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3D BLOCK ROUTING SCHEME WITH APPLICATION TO IMAGE ENHANCEMENT

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ABSTRACT :

Lung cancers are malignant lung tumors resulting from uncontrolled growth of lung cells that metastasizes to other parts of the body and can cause death. Although lung cancer cannot be prevented, the risk of cancer development can be lowered. Early detection of lung cancer is essential for patient survival, and machine learning-based prediction models have potential use in predicting lung cancer. Ensemble techniques are compelling and powerful techniques in Machine Learning to improve the prediction accuracy as classifiers. This paper reviewed some research articles on lung cancer prediction models that used machine learning and ensemble learning techniques. Furthermore, we added our newly developed ensemble learning techniques to this paper which was developed based on a survey dataset of 309 people with or without lung cancer by oversampling SMOTE method. The ensemble techniques we used are XGBoost, LightGBM, Bagging, and AdaBoost by k-fold 10 cross-validation method and the attributes our lung cancer prediction models used are age, smoking, yellow fingers, anxiety, peer pressure, chronic disease, fatigue, allergy, wheezing, alcohol, coughing, shortness of breath, swallowing difficulty, and chest pain.

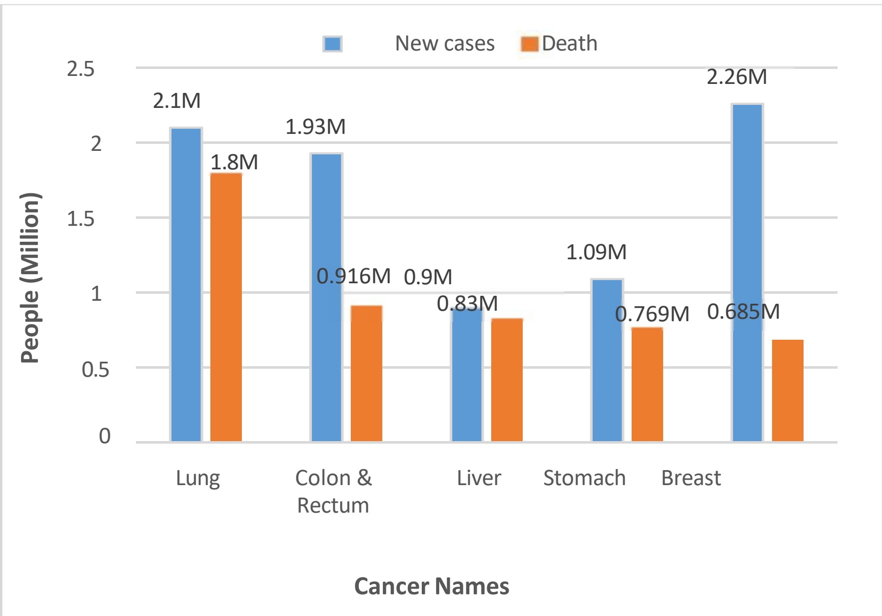
Results: According to our analysis, the XGBoost technique performed better than other ensemble techniques and achieved an accuracy of 94.42 %, precision of 95.66%, recall of 94.46%, and AUC of 98.14%, respectively.

Keywords—Ensemble Learning, Machine Learning, XGBoost, LightGBM, Bagging and AdaBoost, Lung cancer classification.

Introduction :

Lung cancer is one of the most common and deadliest cancer worldwide. It starts as an abnormal growth of cells in the lungs which can spread to other body regions through a process known as metastasis [1].
As it begins in the lining of the bronchi and bronchioles, it obstructs gas exchange in the lungs and causes breathing difficulties.
Smokers exposed to tobacco smoke are more likely to develop lung cancer. According to the WHO report, lung cancer was the deadliest cancer, and almost 1.80 million people died from lung cancer in 2020, affecting 2.21 million [2]. In Figure 1, some cases of cancer against death have been demonstrated.

Fig 1: Cancer in 2020 (New cases against death)



Lung cancer cannot be prevented, and the possible survival rate is only approximately 15.5% after five years of diagnosis [3]. Lung cancer usually begins in the lungs, and in some cases, starts showing the initial symptoms before metastasis. Therefore, one can choose suitable treatment if cancers are detected in a timely manner. Aside from that, this type of cancer has several risk factors and once these elements are clarified, an individual can also take appropriate preventive measures.

