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RESEARCH ARTICLE

Enhanced Stacking Ensemble Model for Cervical Cancer Prediction

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ABSTRACT - Early prediction of cervical cancer is crucial for positive outcome of treatments and reducing high mortality rate among women. This research aims at enhancing ensemble Machine Learning model to improve existing methods so as to have early diagnosis of the disease. Traditional methods have limitations in terms of sensitivity and specificity hence, there is need for more accurate and reliable predictive models. Existing machine learning models often face challenges such as overfitting, underfitting, and variability in prediction performance, this research which integrates different Machine Learning techniques in improving prediction, offers a potential solution to these challenges. In this study, an ensemble approach was used to develop an enhanced ensemble Machine Learning model using Support Vector Machine (SVM), Extreme Gradient Boosting (XGB) and Random Forest (RF). The three algorithms where chosen for their robustness against overfitting and improving accuracy of prediction. Furthermore the study Overcome issues of imbalanced datasets by applying Synthetic Minority Oversampling Technique (SMOTE) and Random Under Sampling (RUS) before training and testing the Machine Learning algorithms so as to obtain better result and improve accuracy of the model. This study achieved a higher accuracy of 95%, 97% precision, recall of 96% and 97% F1-score. The result indicates that the enhanced ensemble approach correctly identifies large majority of cervical cancer cases showing its reliability in prediction, assisting medical experts on early diagnosis. However, this study is limited to secondary datasets which involves collection of only secondary source datasets from the UCI repository for training and validating Machine Learning models. Future work should focus on advancing to Deep Learning to overcome limitation of utilising a feature extraction in Machine Learning algorithms technique and adding a lot more medical images to the dataset.

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1.0 INTRODUCTION

The world has achieved a lot with the improvement in innovation together with efforts of healthcare services. Machine learning models are now improving existing methods to achieve reliable results in the medical field. Cervical cancer being one of the recurring cancers related to a Sexually Transmitted Disease (STD) known as Human Papillomavirus (HP). It is an ailment whereby early prediction is very important to have the positive outcome of treatment and also to reduce the rate of mortality among women. With early diagnosis of the virus that causes the disease, this virus can be eliminated at an early stage and cervical cancer becomes preventable; but when prediction is delayed, treatment becomes very expensive and complicated thus, increases the rate of mortality among the patients [1].

Computer science as a field of study is evolving with emerging technologies and new domains are continuously discovered which include machine learning (ML). Recently, machine learning algorithms are increasingly applied for predicting cancers and identifying high-risk individuals that need immediate medical attention [2]. These algorithms are very useful tools that operates by learning patterns from large dataset and those patterns are used in making predictions. As regards to cervical cancer prediction, the algorithms can learn from patients' data and identify features associated with the increased rate of the disease. Ensemble method integrates results of individual machine learning algorithms so as to bring out a precise and improved prediction [3].

This research shows an ensemble approach for predicting cervical cancer by developing an enhanced ensemble machine learning model. This involves identifying risk factors associated with the disease and then collecting data and preprocessing it to address missing values and imbalanced data. After this, the preprocessed datasets are used to train the predictive models; performance of the predictive model is analyzed so as to have predicted results that are compared with existing results in order to assess the model's performance. Enhanced prediction models directly impact healthcare decision making by correctly predicting a high proportion of actual positive cases; and having early correct predictions improves patient's treatment outcome. Existing ensemble models for predicting cervical cancer remain suboptimal in terms of accuracy, necessitating further study to improve or enhance the performance. Also, previous studies reported issues of imbalanced datasets; however, this research uses SMOTE and RUS techniques to overcome issues of imbalanced datasets so as to enhance accurate prediction of the existing ensemble models.

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Cervical cancer has been a health concern worldwide, resulting to high mortality rate among women. Prompt identification and precise diagnosis of the disease will lead to prevention of the disease and better outcome of treatment. Traditional methods have limitations in terms of sensitivity and specificity [1]. Hence, there is need for more accurate and reliable predictive models.

