Bima Journal of Science and Technology, Vol. 8(1B) Apr, 2024 ISSN: 2536-6041

DOI: 10.56892/bima.v8i1.627

Hybrid Ensemble Machine Learning Approach for Cancer Prediction

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ABSTRACT

Cancer has been one of the major health challenges worldwide in recent times, with millions of new cases and even fatalities recorded annually. Several studies were conducted previously to detect cancer using various machine learning. Here, the hybrid ensemble model has not been extensively considered. As a result, this work constructed a hybrid ensemble model by combining multiple individual models such as random forest, gradient boost, and logistics regression also known as base learners or weak learners, to create a more powerful and robust model known as the hybrid ensemble model. The foremost objective of ensemble model design is to leverage the diversity and complementary strengths of base learners to improve overall predictive performance. The study revealed that hybrid ensemble machine-learning models consistently outperformed single models in terms of prediction accuracy and precision. The proposed ensemble model achieved a sensitivity, specificity, Area Under the Curve (AUC), precision, F1-score 0.92, 1.0, 0.98, 1.0, 0.98 respectively, and accuracy of approximately 0.97. To further check the stability of the model, we carried out a cross-validation, and an average accuracy of 96.072% was obtained. The proposed hybrid ensemble model will help predict cancer patients' to save lives altogether and preclude being taken for granted.

Keywords: Hybrid, Ensemble, Cancer, Machine Learning, Prediction

INTRODUCTION

Cancer is a major health challenge globally, with millions of new cases and fatalities recorded each year (Abubakar et al., 2020). The second most common cancer globally is breast cancer (Sharma et al., 2019). Early detection and accurate prediction of cancer can significantly improve treatment outcomes and increase the chances of survival for patients. Machine learning has shown great capacity in cancer prediction, with several models developed to classify and diagnose different types of cancer(Adeoye et al., 2021).

One of the promising approaches in machine learning for cancer prediction is the use of hybrid ensemble models (Aieb et al., 2022). These models combine the strengths of multiple machine learning algorithms to improve prediction accuracy and reduce the risk of over-fitting. Hybrid ensemble models have been successfully applied in various cancer prediction tasks, including breast cancer, lung cancer, and prostate cancer (Almulihi et al., 2022).

In this paper, we review the latest developments in hybrid ensemble machine learning models for cancer prediction. We discuss the various techniques used to construct hybrid models, including bagging, boosting, and stacking. We also examine the performance of these models in different cancer prediction tasks and compare them with other machine-learning approaches.

The study also considers designing and implementing a hybrid ensemble framework; through the development of a hybrid ensemble framework that combines the predictions of multiple base classifiers, leveraging their complementary strengths, to enhance the accuracy, robustness, and generalization capability of the cancer detection system. Lastly, the study would compare the performance of the hybrid ensemble system with the individual base classifiers to further demonstrate the superiority of the ensemble approach in terms of accuracy, reliability, and efficiency.

The potential of hybrid ensemble machine learning to enhance clinical outcomes, push the boundaries of predictive modeling (Kumar et al., 2022), and deepen our knowledge of cancer biology and treatment is what spurs researchers to investigate this approach to cancer prediction. In general, this paper aims to provide a comprehensive overview of the current state of hybrid ensemble machine-learning models for cancer prediction. It highlights the potential of these models to improve the accuracy of cancer prediction and contribute to the development of more effective cancer diagnosis and treatment strategies.

The rest of the paper is organized thus, section II presents the materials and method employed in this study, results and discussion were provided in Section IV and lastly, the conclusion was drawn in section V.

MATERIALS AND METHODS

Dataset and Data Preprocessing

The dataset was obtained from the Kaggle machine learning repository. It is made up of sixteen features and over three hundred samples. It has been applied to various machine-learning projects for cancer detection and analysis (Inan et al., 2021).. The next step after data acquirement was to preprocess the data, that is to prepare it for analysis. The data was cleaned by removing duplicates, checking for null values, and finally transformed it into a form suitable for hybrid ensemble prediction algorithms.