A variety of techniques are being used to diagnose cancer, predicting the results of cancer treatment and patient survival after a cancer diagnosis. Doctors and scientists have used screening, identification, and classification techniques to diagnose different types of cancer at an early stage, even before symptoms appear. In addition, scientists discovered several innovative ways of predicting the result of cancer treatment at an early stage [4]. In contrast, Predictor models are used to predict whether a patient will survive for a certain amount of time or not after being diagnosed.

Ensemble learning techniques [5] are a subgroup of machine learning algorithms used to improve the output of basic classifiers by constructing an ensemble of multiple classifiers and adding the results. Nowadays, ensemble learning techniques and machine learning are widely used for critical health diagnosis [6]. Therefore, it can be used as an effective method for creating prediction and classification models.

In this research work, we used four types of ensemble learning: XGBoost, LightGBM, AdaBoost and Bagging classifier techniques, and we compared the results in terms of accuracy, precision, recall, F1-score and AUC.

The construction of this research paper is as follows: In Section 2, a related literature review has been discussed with proper explanations and results. Section 3 presents the appropriate methodology, source of the dataset, pre-processing of the dataset, and features selection. Section 4 includes the results of our prediction model and relevant discussions. Finally, in section 5, the concluding remarks and future direction of our work have been discussed.

Literature Review :

Alsinglawi et al. [7] introduced a predictive framework of the length of stay (LOS) for lung cancer patients using supervised machine learning classifiers such as Random Forest, XGBoost, and Logistic Regression, respectively, by K-fold 10 cross-validation. The authors used the MIMIC-III dataset for observing LOS from the ICU hospitalization patients. The dataset is imbalanced, and they used over-sampling techniques (SMOTE) for the validation. The conducted study had 53,423 adult patient subjects. The authors observed that Random forest with SMOTE class balancing technique performed better than the other two classifiers and achieved AUC of 98% (95.3%- 100%) and recall of 98% (95.3%-100%).

Venkatesh et al. [8] proposed ensemble learning methods for lung cancer prediction using the Surveillance, Epidemiology and End Results (SEER) dataset, containing 1000 samples with 149 attributes. The authors used ensemble techniques of Bagging and Adaboost and some other machine learning classifiers such as K-Nearest Neighbors, Decision Tree, and Neural Networks to evaluate lung cancer prediction. The authors observed that Adaboost performed better and achieved 98.2% accuracy.

Vikas et al**.** [9] used two machine learning algorithms, Support Vector Machine and Random Forest, to predict lung cancer. Authors compared the algorithms with and without feature selection named Chi-square. They found that the Support Vector Machine performed better in terms of accuracy and less execution time for predicting. The algorithm obtained an accuracy of 98%, precision of 100%, recall of 100%, and F1- Score of 100% with an execution time of 0.010 seconds. The dataset was collected from the "Data World" website, and it had 1000 samples with 25 attributes.

Puneet et al**.** [10] worked on the lung cancer prediction model using machine learning techniques based on routine blood indices. They used XGBoost, GridSearchCV, Logistic Regression, Support Vector Machine, Gaussian Naïve Bayes, Decision tree, and K-Nearest Neighbor classifiers by K-fold 10 cross-validation for predicting the results. The dataset was collected from Lanzhou University, whereas 277 patients were part of this dataset. Authors found that XGBoost performed better than other classifiers in terms of accuracy (92.16%), recall (96.97%), and AUC (95%).

Sim et al. [11] proposed a study of health-related quality of life (HRQOL) in 5-year survival of lung cancer prediction model using different machine learning models. Authors used Decision Tree, Logistic Regression, Bagging, Random Forest, and AdaBoost for evaluating models' performance by K-fold 5 cross-validation into two types of feature sets. The model performance was compared with the clinical (HRQOL) data of 809 survivors who underwent surgery for lung cancer. According to the analysis, AdaBoost and Random Forest outperformed the other models. AdaBoost achieved the highest accuracy of 94.8% and 94.9% of AUC.

Patra [12] used different types of machine learning classifiers such as Radial Basis Function Network (RBF), K- Nearest Neighbors (KNN), J48, Support Vector Machine (SVM), Logistic Regression, Artificial Neural Network (ANN), Naïve Bayes and Random Forest using WEKA tools for lung cancer prediction. The dataset was collected from the "UCI repository," containing 32 instances with 57 attributes. By comparing those results, the authors found that RBF performed better than all the other algorithms and achieved an accuracy of 81.25%, precision of 81.3%, recall of 81.3%, F1-score of 81.3%, and AUC of 74.9%, respectively.

