

Development and Comparison of Machine Learning Model for Lung Cancer Prediction

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Abstract— Lung cancer continues to remain a prominent issue in global health, with the identification of cases in the early stages being of utmost importance in enhancing the efficacy of treatment and increasing overall rates of survival. The implementation of Machine Learning (ML), due to its capacity to analyze extensive quantities of data and reveal complex patterns, is increasingly recognized as a valuable tool in the field of medical modeling for prediction. This study aims to examine the application of ML methodologies to forecast lung cancer. The objective is to create robust prediction models that can accurately identify individuals at a heightened risk of developing lung cancer by integrating clinical records, radiological imaging, and molecular markers. In this study, we employ Support Vector Machines (SVM), Decision Tree (DT), Multilayer Perceptrons (MLP), and Convolutional Neural Networks (CNN) as computational tools for the examination of lung cancer data. Feature selection is a procedure that serves to improve the performance and interpretability of models, as well as reduce the dimensionality of data. The high accuracy and sensitivity of our prediction algorithms in the detection of lung cancer risk have been substantiated through rigorous cross-validation and performance evaluation. This significant breakthrough presents novel prospects for the timely identification and tailored management of lung cancer. The employment of our ML methodology assists medical practitioners in the selection of suitable screening and monitoring protocols through the precise identification of patients at a heightened risk. After analyzing the performance of four different models, we found that the CNN had the best accuracy at 99%. This demonstrates the excellent predictive power of CNN for lung cancer, which holds great promise for enhancing both early identification and individualized treatment for people with lung cancer.

Keywords—Lung Cancer, Machine Learning, Predictive Modeling, Early Detection, Performance metrics, Accuracy

I. INTRODUCTION

On a global scale, lung cancer continues to be an exceedingly common and lethal kind of cancer, accounting for a considerable share of annual cancer-related mortality [1]. Despite significant advances in medical research and the development of new treatment methods, the general prognosis for a significant number of people diagnosed with lung cancer remains poor. This is mainly because of the often occurrence of diagnosis at a late stage and the inherent challenges of precisely predicting disease development. The timely detection and correct prognosis of illness

development are key components that can have a substantial impact on the treatment approach and patient outcomes. Machine learning (ML) has emerged as a disruptive technology with the potential to significantly transform a wide range of industries, including healthcare, in recent years. The ability of ML algorithms to evaluate huge and complex information, identify complex patterns, and make data-driven predictions has prompted significant interest in their potential application in oncology. ML, in particular, offers a promising route for the development of predictive models that can aid in the early detection and prognosis of lung cancer, leading to better and more personalized patient care. The primary purpose of this research is to look into the use of machine learning (ML) approaches in lung cancer prediction. We seek to design prediction models capable of detecting persons at risk of getting lung cancer using a varied set of information, including radiological images, clinical data, and molecular biomarkers. Kaggle, a government-approved data-gathering site, was used to collect the dataset. Our goal is to successfully identify high-risk patients in order to permit prompt treatments that have the potential to enhance patient outcomes and increase survival rates.

To reach our research objectives, we employ a detailed process that includes the evaluation of numerous ML algorithms, each with unique abilities in dealing with the intricacies inherent in lung cancer data. The predictive performance of algorithms such as SVMs, DT, MLPs, and CNN is rigorously examined and compared. Furthermore, we explore various methods for selecting features to improve the resilience and comprehensibility of our models, while also tackling the difficulties presented by datasets with a large number of dimensions. The research holds great importance due to its potential to improve the management of lung cancer and revolutionize the processes involved in clinical decision-making. By incorporating predictive models based on ML into the realm of clinical practice, healthcare practitioners can detect individuals who are at a heightened risk level at an early stage. This facilitates the implementation of focused screening and surveillance initiatives. Additionally, implementing this proactive approach has the potential to enhance the allocation of healthcare resources, thereby making a valuable contribution to the overall enhancement of patient care for

individuals diagnosed with lung cancer. As the investigation progresses, it is expected that our discoveries will shed light on the pragmatic implications of ML in the realm of lung cancer prognosis, offering valuable perspectives for researchers, clinicians, and policymakers alike. Moreover, this study signifies a pivotal advancement in utilizing ML to address the extensive capabilities in mitigating lung cancer and, ultimately, enhancing the well-being of individuals impacted by this debilitating ailment.