Feature Selection

The relevant features were selected from the data using machine learning algorithms. The target distribution variable features were checked and arranged. From the data, we discovered that the people with lungs are higher in number compared to those without it. The male and female patients were seen to be male having a higher percentage compared to their female counterparts (Kumar et al., 2022). The right features for the experiment to obtain a better performance model were selected.

Algorithm Selection

Here in this study, three different algorithms selected are complementary in terms of their strengths and weaknesses for the development of a hybrid ensemble model for cancer detection. These machine learning models include random forest classifier, gradient boosting classifier, and extreme gradient boosting methods.

Random Forest Classifier

The Random Forest is a machine-learning method that combines multiple decision trees to make predictions (Ajuji et al., 2021). Each tree is trained on a different subset of the data, and the final prediction is determined by aggregating the predictions of individual trees (Chen, 2012). The Random Forest formula can be explained by breaking it down into the following steps:

a. Randomly select a subset of features from the input dataset.

b. Build multiple decision trees using the selected features and a random subset of the training data.

c. Each tree is trained by recursively partitioning the data based on feature splits that maximize information gain or decrease impurity.

d. During prediction, each tree independently classifies the input data point.

e. The final prediction is determined by taking the majority vote (for classification) or the average (for regression) of the predictions from all the trees (Cheng et al., 2021).

Gradient Boosting Classifier

Gradient Boosting is another ensemble method that combines multiple weak learners, typically decision trees, to create a strong predictive model. Unlike Random Forest, Gradient Boosting builds the trees sequentially, with each subsequent tree aiming to correct the mistakes made by the previous trees (Kim et al., 2021). The Gradient Boosting formula can be itemized as summarized as follows:

i. Initialize the model with a simple weak learner such as a decision tree
ii. Fit the weak learner to the training data and compute the residuals (the difference between the predicted and actual values).
iii. Train the next weak learner on the residuals, attempting to minimize the residual error.
iv. Repeat steps b and c until a predefined number of weak learners are trained.
v. Combine the predictions of all the weak learners, typically using a weighted sum, to obtain the final prediction.

The key idea behind Gradient Boosting is to iteratively update the model by placing more emphasis on the samples that are difficult to predict (Inan et al., 2021).

Logistic Regression

Logistic Regression is a popular classification algorithm that models the relationship between the input features and the probability of belonging to a particular class. It is a linear model that uses the logistic function (sigmoid function) to transform the output into a probability (Li & Abdel-Aty, 2022).

The equation for Logistic Regression is as follows:

$$P(y=1|x)=\frac{1}{1+e^{-w^{T}x}} \qquad \ldots 1$$

In the equation 1 above, $P(y = 1 \mid x)$ represents the probability of the input vector x belonging to the positive class $P(y = 1)$. w Denotes the weights assigned to each feature, and x is the input vector. The logistic function $(1\,/\,(1\,+\,e\hat{}(-w\hat{}T * x)))$ transforms the weighted sum of the features into a value between 0 and 1, representing the probability.

During training, the model adjusts the weights w to maximize the likelihood of the observed labels given the input features (Destere et al., 2022). This is typically done using optimization algorithms such as maximum likelihood estimation or gradient descent (Doppalapudi et al., 2021).

Hybrid Machine Learning Model

A hybrid machine learning model is chosen for this study because it combines two or more dissimilar base types of machine learning model approaches to create a hybrid model, which could result in improved prediction accuracy, robustness, or interpretability (Khalid et al., 2023; Lin et al., 2022). It leverages the strengths of multiple models and techniques to overcome the limitations of individual models, which could result in enhanced general performance

(Sharma et al., 2021). There are many ways to build a hybrid machine learning model, here are a few common approaches: ensemble models, stacking models, future engineering, and transfer learning. For this study, the Ensemble method was used. The ensemble method techniques include Voting; that is combining predictions by the majority voting or weighted voting. Bagging; refers to building multiple models on dissimilar subsets of the training data and averaging their predictions (e.g., Random Forest and Logistic Regression) lastly Boosting; is used to successively build models, with each model correcting the mistakes of its previous or predecessor (e.g., Gradient Boosting) model (Tran, 2022).