P.R. et al**.** [13] predicted lung cancer using four types of Machine Learning algorithms such as Naïve Bayes, Support Vector Machine, Decision Tree, and Logistic Regression. The main goal of this research work is to early diagnosis of lung cancer and performance analysis of the algorithms. The authors collected the dataset of 1000 instances and attributes of 25 from the "Data World" website. They observed that Support Vector Machine algorithm achieved an accuracy of 99.2% and performed better than other classifiers.

Wu et al. [14] proposed Random Forest model for lung cancer identification based on routine cancer indices. The model was validated by K-fold 10 cross-validation. The authors collected the dataset from Lanzhou University, whereas 277 patients were part of this dataset. They observed accuracy of 95.7%, recall of 96.3%, and AUC of 99.01%.

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Faisal et al**.** [15] used several machine learning and ensemble learning methods for detecting and predicting lung cancer. For observing the performance, the authors used MLP, Neural Network, Naïve Bayes, Support Vector Machine, Majority Voting, Gradient Boosted Tree, and Random Forest by K-fold 10 cross-validation. The authors observed that Gradient Boosted Tree (Ensemble Learning technique) outperformed all other individual classifiers and achieved an accuracy of 90%, precision of 87.82%, recall of 83.71%, and F1-score of 85.71%.

Dataset used here was collected from the UCI repository, which contains 32 instances and 57 attributes.

Safiyari et al. [16] used different types of ensemble learning techniques such as Bagging, Dagging, AdaBoost, MultiBoosting, and Random SubSpace, along with some other classification techniques like RIPPER, Decision Stump, Simple Cart, C4.5, SMO, Logistic Regression, Bayes Net and Random Forest were also executed for predicting survival of lung cancer. The authors evaluated the prediction model using the under-sampling method on Surveillance, Epidemiology, and End Results (SEER) dataset which contains 643,924 samples with 149 attributes. They compared the results and found that the AdaBoost algorithm outperformed other algorithms in both AUC and accuracy metrics which are 94.9% and 88.98% respectively.

TABLE I. Lung cancer prediction model's performance

Authors(year)	**Dataset Collection (samples)**	**Models**	**Performance (Proposed model)**
Alsinglawi et al. (2022) [7]	MIMIC-III data (53,423)	**Random Forest (proposed),** XGBoost, and Logistic Regression,	AUC: 98% (95.3%-100%), Recall: 98% (95.3%-100%).
Venkatesh et al.(2022) [8]	SEER dataset (1000)	Bagging, **Adaboost (proposed),** K-Nearest Neighbors, Decision Tree, Neural Networks	Accuracy: 98.2%
Vikas et al**.**(2021**)** [9]	Data World dataset (1000)	**Support Vector Machine (proposed),** and Random Forest	Accuracy: 98% Precision: 100% Recall: 100% F1-Score: 100%
Puneet et al**.** (2020) [10]	Lanzhou University (277)	**XGBoost (proposed),** GridSearchCV, Logistic Regression, Support Vector Machine, Gaussian Naïve Bayes, Decision tree, and K-Nearest Neighbor	Accuracy:92.16% Recall: 96.97% AUC: 95%
Sim et al. (2020) [11]	HRQOL data (809)	Decision Tree, Logistic Regression, Bagging, Random Forest, and **AdaBoost (proposed)**	Accuracy: 94.8% AUC: 94.9%
Patra (2020) [12]	UCI repository (32)	**Radial Basis Function Network (proposed),** K-Nearest Neighbors, J48, Support Vector Machine, Logistic Regression, Artificial Neural Network, Naïve Bayes, and Random Forest	Accuracy:81.25% Precision:81.3% Recall: 81.3% F1-score: 81.3% AUC: 74.9%
P.R. et al**.** (2019) [13]	Data World dataset (1000)	Naïve Bayes, **Support Vector Machine (Proposed),** Decision Tree, and Logistic Regression	Accuracy: 99.2%
Wu et al.(2019)[14]	Lanzhou University (277)	**Random Forest (proposed)**	Accuracy: 95.7% Recall: 96.3% AUC: 99.01%

