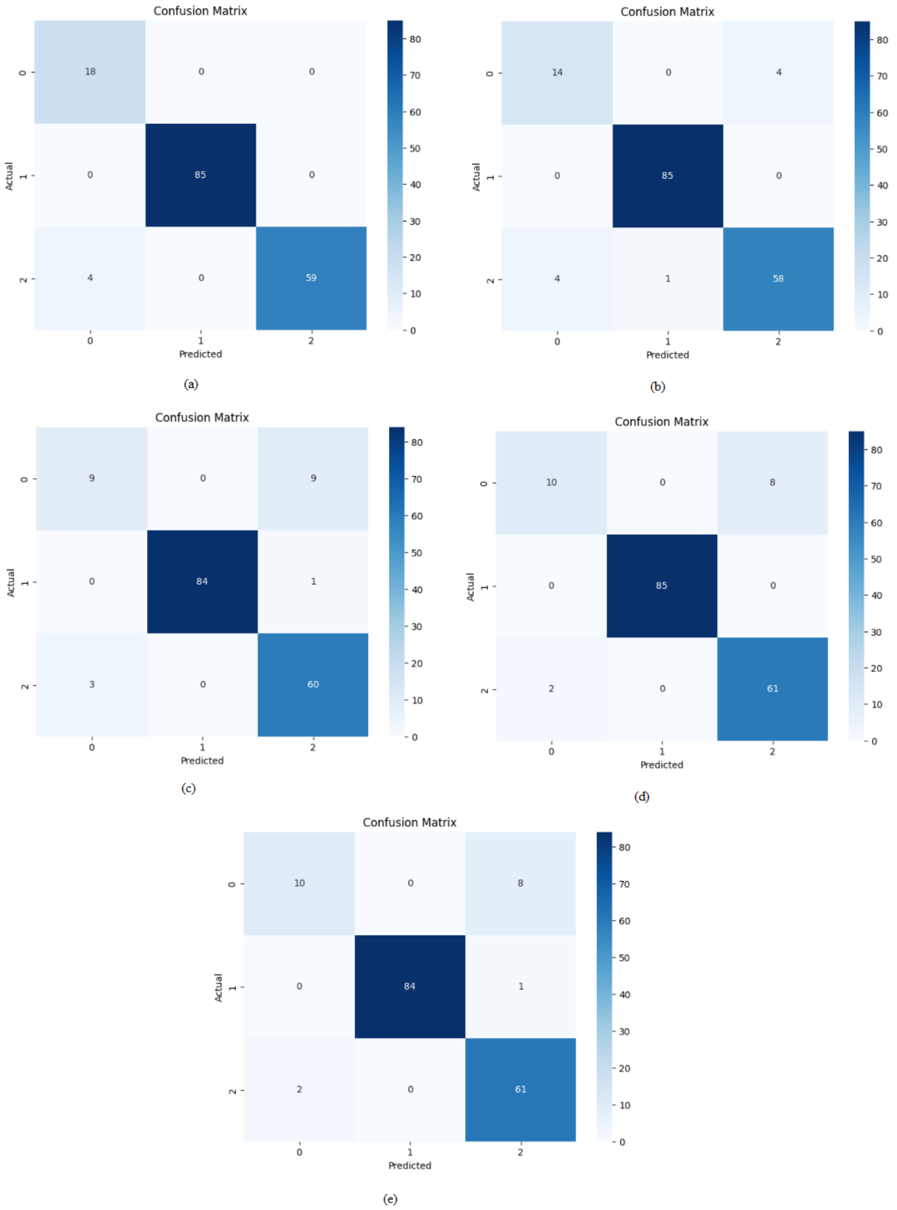
(e)

Figure 4.7: (a) DenseNet 201, (b) EffieientNet B7, (c) VGG 16, (d) MobileNet V1, and (e) VGG 19, Showing Accuracy and Loss.