Ensemble Machine Learning Model

An ensemble machine-learning technique model intersects multiple individual models to make predictions jointly. It is known for its ability to improve prediction accuracy and generalization by leveraging the diversity and collective intelligence of the constituent models (Kim et al., 2021). Some common ensemble machine-learning approaches are bagging, boosting, stacking, and voting.

Ensemble models are effective in reducing over-fitting, increasing stability, and capturing complex patterns in the data (Geetha & Prasad, 2021; Khazaee Fadafen & Rezaee, 2023). They are widely used in various domains and have achieved significant success in competitions and real-world scenario applications. The choice of ensemble technique for cancer prediction depends on the specific nature of the disease, the data attributes, and the base models used.

Hybrid Ensemble Machine Learning Model

The idea of hybrid models and ensemble models are combined in a hybrid ensemble machine learning model (Dalal et al., 2023). It makes use of the advantages of many models, approaches, and/or algorithms to build a strong predictive model with increased performance, resilience, and flexibility. This kind of model combines many strategies to get around the shortcomings of separate models and get better outcomes (Elshafey & Ghoniemy, 2021). There are several approaches to building a hybrid ensemble model; here are a few typical ones: Algorithm combination, data combination, Ensemble of Ensembles, and meta-learning. Different kinds of base models can be combined via hybrid ensemble approaches to produce a variety of models. For instance, here, the three base models used are logistic regression, random forest, and gradient boosting. Each base model gives a distinctive perspective and captures various facets of the data, resulting in a deeper comprehension and enhanced predictive power.

Figure 1 below described the architecture of the study, a preprocessed dataset was divided into two sets; one for training and the other for testing, various models used are random forest (RF), gradient boosting (GB) and logistic regression (LR) were trained, tested and evaluated individually and also merged together to form the hybrid ensemble (HE) model. The performance result of the hybrid model was evaluated using metrics such as accuracy, precision, recall and so on as shown in in table 1 below. It was discovered that the hybrid ensemble model has outperformed the individually models.

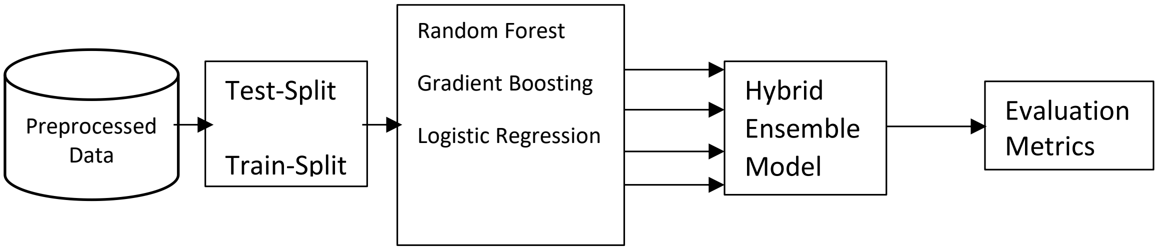

Figure 1: Architecture of the proposed system

Metrics for Evaluation

a. Accuracy

The percentage of correctly identified cases within the total number of examples in the dataset is known as accuracy. The formula in equation 2 is used to compute it.

$$Accuracy = \frac{True\ Positive\ (TP) + TrueNegative\ (TN)}{Total\ number\ of\ instances} \qquad \ldots 2$$

b. Precision

The precision of the model is determined by dividing all of its positive predictions by the percentage of true positive forecasts. Equation 3 present it the formula.

$$Precision = \frac{True\ Positive\ (TP)}{True\ Positive\ (TP) + False\ Positive\ (FP)} \qquad \ldots 3$$

c. Recall

Recall, which is often referred to as sensitivity or true positive rate (TPR), quantifies the percentage of real positive cases that the model properly identifies. The formula is used to compute it:

$$Precision = \frac{True\ Positive\ (TP)}{True\ Positive\ (TP) + False\ Negative\ (FN)} \qquad \ldots 4$$

d. F1-Score

The harmonic mean of recall and precision is the F1 score. It offers a solitary score that harmonizes recall and precision. Its mathematically define as shown in equation 5.

$$F1 - Score = 2\left(\frac{Precision * Recall}{Precision + Recall}\right) \qquad \ldots 5$$

When assessing how well binary classification models work, these indicators are crucial. While accuracy provides a broad overview of the model's performance, precision and recall offer more detailed information about the model's performance for each specific class. Because it combines recall and precision, the F1 score offers a balanced metric that is particularly helpful for handling unbalanced datasets.