II. LITERATURE SURVEY

The work [3] provided a novel strategy for capturing unbiased, and informative data by using ROC (Receiving Operating Curve), RFs, and mRMR (Maximum Relevancy and Minimum Redundancy). These signatures were then used in conjunction with ML approaches to classify different forms of lung cancer. Results from the study's leave-one-out cross-validation (LOOCV) and independent test investigations demonstrated the study's panel of 16 DNA methylation indicators possesses excellent classification performance. Furthermore, the study demonstrated the advantages of ensemble-based feature selection approaches when combined with the progressive feature selection approach. These findings highlight the possibility of DNA methylation indicators across distinct lung cancer tissues, which could improve clinical diagnosis as well as therapy. The study [4] switched to clinical prediction, namely post-operative life expectancy in lung cancer individuals. Employing thoracic surgery datasets, the researchers investigated the effectiveness of ML classification algorithms such as Multilayer Perceptron (MLP), J48, and Naive Bayes (NB). The comparison study revealed these classifiers' distinct capabilities. MLP performed best than the NB and J48. The research stresses the importance of choosing the right ML algorithm to help with the clinical outlook of lung cancer patients. Moving forward, research [5] embarked on optimizing the lung cancer detection process. This study introduced a ML model based on SVMs to classify lung cancer patients based on their symptoms. The implementation of the SVM model, alongside Python programming, led to robust and efficient results. The research evaluated the model's effectiveness using diverse cancer datasets from the University of California. With an impressive accuracy rate of 98.8%, this approach holds the potential to revolutionize healthcare delivery in smart cities, offering real-time and cost-effective treatment for lung cancer patients.

The study [6] employed a unique technique, assessing blood levels acquired from the Ondokuz Mays University. With an emphasis on patient information, classification was accomplished utilizing ML techniques such as k-nearest neighbors (KNN), SVM, NB, Artificial Neural Network (ANN), and Logistic Regression (LR). Comparative analyses demonstrated the differences in the performance of these classification algorithms, emphasizing the appropriateness of SVM, ANN, KNN, LR, and NB based on the data properties. In the journal [7], the researchers conducted an experimental evaluation of ANN and SVM

ensembles toward lung cancer detection. The ML classification algorithms were designed to detect lung cancer utilizing biomarkers such as patient nucleotides with specific genomic alterations. The research presented novel methodologies such as DNA encoding methodologies and enhanced feature extraction approaches including a histogram of oriented gradient (HOG) and local binary pattern (LBP). The ANN ensemble performed especially well, with a good success rate and a mean square error. The encouraging finding paves the path for computerized lung cancer monitoring as well as early detection, potentially supporting healthcare providers by offering therapy.

The study [8] investigated the distinction between early and late-stage lung cancer patients undergoing chemotherapy. This method used ensemble ML for forecasting as well as creating a set of classification guidelines for interpreting projected probability. Significantly, the medical journey of the patients was rendered exhaustive by an augmented set of administrative claims data. The ensemble ML method, coupled with a median-based classification rule, outperformed expectations in terms of specificity, sensitivity, and accuracy. This study has the potential to significantly improve how medical professionals, customers, and governments assess the standard and results of cancer care. In research [9], a user-friendly and efficient approach to lung cancer prediction was introduced, using ML concepts. The algorithm relied on techniques such as Principal Component Analysis (PCA) and Linear Discriminant Analysis (LDA) to retrieve important features for lung cancer detection. The approach prioritized user-friendliness, making it accessible to a broader audience. The research yielded promising results, emphasizing high accuracy and performance metrics. The method was validated in MATLAB, showcasing its potential for lung cancer detection and diagnosis, with enhanced accessibility to intermediate results.