The confusion matrix results of different models are shown in figure 4.8 where label 0 indicates Benign cases, 1 indicates Malignant cases and 2 indicates Normal cases. Each matrix compares the predicted classifications against the actual classifications. Model 4.8(a) correctly classifies 100% of benign, 95.5% of malignant cases, and 92.2% of the normal cases. Model 4.8(b) correctly identifies 77.8% of benign cases, 95.5% of malignant cases, and 90.6% of normal cases. Model 4.8(c) identified 50% of benign cases, 94.4% of malignant cases, and 93.8% of normal cases. Model 4.8(d) had an accuracy for benign cases at 55.6%, for malignant cases, it was 95.5%, while that of normal cases was 95.3%. For model 4.8(e), the accuracy for benign cases was 55.6%; for malignant it was 94.4%; and for normal cases, it stood at 95.3%. Thus, on average, the models are accurate in malignant and normal cases but varied in correctly identifying benign cases.

4.4.2 Results of the Proposed Ensemble Model and Weighted Average Ensemble Model Assisted with Grid Search (DEV-MV)

An ensemble of predictions by five independent CNN models—DenseNet201, EfficientNet B7, VGG16, MobileNet V1, and VGG19 was prepared to enhance model accuracy. A comparative analysis was taken while deciding on the 5 CNN models, to check their complementary strengths. Even though VGG19 is the extended version of VGG16, it also pushes forward its deeper architecture in capturing more complex features. VGG16, however, is a shallower network and may generalize better on other datasets, especially relating to the computational resources or nuances of the particular task at hand.



(a) (b) (c) (d) (e)

Figure 4.8: Confuion Matrix for (a) DenseNet 201, (b) EffieientNet B7, (c) VGG 16, (d) MobileNet V1, and (e) VGG 19.

Since all the five CNN models used in this study have an error rate of less than 50% (as the accuracy of all individual models is more than 50%), they meet the criteria mentioned by Sebastian Raschka [136]. According to Raschka, ensemble methods consistently outperform individual classifiers if the base classifiers are at least moderately accurate, with error rates below random guessing ($\varepsilon < 0.5$). Raschka explains this using combinatorics, where the error probability of an ensemble is calculated through a binomial distribution. The ensemble error rate,

P_{ensemble}, is represented by the formula:

$$P_{\text{ensemble}}(y \geq k) = \sum_{k=\lceil \frac{n+1}{2} \rceil}^{n} \binom{n}{k} \cdot \varepsilon^{k}(1-\varepsilon)^{n-k} \tag{4.1}$$

This formula demonstrates that combining multiple classifiers (such as VGG16 and VGG19) can reduce the overall error rate, as the ensemble is less likely to make incorrect predictions than any single base classifier.

The table 4.8 presents the performance metrics of the models: Proposed Ensemble and Proposed Weighted Average Ensemble with Grid Search (DEV-MV). It contains accuracy, weighted F1-score, weighted precision, and weighted recall in percentages. The proposed ensemble attained an accuracy of 98.20%, a weighted precision of 95.96%, a weighted recall of 97.16%, and a weighted F1-score of 96.53%. The Proposed Ensemble with Grid Search—the improved model—gave an accuracy of 99.40%, a weighted precision of 98.25%, a weighted recall of 99.47%, and a weighted F1 score of 98.85%. These results further validate that although both models demonstrated good performance, the Proposed Ensemble with Grid Search had better accuracy and precision, evidencing that grid search optimization improves the performance of the model.

Table 4.8: Performance Metrics of Proposed Ensemble Model and Proposed DEV-MV.

Model	**Accuracy (%)**	**Weighted Recall (%)**	**Weighted Precision (%)**	**Weighted F1-Score (%)**
Proposed Ensemble	98.20	97.16	95.96	96.53
Proposed DEV-MV	99.40	99.47	98.25	98.85

The figure 4.9 illustrates the performance metrics of the three models: DenseNet 201, Proposed Ensemble, and Proposed Ensemble with Grid Search. The metrics included were Accuracy, Recall, Precision, and F1 Score. The DenseNet 201 model outperformed other models initially taken; it turned in quite a good result on all metrics. The Proposed Ensemble model could not perform well on both Precision and Recall. The proposed ensemble method with grid search had the highest among all metrics, significantly higher than the other two models: it had an accuracy and a recall close to 100%, an extremely high F1 score, and precision was the highest.