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RESULTS AND DISCUSSION

Training and Testing

Cross validation when compared to a single train-test split, it helps to provide a more accurate estimate of a model's performance (Inan et al., 2021). It makes it possible to evaluate how effectively the model generalizes to previously unseen data and assists in identifying problems such as underfitting or overfitting (Dalal et al., 2023). Furthermore, cross-validation makes greater use of the data that is available possible, particularly when the dataset is small. It is a key instrument in the assessment of machine learning models performance, cross-validation is frequently used to evaluate and contrast the performance of several models or algorithms. Figure 2 below shows the density plot of cross validation result obtained.

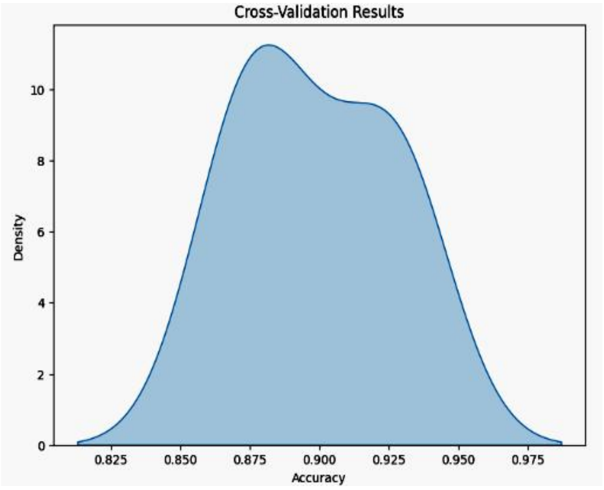

Figure 2: Density plot of Cross-Validation results

Ensemble Construction

The hybrid Ensemble model was constructed by combining multiple individual models such as random forest, decision tree, support vector machine, gradient boost, and logistics regression also known as base learners or weak learners, to create a more powerful and robust model known as ensemble. The foremost objective of ensemble model construction is to leverage the diversity and complementary strengths of base learners to improve overall predictive performance (Sarwar et al., 2015) and (Shakhovska et al., 2022). There are various techniques for ensemble model construction, including voting-based ensembles, bagging, boosting, and stacking. However, for this study, the voting-based ensembles were used. Here, multiple-based models were trained autonomously and their extrapolations are joint using a voting scheme. Two voting techniques are available, these include; Majority voting where the individual base model predicts the class label, and the class with the majority of votes is selected as the final prediction. Weighted voting, in weighted voting, the individual base model assigns a weight to its forecast, and the final prediction is computed as a weighted average of the predictions (Thanka et al., 2023). The ensemble construction technique was chosen because of various factors such as the nature of the problem, the availability of data, the diversity of base models, and the computational resources (Tuia et al., 2022).

Model Evaluation

The performance of the hybrid ensemble machine learning model was evaluated and analyzed on a test dataset. The dataset obtained was divided into training and testing, that is eighty and twenty percent respectively. This was achieved using common evaluation metrics such as accuracy, precision, recall, and F1-score. These measurements shed light on the various facets of the model's functionality (Sarkar & Mali, 2022) and (Singh et al., 2023). F1-score is the harmonic mean of precision and recall, providing a balanced measure between the two. Accuracy measures the overall accuracy of the predictions, precision measures the ability to correctly identify positive cases, and recall measures the ability to correctly identify all positive cases. These can be obtained on the following Table 1 which compared performances of the individual weak learner models to the hybrid ensemble learner.