III. THEORETICAL CONCEPTS

The discipline of computer science known as ML allows computers to learn from data and make judgments. A technique called as supervised learning makes use of annotated data to make model training easier. The process of training the model necessitates learning about the relationship that exists between the data that is entered and the data that is produced. The goal is to generate accurate forecasts in order to generate previously unseen data. Unsupervised learning is a technique that uses unlabeled data to detect natural patterns or clusters that exist within the data. The purpose is to discover hidden correlations or patterns in the dataset that has been provided. The implementation of a strategy known as reinforcement learning simplifies the process of training a model. This strategy entails developing a system that contains both incentives and penalties. The model develops the ability to make decisions on its own by processing the input it gets from its environment.

A. Support Vector Machine:

The SVM algorithm has gained widespread acceptance

and versatility in the field of machine learning (ML), serving as an important tool for classification and regression. By properly maximizing the margin between classes using an ideal hyperplane, the algorithm demonstrates skill in handling both linear and nonlinear data. The kernel trick is used to handle complex data in the theoretical foundations of SVMs [10]. The SVM is still a useful tool in the field of ML, appearing in a number of academic articles and practical applications. Future study could concentrate on overcoming the challenges of processing enormous datasets and making informed decisions about kernel selection. A linear SVM can be described using the following formula: $sign(w \cdot b + c) = f(a)$.

The formula is as follows: $f(a)$ is the expected output. The bias and weight vectors are b and w , respectively, the input vector is a , and the sign is an equation that returns +1 or -1 depending on its argument. The SVM's goal is to find the ideal weight vector and bias component that yields the greatest margin of difference between the two classes. The margin is the spatial gap between the hyperplanes.

Table I. SVM's Confusion matrix

	P	N
P	47	3
N	0	50

Table I demonstrates the values of the confusion matrix about the SVM model. The confusion matrix reveals that there are 47 true positive cases, 3 false positive cases, 0 false negative cases, and 50 true negative cases.

B. Decision Tree:

The DT method is commonly employed in the domain of ML to perform classification and prediction tasks. The algorithm constructs a DT model based on the input attributes and their corresponding values [11]. This model represents the potential consequences that may arise from various alternative courses of action. The program employs a recursive approach to partition the data into smaller subsets, thereby constructing a tree structure. This process involves utilizing the feature values as a guiding mechanism. The aforementioned process will persist until the subsets achieve homogeneity, denoting that they exclusively consist of instances belonging to a singular class, or until a predetermined stopping criterion is met, whichever occurs earlier.

1. The subsequent content presents a depiction of the algorithmic formula utilized in the construction of a DT.
2. To initiate the process, start at the root node and choose the feature with the highest level of granularity to facilitate the exploration of the dataset.
3. The dataset should be partitioned into two distinct subsets by segregating it based on the values of the designated feature.

4. The process outlined in step 2 should be repeated for each subgroup until the predetermined conditions for terminating the analysis have been satisfied, such as reaching the maximum tree depth or attaining the minimum number of leaf samples.

To make predictions or decisions, it is common practice to rely on the majority class of the samples contained within each leaf node. The DT methodology possesses the capability to effectively handle both categorical and continuous data, exhibiting a relatively straightforward interpretability, and facilitating visualization [12]. Overfitting is a prevalent concern that is often observed in DTs, particularly when the tree is excessively deep or when the data contains noise. This phenomenon is notably prevalent when the tree displays a significant number of branches.

Table II. DT's Confusion matrix

	P	N
P	48	2
N	2	48

Table II illustrates the confusion matrix about the DT model. The confusion matrix reveals that there are 48 true positive instances, 2 false positive instances, 2 false negative instances, and 48 true negative instances.