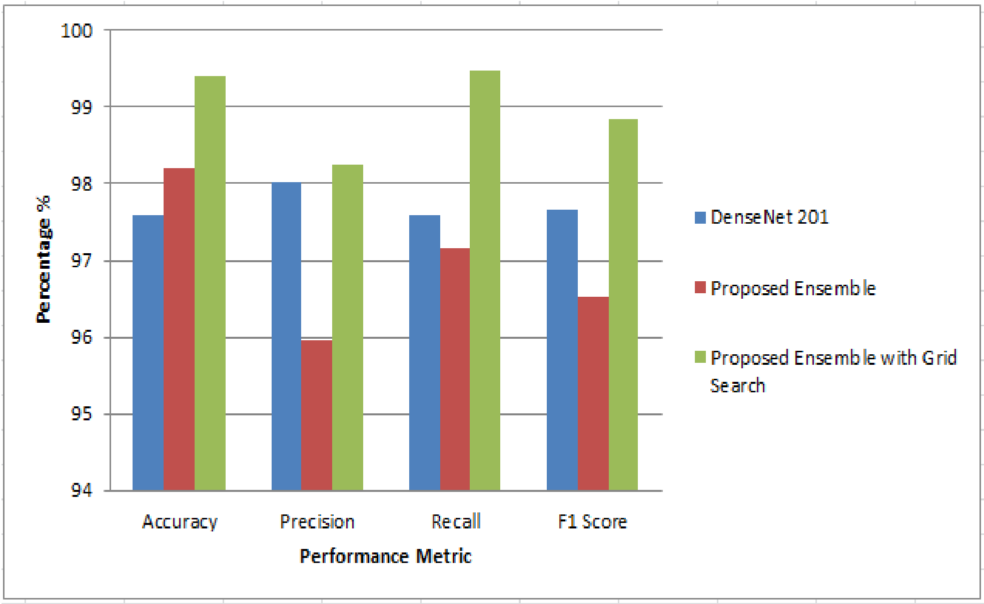


Figure 4.9: Comparison of Performance Metrics of DenseNet 201, Proposed Ensemble and Weighted Average Ensemble with Grid Search (DEV-MV).

Two confusion matrices representing the performance of the proposed Ensemble model and Weighted Average Ensemble model using grid search are shown in figure 4.10 where label 0 indicates Benign cases, 1 indicates Malignant cases, and 2 indicates Normal cases. In the first confusion matrix figure 4.10(a), the model showed strong performance with true predictions comprising 94.44% for class 0, 100% for class 1, and 96.88% for class 2, indicating that most instances in every class were correctly classified by this model. The accuracy for this model was 98.20%. On the second confusion matrix, figure 4.10(b) showed slightly improved performance, predicting correctly class 0 with 100%, class 1 with 100%, and class 2 with 98.41%. The total accuracy accomplished by the use of this model is 99.40%. These are very excellent percentages of the true predictions that prove both models are very efficient; however, the second model shows a slight improvement in accuracy and precision.

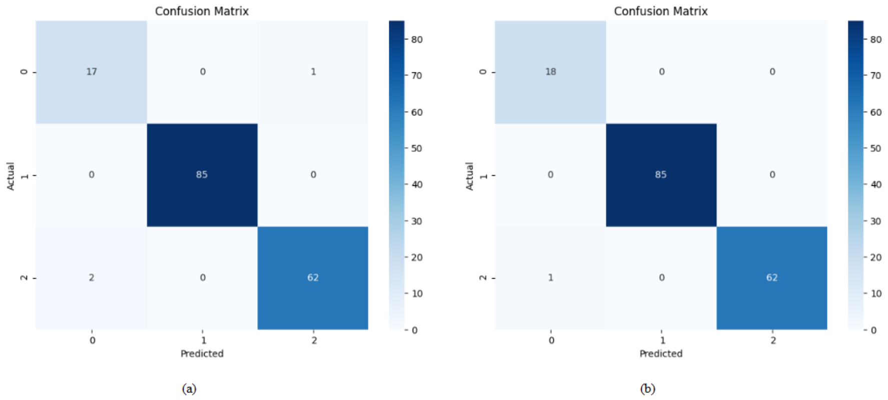


Figure 4.10: Confuion Matrix for (a) Proposed Ensemble Model, (b) Proposed Ensemble Model Assisted with Grid Search (DEV-MV).