Table 1: Comparison of Models Performances Metrics

Model	Accuracy	Precision	Recall	F1_Score	Sensitivity	Specificity	AUC
Random Forest	0.95	1.00	0.94	0.96	0.91	1.0	0.96
Gradient Boosting	0.96	1.00	0.96	0.97	0.89	1.0	0.95
Linear Regression	0.93	0.94	0.98	0.96	0.95	0.6	0.77
Hybrid Model	0.97	1.00	0.96	0.98	0.92	1.0	0.98

Figures 3 – 11 shows the graphical (plot) representation of the various metrics used in this work. In figure 3, the accuracies of all the individual model plus the hybrid model was shown and it clearly shows that the proposed hybrid ensemble outperformed the rest in terms of accuracy. Figure 4 and figure 5 compared the precision and recall of the various models used. Figure 6 shows the comparison of f1-score while figure 7 showcase and compared the sensitivity of the models. Comparison of specificity was shown in figure 8 whereas the Area Under the Curve (AUC) is shown in figure 9.

Also, figure 10 shows the graphical representation called the Receiver Operating Characteristic (ROC) curve. It was used to show how well a binary classification model can diagnose problems as its discrimination threshold is changed. Plotting the genuine positive rate (sensitivity) versus the false positive rate (1 - specificity) at different threshold values is how it was developed.