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Faisal et al. (2018) [15]	UCI repository (32)	MLP, Neural Network, Naïve Bayes, Support Vector Machine, Majority Voting, **Gradient Boosted Tree(proposed),** and Random Forest	Accuracy: 90%, Precision: 87.82% Recall: 83.71% F1-score: 85.71%
Safiyari et al. (2017) [16]	SEER dataset (643,924)	Bagging, Dagging, **AdaBoost (proposed),** MultiBoosting, Random SubSpace, RIPPER, Decision Stump, Simple Cart, C4.5, SMO, Logistic Regression, Bayes Net and Random Forest	Accuracy: 88.98% AUC: 94.9%
Our (2022)	Kaggle dataset (309)	**XGBoost (proposed),** LightGBM, Bagging, and AdaBoost	Accuracy:94.42% Precision:95.66% Recall: 94.46% AUC: 98.14%

Methodology :

The proposed methodology begins with data collection and then moves on to pre-processing. The selected classifiers such as XGBoost, AdaBoost, Bagging, and LighGBM are then trained and tested on the lung cancer dataset using standard 10- fold cross-validation approach. The findings are computed and analyzed to determine the most effective lung cancer prediction method. Figure 2 depicts the overview of the proposed strategy.

Dataset Collection

In this paper, we used a dataset named "Lung Cancer" collected from the Kaggle online website. This dataset has 309 instances, and 16 attributes, whereas 1 class attribute and 15 attributes are predictive. Proper lung cancer prediction is conducted by appropriately using attributes, where the attributes describe the symptoms. The predictive attributes are gender, age, smoking, yellow fingers, anxiety, peer pressure, chronic disease, fatigue, allergy, wheezing, alcohol, coughing, shortness of breath, swallowing difficulty and chest pain, respectively and the class attribute is lung cancer.

Dataset pre-processing

Dataset pre-processing has been done by using feature extraction, data cleaning, missing values handling, and categorical variables transformation. Because the dataset is unbalanced, we used the oversampling method by SMOTE [17] to balance the dataset and expect an accurate model performance with zero biasness.

Validation process:

Selecting the appropriate validation process for a particular dataset is crucial. The K-fold cross-validation is most effective for getting the appropriate results when the dataset is small [18]. We applied K-fold cross validation process using K=10 for our dataset, where K is the number of folds. Using this validation process, we figured out the performance matrix of accuracy, precision, recall, area under curve and F1-Score for every ensemble techniques.

Ensemble learning approaches:

We applied four types of ensemble learning techniques such as XGBoost, AdaBoost, Bagging and LightGBM classifiers to predict lung cancer. The short description for those ensemble classifiers is as follows:

- XGBoost is eXtreme gradient boosting ensemble learning classifier. It uses the Gradient Boosting framework to create machine learning algorithms and has been developed for high efficiency, flexibility, and portability. It [19]. XGBoost is a parallel tree boosting (known as GBDT, GBM) algorithm that solves a variety of data science issues quickly and accurately.
- AdaBoost provides a straightforward and efficient method for generating ensemble classifiers. The ensemble's performance is determined by the diversity of the member classifiers and the performance of each individual classifier. On the other hand, the existing AdaBoost algorithms are developed to fix error minimization problems [20].
- Bagging classifiers are ensemble meta-estimators that fit base classifiers to random subsets of the original dataset and then combine their individual predictions (either by voting or average) to generate a final prediction [21].