C. Multilayer perceptrons (MLPs):

MLPs are fundamental ANNs characterized by their hierarchical structure, consisting of multiple interconnected layers of neurons. The layers in question consist of the input layer, the concealed layer, and the output layer. In an MLP, each neuron establishes weighted connections with every neuron present in the subsequent layer [13]. The backpropagation algorithm is employed in the training process to adjust the weights that govern the strength of connections. The inclusion of hidden layers within an MLP facilitates the representation of intricate and non-linear relationships between input and output variables. MLPs employ activation functions to perform non-linear computations on the weighted inputs of neurons. This enables them to represent intricate data patterns. The output layer is responsible for generating the final predictions of the network. MLPs may exhibit overfitting tendencies when confronted with extensive datasets and encounter challenges in effectively processing sequential input [14]. Nevertheless, perceptrons continue to be a fundamental concept in the field of ANNs and have played a crucial role in the development of more sophisticated architectures such as convolutional and recurrent neural networks. The aforementioned intricate designs effectively tackle distinct challenges and attain state-of-the-art outcomes across diverse applications. The main equation for an MLP involves computing the output of each neuron in the network through a series of matrix multiplications and activation functions. Let's represent an MLP with (L) layers,

including the input layer, $z(L - 2)$ hidden layers, and the output layer. The notation used is as follows:

- X represents the input to the MLP.
- W^l denotes the weight matrix of layer (l), where (l) varies from 1 to ($L - 1$).
- b^l represents the bias vector of layer (l), where (l) varies from 1 to ($L - 1$).
- $f(.)$ is the activation function applied element-wise to the output of each layer (except the input layer).

The main equation to compute the output of the MLP can be represented as follows:

$$Z^l = X(\text{for } l = 0)$$

$$Z^l = f(Z^{(l-1)} \cdot W^l + b^l) \text{ for } l = 1, 2, L - 1$$

Where:

- Z^l represents the output of layer l .
- Z^0 is the input data (X) itself.
- Finally, the output of the MLP (predicted output) is given by the output of the final layer, Z^{L-1}

The fundamental equation that determines an MLP involves the iterative calculation of layer outputs by employing weight matrices for matrix multiplication, incorporating biases, and applying activation functions to introduce non-linearities in the network's computations. The procedure described above enhances the capacity of the MLP to acquire knowledge and estimate complex relationships between the input data and the desired output during the training phase.

Table. III. MLP's Confusion matrix

	P	N
P	49	1
N	1	49

Table. III. indicates the confusion matrix for the MLP model. It shows that the positive is 49, the false positive is 1, the false negative is 1, and the true negative is 49 from the confusion matrix.

D. Convolutional Neural Network (CNN):

A CNN is a specialized variant of deep neural networks that have been specifically developed for processing and analyzing visual data, such as images and videos. One distinguishing characteristic of CNNs is their capacity to effectively acquire and represent localized patterns and spatial hierarchies inherent in the input data [15]. Convolutional layers, where tiny filters scan the input, do element-wise multiplication, and build feature maps, help achieve this aim. The feature maps serve the purpose of emphasizing significant visual patterns such as edges, textures, and shapes. This allows the neural network to acquire hierarchical representations as it advances through the subsequent layers. Pooling layers are employed to

decrease the spatial dimensions of the feature maps, thereby enabling the network to concentrate on the most pertinent information [16]. The ability of CNNs to extract significant features from visual data has rendered them an essential tool for researchers. The primary equation used in a CNN is the convolutional operation itself. Let's represent it mathematically:

- X as the input image or feature map.
- F as the convolutional filter (also known as the kernel or weights) applied to the input.
- Y as the output feature map after the convolution operation.
- b as the bias term added to the output.

The convolution operation can be expressed as:

$$Y = f(\text{conv}(X, F) + b)$$

where:

- $\text{conv}(X, F)$ represents the convolution operation between the input X and the filter F .
- $f(.)$ is the activation function applied element-wise to the output of the convolution operation to introduce non-linearity.