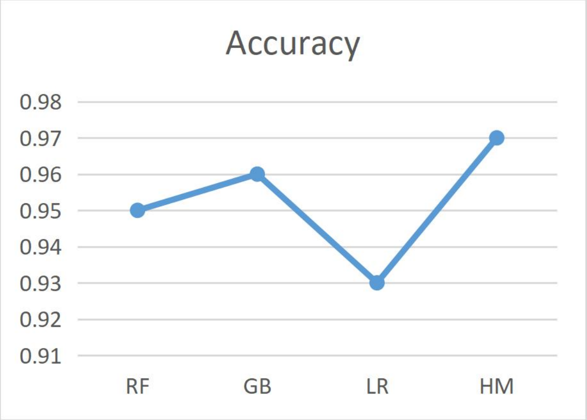

Figure 3: Comparison of Accuracy Results

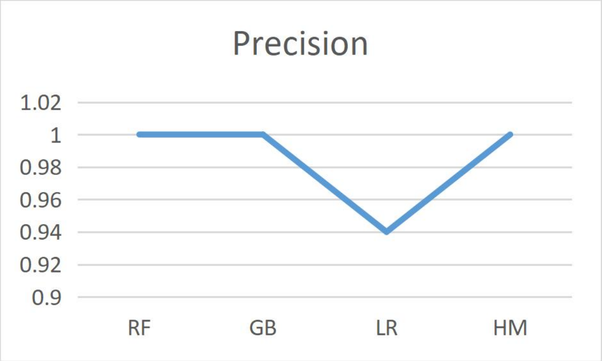

Figure 4: Comparison of Precision Results

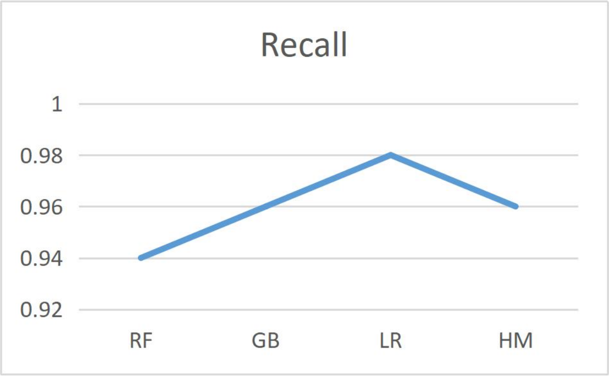

Figure 5: Comparison of Recall Results

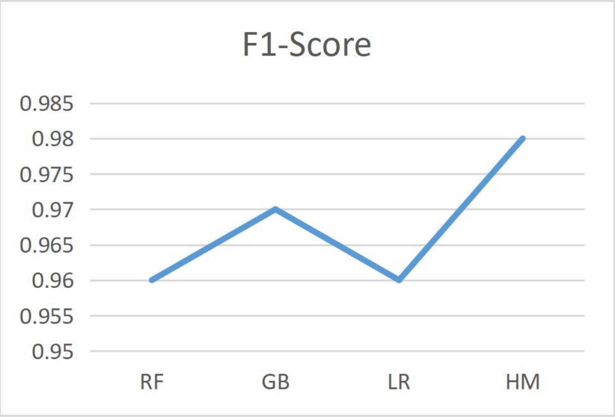

Figure 6: Comparison of F1-Score Results

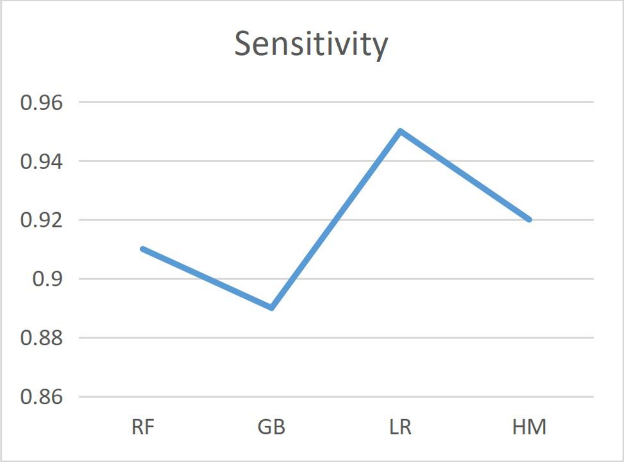

Figure 7: Comparison of Sensitivity Results

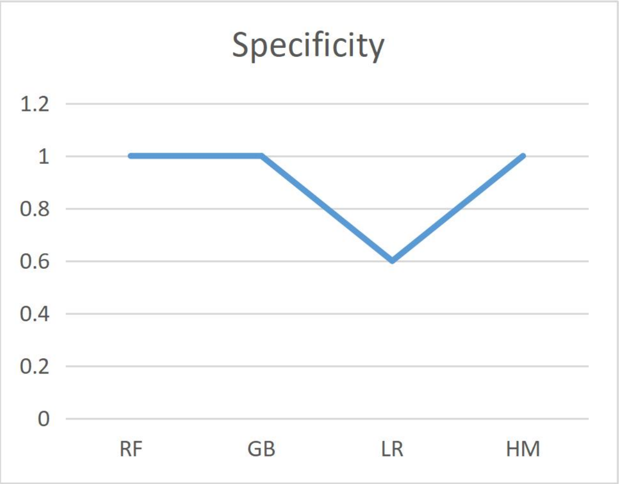

Figure 8: Comparison of Specificity Results

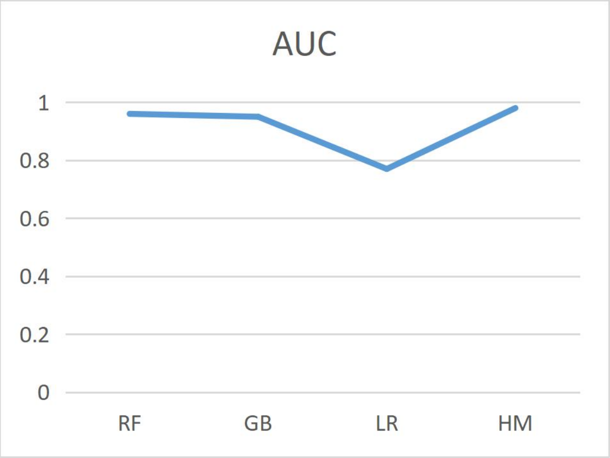

Figure 9: Area Under the Curve (AUC)