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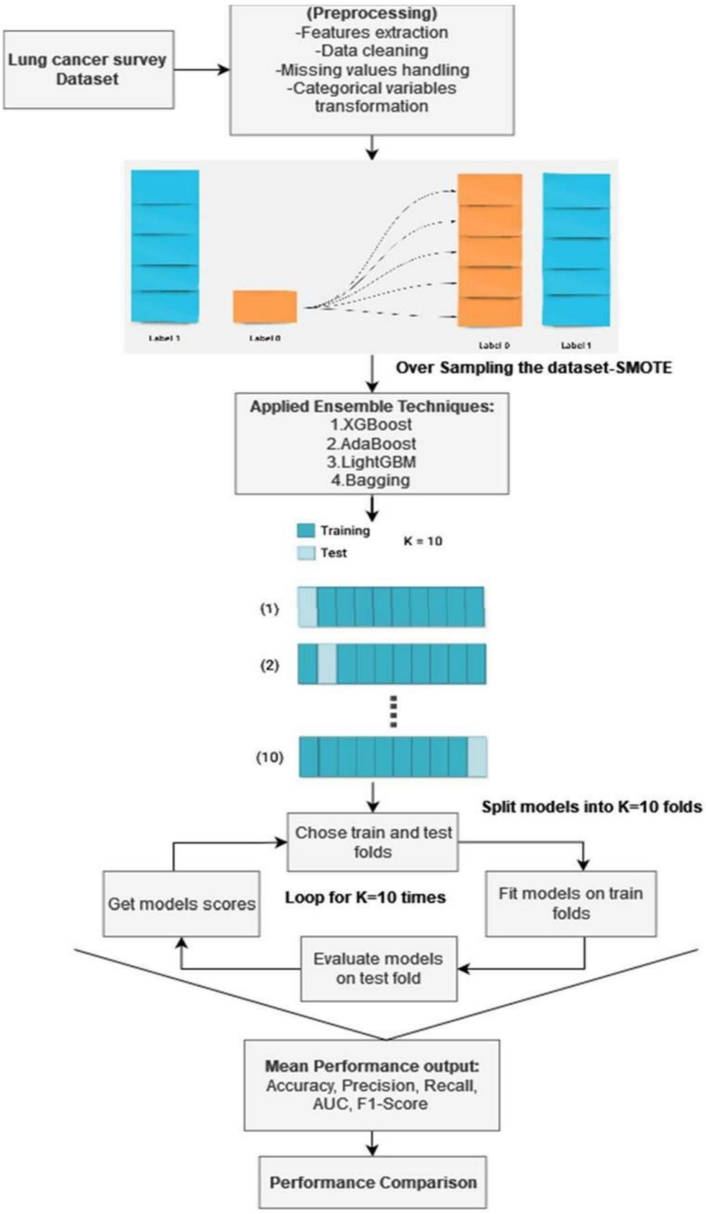
- LightGBM is a gradient boosting framework that uses tree based learning algorithms. It's built to be distributed and efficient, with characteristics like faster training speeds and higher efficiency, lower memory use, improved accuracy, support for parallel, distributed, and GPU learning, and the ability to handle enormous amounts of data [22].
  In the Figure 2, we explained the overview of the research work step by step in a flowchart.

Fig 2: An overview of study



Results and Discussion

The performance of various ensemble learning techniques –
i.e. XGBoost, LightGBM, AdaBoost and Bagging classification methods on the lung cancer dataset has been computed in the TABLE II and comparison made in the Figure 3 and Figure 5. For the performance observation of the models, we have provided the results of Accuracy, Precision, Recall, F1-Score and Area under curve (AUC) in the TABLE II.

TABLE II. Values of different measures for different ensemble learning techniques for predicting lung cancer.

Model	Accuracy (%)	Precision (%)	Recall (%)	F1-Score (%)	AUC (%)

1.XGBoost	94.42	95.66	94.46	94.74	98.14
2.LightGBM	92.558	93.926	92.10	92.71	97.74
3.AdaBoost	90.70	92.53	90.26	90.89	97.62
4.Bagging	89.76	91.88	89.35	90	95.30

From Figure 3, we can observe that XGBoost achieved the highest accuracy of 94.42%, whereas LighGBM, AdaBoost and Bagging achieved 92.55%, 90.70%, and 89.76%, respectively. For predicting lung cancer, XGBoost performed well in terms of accuracy.

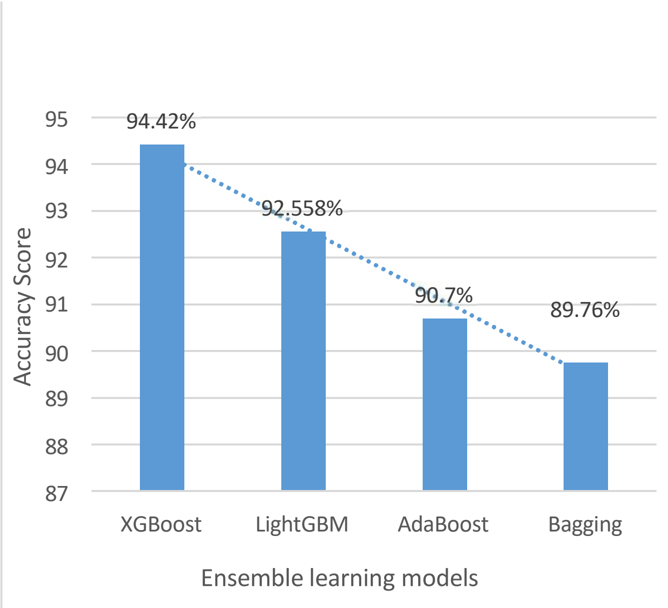
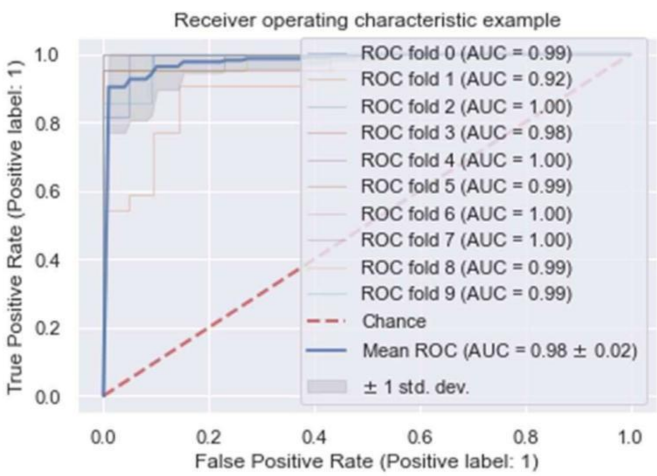