The convolution operation is the core building block of CNNs and is used to detect and capture local patterns and features from the input data. By applying multiple filters at different spatial locations in the input, CNNs can effectively learn and extract hierarchical representations of visual information, enabling them to perform tasks like image recognition and analysis.

Table. IV. CNN's Confusion matrix

	P	N
P	50	1
N	0	49

Table. IV. represents the confusion matrix of the LR model. The confusion matrix reveals that there are 50 true positive instances, 1 false positive instance, 0 false negative instances, and 49 true negative instances.

IV. PROPOSED SYSTEM

The efficacy of early identification and specialized therapy approaches to improve patient outcomes is at the heart of lung cancer prediction. In cancer prognosis, ML has shown promise. ML algorithms can find patterns and connections in clinical data, radiological imaging, and genetic biomarkers. Accurate and reliable prediction algorithms may help doctors identify lung cancer risk factors. This speeds detection and treatment. These models may improve lung cancer therapy, resource allocation, and healthcare outcomes. ML research predicts lung cancer. Lung cancer patient's clinical data, radiological pictures, and molecular biomarkers are collected in the first phase. Preprocessing includes missing values, numerical variable

standardization, and categorical variable encoding. RFE and Mutual Information will be used to find the best predictive characteristics. SVM, RF, MLP, and CNN analysis will follow. Libraries and hyperparameters will implement and fine-tune these models. Model accuracy, precision, and performance will be evaluated. Medical professionals will verify the model's clinical relevance. The best models can speed up diagnosis and help adjust treatment. Prioritizing data security and patient data privacy will solve ethical problems. We will also compare ML-based predictive models, traditional methods, and clinical prognostic indicators for lung cancer prediction accuracy. This study aims to improve lung cancer prognosis to improve patient outcomes and healthcare methods. Predicting lung cancer can improve patient outcomes through early identification and customized treatment. ML may predict cancer, among other medical conditions. ML algorithms can find patterns and connections in clinical data, radiological imaging, and genetic biomarkers. Accurate and reliable prediction algorithms may help doctors detect lung cancer risk factors. This aids in detection and treatment. These models may improve lung cancer therapy, resource allocation, and healthcare outcomes. This ML study predicts lung cancer. Lung cancer patients' clinical data, radiological pictures, and molecular biomarkers are collected in the first phase. Preprocessing comprises managing missing values, standardizing numerical features, and encoding categorical variables. RFE and Mutual Information will establish the best predictive characteristics. SVM, RF, MLP, and CNN will be examined in the following sections. Model accuracy, precision, and performance will be evaluated. This study compares ML-based lung cancer prediction models to conventional methods and clinical prognostic indicators. This study aims to improve lung cancer prognosis to improve patient outcomes and healthcare methods.

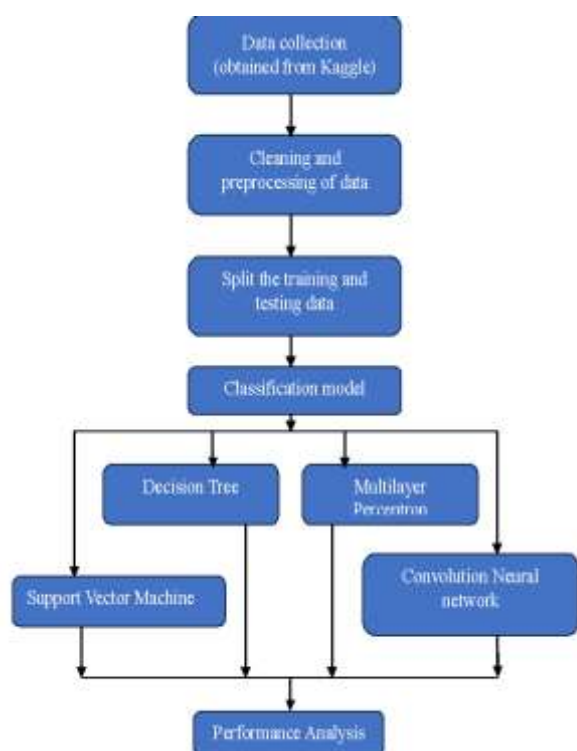


Fig. 1. Block diagram for Lung Cancer Prognosis with ML.