We compared the proposed method with previous studies discussed in related work to show the effectiveness and robustness of the proposed weighted average ensemble model with grid search. The comparison of the findings for the detection of lung cancer disease cases is depicted in table 4.9. We chose those studies from the literature that considered multiclass datasets for comparison with the proposed method. The accuracy column presents the performance of each model in percentage terms. Specifically, the proposed model from this paper achieved the highest accuracy of 99.40%, outperforming other models such as LungNet22 (98.89%), EfficientNet v2-M (82.15%), VGG 19 + CNN (96.48%), an ensemble of 7 pre-trained CNN models (98.67%), CNN and GoogleNet (98%), and AMP-WSVM(93%).

Table 4.10 illustrates the comparison of the proposed model with other models found in the literature using same dataset.

4.4.3 Discussion

While traditional ensemble methods are widely used, the concept of reinforcement learning (RL) has been relatively less explored in the literature. Compared to previous studies, our proposed Ensemble Reinforcement Learning (ERL) model provides significant improvements in both accuracy and robustness. The proposed approach introduces dynamic model tuning based on feedback using a unique combination of deep learning and reinforcement learning. The proposed integrated reinforcement learning model is based on well-established methods, but has distinct advantages. While previous studies have investigated individual models and reinforcement learning techniques, this approach uniquely integrates several state-of-the-art models (DenseNet201, VGG16, VGG19, MobileNet V1, EfficientNet) into a single integration framework that has not been used in previous works. The ensemble provides the potential benefits of each architectural design to develop a more stable and wider model of deviations and differences in the model.

Table 4.9: Comparison of Proposed Weighted Average Ensemble using Grid Search with Previous Studies.

Reference	**Model**	**Dataset**	**Accuracy**
[112]	LungNet22	Combination of 16 datasets	98.89%
[117]	EfficientNet v2-M	NIH	82.15%
[118]	VGG 19 + CNN	RSNA, SIRM	96.48%
[33]	7 Pre-trained CNN models	Histopathological image dataset	98.67%
[34]	CNN and GoogleNet	Dataset from hospital	98%
[137]	AMPWSVM classifier	LIDC	93%
This Paper	Proposed Model	IQ-OTH/NCCD	99.40%

Table 4.10: Comparison of Proposed Model with Previous Studies Using IQ-OTH/NCCD Dataset.

Reference	**Model**	**Accuracy (%)**	**Recall (%)**	**Precision (%)**	**F1-score (%)**
[119]	SVM	89.88	97.14	98.55	97.84
[120]	VGG16, VGG19, Xception	98.83	98.57	98.83	98.70
[138]	AlexNet	93.54	95.71	97.10	96.40
[139]	Ensemble learning	92.80	-	-	-
[140]	AlexNet, ResNet	98.58	95.50	96.78	96.14
[141]	SMOTE based on CNN	97.00	-	-	-
This Paper	Proposed Model	99.40	99.47	98.25	98.85

The high accuracy and reliability of our proposed integrated reinforcement learning (ERL) framework have promising implications in clinical settings, especially in early lung cancer diagnosis. However, a few challenges need to be overcome. First, the model needs to guarantee generalizability to many different patient populations so that it can be brought to real-world applications.. The dataset used in this study contains a limited number of images from specific demographics. Therefore, expanding the data set in patients with different varieties, age and risk factors are important to improve the pattern of persistence and avoid possible bias.