Fig 3: Accuracy analysis of ensemble learning models

However, only accuracy cannot demonstrate the sufficient measure for analyzing the performance of a model. Besides, AUC value becomes a crucial matrix for identifying the model's performance and measures a model's ability to distinguish between classes. It's a probability curve that compares the True Positive Rate to the False Positive Rate at various thresholds. The AUC indicates how well the model distinguishes between positive and negative classes. The greater the AUC, the better. The range of the values from 0 to 1, where 0 represents a completely inaccurate test, and a value of 1 represents a completely accurate test. In general, an AUC of 0.5 shows no discrimination (i.e., ability to classify patients with and without cancer or condition based on the test), 0.7 to 0.8 is considered acceptable, 0.8 to 0.9 is considered great, and more than 0.9 is considered outstanding performance [23]. We provided the AUC curves and mean results using K-fold 10 cross-validation for the given ensemble techniques models in Figures 4.1, 4.2, 4.3 and 4.4.

Fig 4.1: Area under curve (AUC) of XGBoost.



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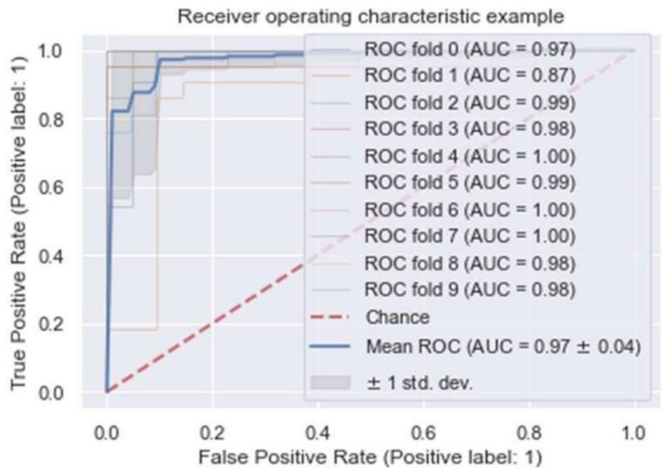

Fig 4.2: Area under curve (AUC) of LightGBM.

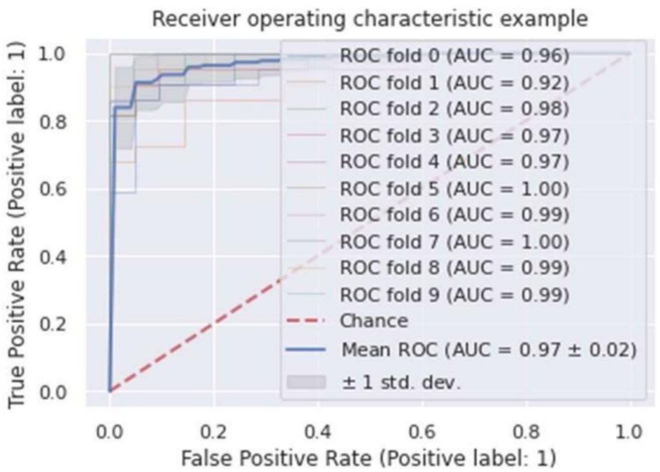

Fig 4.3: Area under curve (AUC) of AdaBoost.