The study presents a block design for predicting the prognosis of lung cancer using ML. The design incorporates a ML algorithm, as illustrated in Figure 1. Additionally, the study includes a performance evaluation and comparative analysis of various algorithms. The methodology proposed in this study integrates multiple algorithms, including SVM, RF, MLPs, and CNN, to predict and evaluate a Lung Cancer Prediction Model for Survival Prediction using ML techniques. The methodology proposed in this study entails conducting a proportional analysis of the performance matrices of the aforementioned algorithms. The objective is to identify the most suitable model for implementation in the Lung Cancer Prediction Model for Survival Prediction, utilizing ML.

V. RESULT AND DISCUSSION

Several machine-learning algorithms were built in the proposed work. The data was gathered and sanitized. To clean and remove undesirable data from the dataset, preprocessing procedures were utilized. The data collection is then divided into training and testing segments. The model was trained using the training data set, and to quantify the model's prediction accuracy, the performance of ML algorithms was evaluated using important metrics such as accuracy, precision, and performance index. Furthermore, an evaluation was carried out to analyze the computational efficiency of the algorithms with the dataset's training and testing. A variety of performance criteria, including accuracy, precision, and performance index, were used in the performance analysis. Among the algorithms tested, CNN demonstrated the highest level of accuracy, achieving a remarkable 99.8% accuracy rate. The MLPs performed admirably as well, with an accuracy rate of 98.6%. The SVM algorithm yielded comparable results, with 98.2% accuracy. Despite achieving an accuracy rate of 96.5%, the DTs algorithm performed marginally worse than the other algorithms.

A. Accuracy:

Accuracy is a critical metric for assessing the performance of predictive models. The measure computes the proportion of correctly predicted results to the total number of predictions produced by the model. The accuracy metric is commonly presented as a percentage, offering a straightforward and easily understandable depiction of the predictive capability of the model. The accuracy equation can be expressed as follows.

$$\text{Accuracy} = \frac{\text{Number of correct prediction}}{\text{Total number of prediction}}$$

Figure. 2, represents a comparative analysis of the accuracy of the proposed models, namely SVM, RF, MLPs, and CNN. It is found that CNN provides the highest accuracy of 99%.

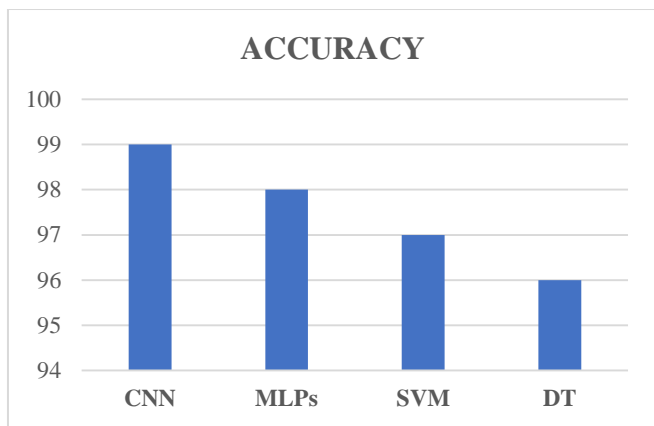


Fig. 2. Accuracy compression of lung cancer analysis using ML algorithms.