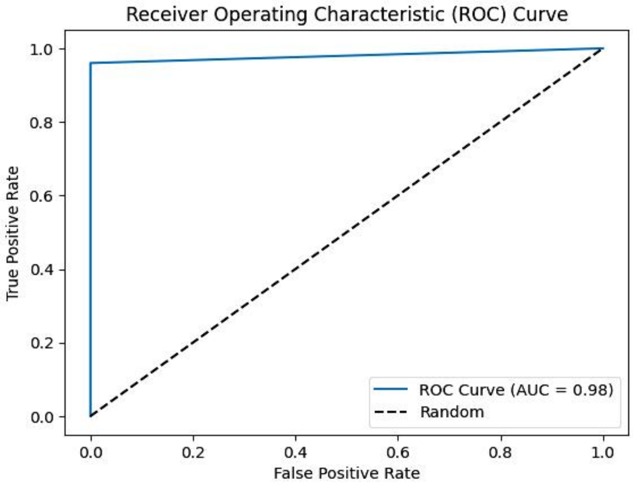

Figure 10: Receiving Area Characteristics Curve (ROC)

Discussion and Interpretation

The results obtained from the study suggested that the proposed ensemble model for cancer prediction achieved an impressive performance across various evaluation metrics used. Sensitivity also known as True Positive Rate or Recall, measures the model's ability to correctly identify positive instances (Abubakar et al., 2021). In this study, the ensemble model attained a sensitivity of 0.96, indicating that it correctly identified 96% of the cancer cases. Specificity, also known as True Negative Rate, measures the model's ability to correctly identify negative instances. The value of 1.0 attained by the model suggests that the model achieved a perfect specificity; that is, it correctly identified all the non-cancer cases. Area Under the Curve (AUC) is a widely used metric for evaluating the performance of binary classification models. It represents the area under the Receiver Operating Characteristic (ROC) curve, which measures the trade-off between the True Positive Rate and the False Positive Rate. The AUC value of 0.98 indicates that the ensemble model's predictions were highly accurate, with a high probability of ranking a randomly chosen positive instance higher than a randomly chosen negative instance. Precision is the ratio of true positives to the total number of positive predictions made by the model. A precision value of 1.0 indicates that all the positive predictions made by the ensemble model were correct.

Other metrics are; the harmonic mean of precision and recall (sensitivity) also called f1-score. It provides a balanced measure of the model's performance. A value of 0.98 indicates a high level of accuracy and balance between precision and recall. And lastly, accuracy; the overall correctness of the model's predictions, is calculated as the ratio of correct predictions to the total number of instances. An accuracy of approximately 0.97 shows that the proposed ensemble model achieved a high level of overall prediction accuracy.

In general, the findings highlight the excellent performance of the proposed ensemble model for cancer prediction. It achieved high sensitivity, specificity, AUC, precision, F1-score, and accuracy, indicating its ability to accurately classify both cancer and non-cancer cases. These results suggest that the ensemble model is promising for cancer prediction and could potentially be useful in real-world applications.

CONCLUSION

Conclusively, the proposed ensemble model for cancer prediction has demonstrated a remarkable performance across various evaluation metrics. With a sensitivity of 0.92, the model accurately identified a significant portion of cancer cases, while achieving a perfect specificity of 1.0, ensuring minimal misclassification of non-cancer cases. The high AUC value of 0.98 indicated the model's ability to accurately rank positive instances above negative instances, further solidifying its predictive power. Moreover, the precision and F1-score of 1.0 and 0.98, respectively, showcased the ensemble model's capability to make precise and balanced predictions. The overall accuracy of approximately 0.97 highlighted the model's strong overall predictive performance. The achievements of the ensemble model have important implications for clinical practice and patient outcomes. The accurate identification of cancer cases can facilitate early detection and timely interventions, which are vital in improving treatment efficacy and patient prognosis. Additionally, the model's ability to predict non-cancer cases accurately reduces the chances of unnecessary diagnostic procedures and treatments, leading to more efficient healthcare resource allocation.

Future Directions

There are several ways to explore this model. First of all, further validation of the ensemble model's performance on larger and more diverse datasets could enhance its generalizability and robustness. Furthermore, incorporating more advanced feature selection techniques or exploring different ensemble strategies may potentially enhance the model's predictive capabilities. Again, the deployment of the ensemble model in real-world clinical settings should be considered, along with addressing practical challenges related to data acquisition, integration, and interpretability. This would enable the assessment of its performance and impact on actual patient populations, fostering evidence-based decision-making and personalized treatment approaches.

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