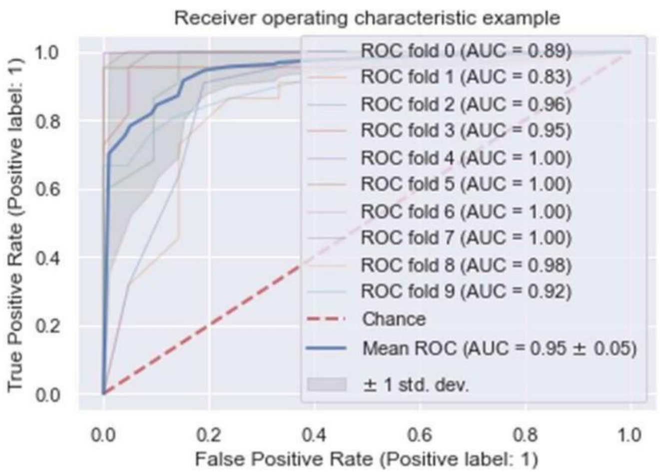

Fig 4.4: Area under curve (AUC) of Bagging.

From the observation in Figure 5, the XGBoost outperformed other ensemble learning models in Accuracy and AUC, 94.42% and 98.14%, respectively. According to our overall performance analysis, this model is considered as our proposed model for lung cancer prediction. Besides, LightGBM and AdaBoost also performed well and achieved an accuracy of 92.55% and 90.70%, AUC of 97.74% and 97.62%, respectively. In addition, Bagging achieved the least Accuracy and AUC, of 89.76% and 95.30%, respectively.

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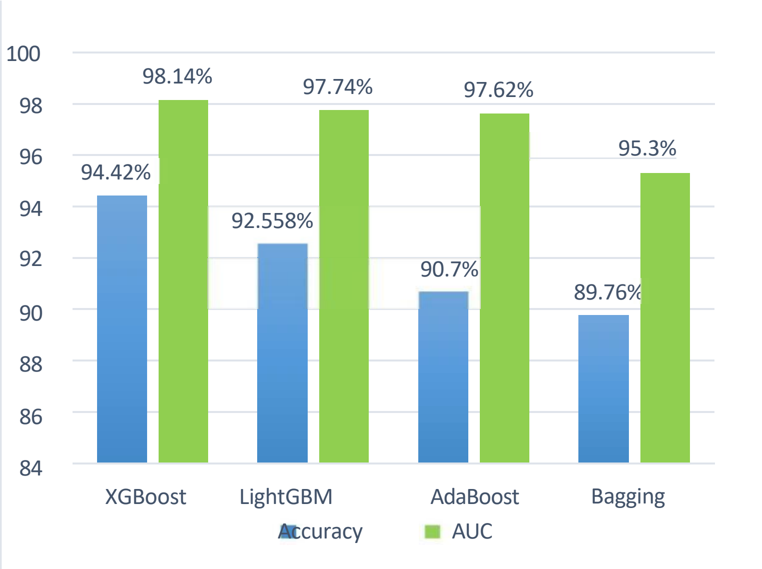

Fig 5: Ensemble learning model's performance analysis in terms of Accuracy and AUC

Conclusion and Future work :

Lung cancer is one of the most common and leading cancers globally, which is very dangerous according to the death rate shown in Figure 1. It cannot be prevented, but an early diagnosis can increase patient life expectancy. In this paper, we reviewed some previous studies related to lung cancer prediction models and compared the performances to our models. We developed four types of ensemble learning techniques: XGBoost, LightGBM, AdaBoost, and bagging, to predict lung cancer using the lung cancer dataset. The dataset was unbalanced, and an oversampling method by SMOTE was used to make it balanced and suitable for the analysis. Besides, we chose K-fold 10 cross-validation for the model validation process. According to our overall analysis, XGBoost outperformed all the models and is considered our proposed model. It achieved an Accuracy of 94.42%, Precision of 95.66%, Recall of 94.46%, F1-Score of 94.74%, and AUC of 98.14%, respectively. Although our results are very promising, we could expect a better output if we get a larger and more balanced dataset. Our proposed method might be beneficial in the early diagnosis and therapy of lung cancer as well as in biomedical research. In the future, we may also work on other health disorders such as respiratory diseases detection by lung sounds using deep neural network with federated learning algorithm for medical data privacy, cancer detection, heart failure prediction, and some other diseases using machine learning algorithms for humankind.

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