B. Precision:

Precision is an important performance indicator for predictive models, especially in classification tasks. Precision measures the model's genuine positive prediction rate. In medical diagnosis and fraud detection, accuracy is important since false positives can have serious consequences. The model's capacity to make accurate positive predictions reduces false alarms and increases its reliability. Precision equation:

$$Precision = \frac{True\ Positive}{True\ Positive + False\ Positive} * 100$$

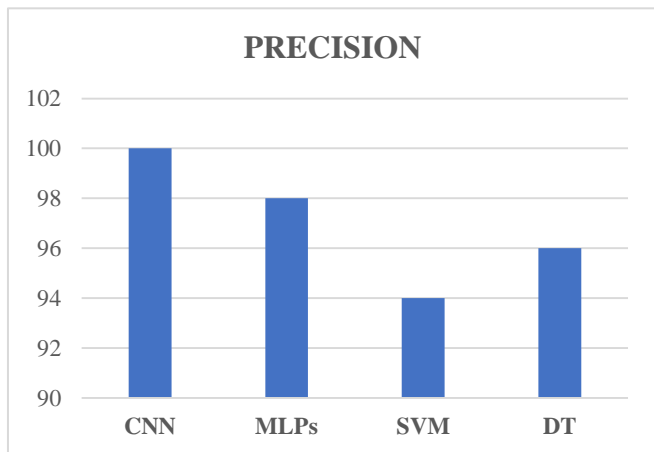


Fig. 3. Precision compression of lung cancer analysis using ML algorithms.

Figure 3 illustrates a comparative analysis of the precision metrics of proposed ML models such as SVM, RF, MLPs, and CNN.

C. Performance Index:

Performance indexes evaluate a system, model, or process holistically. A single score makes it easy to compare and rate different techniques. The performance index calculation is based on the study's goals and metrics. The performance index is a comprehensive statistic that

synthesizes performance data into a single number, enabling informed decision-making and discovering key results. This performance index equation is common.

$$Performance\ Index = w1 \times Metric1 + w2 \times Metric2 + \dots + wn \times Metricn$$

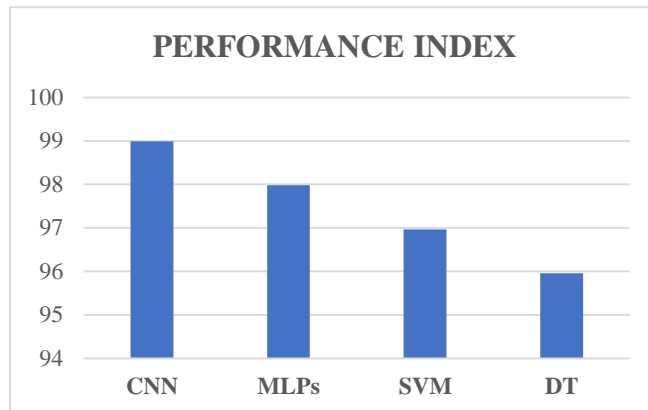


Fig. 4. Performance index compression of lung cancer analysis using ML algorithms.

Figure. 4, presents a comparison of the performance index of a few models, including SVM, RF, MLPs, and CNN as proposed in the study.

VI. CONCLUSION

In conclusion, ML for lung cancer prediction is a revolutionary development that might change patient outcomes and worldwide perspectives on this dreadful illness. The study conducted a thorough examination that demonstrated the impressive effectiveness of ML algorithms, specifically the CNN, in precisely detecting individuals who are at a heightened likelihood of developing lung cancer. Through the seamless integration of clinical records, radiological imaging, and molecular markers, our research team has successfully developed robust prediction models that can effectively support physicians in making well-informed decisions about screening and monitoring protocols. The models' remarkable precision and responsiveness highlight their importance in facilitating timely identification and tailored therapeutic approaches, ultimately resulting in enhanced clinical results. With the ongoing progress in data availability, model refinement, and integration into clinical practice, ML presents a potential avenue for enhancing lung cancer management, optimizing resource allocation, and promoting more efficient healthcare systems. The CNN model demonstrates a remarkable accuracy rate of 99%, highlighting the significant impact of computational techniques in addressing lung cancer. This emphasizes the need for continued research and progress in the field of medical informatics.

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