Another challenge from an operational perspective is integrating the system into the clinical workflow which requires appropriate infrastructure and training. Healthcare professionals, must be trained to interpret the results generated by artificial intelligence and combine them with clinical experience. In addition, computer resources should be used to treat model treatment requirements.

Although there are challenges, it is still possible to use this framework. ERL-based systems may enhance diagnostic accuracy in under-resourced areas where healthcare professionals may not be readily available.Through mitigation of these challenges and an exploitation of the available opportunities, the proposed ERL system has vast promise for transforming diagnosis in lung cancer, and improvement of patient outcomes through enabling more accurate, efficient, and scalable healthcare solutions.

4.5 Summary

The increasing incidence of lung cancer necessitates advancements in diagnostic techniques that can facilitate early detection and treatment. This study presents a comprehensive framework that integrates deep learning with ensemble reinforcement learning to enhance lung cancer diagnosis accuracy from CT scans. The objective is to identify the stages of lung tumors at the earliest possible point through advanced imaging techniques. By combining five powerful CNN architectures—DenseNet201, EfficientNetB7, VGG16, MobileNetV1, and VGG19 along with grid search optimization, our model achieves an outstanding accuracy of 99.40%, surpassing previous benchmarks.

The advanced preprocessing methods are employed together with handling class imbalance using elastic transformations, which increases the strength and generalization of the model. This unique integration of models and reinforcement learning signifies a substantial advancement in lung cancer diagnosis, providing a more reliable and scalable solution for medical use.

Our work not only improved existing methods but also set new standards for the field. In order to ensure the model's adaptability and impact on actual medical care, future work will concentrate on growing the dataset and validating the model across a range of patient demographics.

CHAPTER 5

CONCLUSION AND FUTURE DIRECTIONS

This chapter concludes the thesis, including a summary of work and significant contributions. It then suggests and analyses several potential future directions that can further enhance diagnostic methodologies.

5.1 Conclusion and Discussion

The quest for improved diagnostic methodologies in the healthcare sector has intensified, especially in the context of diseases like lung cancer, which remain among the leading causes of mortality worldwide. This research has focused on developing an advanced diagnostic framework that integrates deep learning with reinforcement learning to enhance lung cancer diagnosis accuracy from CT scans. This section summarizes the key findings of this study, emphasizing performance improvements achieved through various machine learning and deep learning models in disease prediction and lung cancer detection.

In this thesis, to achieve the first objective, the literature survey chapter highlights the extensive application of data mining techniques in healthcare. It explores various machine learning and deep learning methods used for diagnosing lung cancer and other diseases. This chapter also provides a foundation for understanding how data mining can extract meaningful inferences from patient health data, setting the stage for implementing the models proposed in the following chapters.

The implementation of second objective involves the use of predictive models with machine learning, deep learning, and ensemble techniques to recognize lung cancer. To achieve this objective several different machine learning classifiers and deep learning models are implemented and tested for a novel ensemble learning framework. A cloud-based IoMT framework was proposed for remote lung cancer detection, integrating logistic regression, MLP classifier, Gaussian NB, and K-Means with fuzzy logic for intelligent feature selection. A reinforcement learning-assisted deep learning framework was introduced, focusing on diagnosing lung cancer from CT scan images. These procedures enable precise recognition of lung cancer by automating feature selection and optimizing model accuracy through hyperparameter tuning and ensemble learning techniques.

To achieve the third objective a consumer-focused IoMT-based framework is developed that enables remote monitoring and diagnostic capabilities. By integrating machine learning models and ensemble methods into the IoMT architecture, this system provides efficient and accessible healthcare support for lung cancer patients. The proposed model's ability to gather patient data, process it using deep learning techniques, and offer real-time insights enhances patient care. This also demonstrates how data-sharing between healthcare providers and patients can lead to timely and informed decision-making, ensuring the right care pathways are chosen.

To implement the fourth objective, the proposed models focus on predictive analysis for lung cancer detection, achieving high diagnostic accuracy rates of 98.50% and 99.40% for machine learning and deep learning models respectively. The voting classifier ensemble and hyperparameter tuning techniques improved predictive accuracy, and we further refined these methods by introducing weighted average ensemble learning and reinforcement learning. These approaches ensure that the models can predict lung cancer at an early stage, thus facilitating timely interventions and improving patient outcomes. The integration of elastic transformation and data augmentation also ensures robust model generalization across diverse datasets, enhancing its application in real-world healthcare settings.

Each chapter has successfully contributed to the overarching goal of enhancing lung cancer diagnosis using computational intelligence and deep learning frameworks. Through rigorous model development, feature selection, and reinforcement learning integration, the research has demonstrated notable improvements in diagnostic accuracy, making significant strides toward addressing real-world healthcare challenges.

5.2 Future Directions

While this research has made significant contributions to healthcare analytics, several future research directions can further enhance its impact.Given the promising results of this study, several directions for future research can be proposed:

1. **Expansion to Other Cancers:**

   Future studies could validate the framework on datasets for other cancer types, assessing its generalizability and robustness across various diseases. The validation of this model on datasets external to these subsets will confirm the robustness and applicability of this model.

2. **Integration of Multi-Modal Data:**

   Incorporating genomic, clinical, and demographic data into the existing framework could enhance the model's predictive capabilities and provide a more comprehensive understanding of patient health. Additionally, various types of feature data will improve resilience and diagnostic precision.

3. **Development of Real-Time Detection Systems:**

   Future work could focus on building real-time monitoring systems that leverage the proposed framework for continuous patient assessment.

4. **Exploration of Explainable AI:**

   Further research into explainable AI methods could enhance the interpretability of the model's predictions, fostering greater trust among healthcare professionals. This enhancement will make it easier for healthcare professionals to understand and depend on the result produced by the model. Further, the incorporation of XAI into the system will help with following the medical monitoring regulations thus enhancing the applicability of the system in a clinical environment.

5. **Cross-Validation Across Diverse Populations:**

   Conducting extensive cross-validation on diverse patient populations will help ensure the model's effectiveness in varied clinical settings.

6. **Multi-task Reinforcement Learning:**

   Exploring the integration of multi-task reinforcement learning could optimize performance across different medical imaging tasks, improving the framework's adaptability and generalizability. This could allow for joint optimization across various medical imaging tasks, further enhancing the model's robustness.

This thesis has made significant strides in enhancing lung cancer diagnosis through the integration of deep learning and reinforcement learning techniques. The study demonstrates that advanced computational methods can yield impressive diagnostic accuracy, addressing critical challenges in lung cancer detection and predictions.

The results underscore the transformative potential of ML and DL in healthcare, paving the way for improved diagnostic practices that can ultimately lead to better patient outcomes. The proposed framework not only sets new benchmarks for accuracy but also provides a scalable solution for the early detection of lung cancer. As the field of medical diagnostics continues to evolve, the findings from this research will contribute to ongoing advancements in automated detection and treatment paradigms, heralding a new era of precision medicine sets.

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LIST OF PUBLICATIONS

- **Richa Jain,** Devendran V., “Data Mining Algorithms in Healthcare: An Extensive Review”, *Fifth International Conference on I-SMAC (IoT in Social, Mobile, Analytics and Cloud) (I-SMAC)* (Published), 2021. (Scopus)
- **Richa Jain,** V. Devendran, and Parminder Singh, “Evaluation of Machine Learning Classifiers for Multiple Disease Prediction.”, *Computer Science Engineering and Emerging Technologies: Proceedings of ICCS* (Published), 2024.
- **Richa Jain,** Parminder Singh, Mohamed Abdelkader, and Wadii Boulila, “Efficient lung cancer detection using computational intelligence and ensemble learning”, *PloS one* (Published), 2024. (Scopus, SCIE 2.9 IF)
- **Richa Jain,** Parminder Singh, and Avinash Kaur, “An Ensemble Reinforcement Learning-Assisted Deep Learning Framework for Enhanced Lung Cancer Diagnosis”, *Swarm and Evolutionary Computation* (Published), 2024. (Scopus, SCIE 8.2 IF)