Machine learning is enhancing cervical cancer prediction by leveraging large datasets and identifying complex patterns that may be missed by conventional methods. However, individual machine learning models often face challenges such as overfitting, underfitting, and variability in prediction performance. Ensemble Machine Learning, which integrates different Machine Learning techniques in improving prediction, offers a potential solution to these challenges [4]. This study's goal is to enhance ensemble Machine Learning approach to predict cervical cancer. This model achieves higher accuracy hence more reliable than the existing methods. This research aims to enhance early detection, reduce mortality rates, and enhance better outcome of treatment.

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This study's goal is to enhance ensemble Machine Learning approach to predict cervical cancer. This model aims to realize higher accuracy and to be more reliable than the existing methods. The main aspect of this study includes: data collection and preprocessing, training the algorithms to learn from data and testing, developing the ensemble model, model validation and evaluation. This research aims to enhance early detection, reduce mortality rates, and enhance better outcome of treatment. This paper is organized as follows: Section 1 provides the background of the study, followed by section two which discuss about related works, section three talks about materials and methods, section four contains results and discussion and section five contains the conclusion.

2.0 RELATED WORKS

Cervical cancer is one of the diseases with high mortality rate globally among women. Identifying women who are most susceptible to cervical cancer will improve the screening strategies so as to have effective prevention and also to have effective treatment of patients with the disease at precancerous stage. Algorithms for machine learning offer promise. In predicting cervical cancer using various features that includes Human Papillomavirus (HPV), weakened immune system, HIV and AIDS, smoking habits, long term use of contraceptives, sexually transmitted diseases (STDs) and a number of other causes [5]. This literature review is committed to provide a summary of the current research in cervical cancer prediction using Machine Learning techniques.

Supervised Machine Learning is acquiring knowledge under supervision; like teaching a kid to walk. Until the child can walk independently, you will hold his hand, show him how to advance his foot, walk yourself as a demonstration, and so on [6]. This type of learning uses algorithms for supervised learning. Making a function or mapping out of labeled training data is the aim. An input vector (X) and an output vector (Y) make up the training data, which contains tags or labels. Each tag or label in vector Y explains its corresponding input example in vector X. These two vectors together form a training example. If there is no labeling for the input vector X, it is considered unlabeled data. In supervised learning, neural networks, decision trees, and linear regression are often utilized techniques [7].

[8] suggested a model in which the performance of four classifiers was assessed to estimate the probability of eventually being diagnosed with cancer. With an AUC ranging from 0.70 one year before to diagnosis to 0.97 one day prior, Random Forest yielded the best results. They conclude that although their approach is reasonable and showed good diagnostic discrimination, it had only a limited potential for discriminating earlier. Since the goal of their study was to predict diseases before they manifested, we suggest that future research look at including basic health records before a hospital referral to broaden patient histories, for instance.

Five Machine Learning algorithms, namely Decision Tree, Random Forest, Gaussian Naïve Bayes, K-Nearest Neighbor, and Logistic Regression, have all been examined in a different study by [9]. Seventy percentage of the data set is meant for training, while thirty percent is meant for testing. With default parameters, Random Forest outperformed the other algorithms; Decision Tree, the least successful algorithms were GNB, KNN, and logistic regression, which came in last.

In another study by [10], the accuracy results from the ensemble approach were 1.72% higher than the average accuracy values from SVM, MLP, and KNN. When it came to sensitivity results, the ensemble method's outcomes outperformed the average of the three single classification approaches by a margin of 0.74%. The specificity results can be increased by 3.4% using the ensemble approach. The study's findings indicate that, when it comes to classifying anomalies related to Pap smear images to detect cervical cancer, the ensemble technique with the most votes can outperform the single classification method related to classification performance.

In another study by [12] the ANN model, enhanced by SMOTE and GA, achieves 87% accuracy and 0.85 AUC, demonstrating AI's potential to lower cervical cancer mortality in Nigeria. It provides scalable solutions for public health. The study [13] demonstrates ML's potential in resource-limited settings, with bagging offering reliable predictions, though larger datasets could improve generalizability.

The performance of the existing models for predicting cervical cancer in above literature review remains suboptimal in terms of accuracy, necessitating further study and improving ensemble machine learning models. [1] applied K-Nearest Neighbor (KNN) and Decision Tree (DT) using class balancing technique and suggested that other machine learning methods can be applied in future to observe the performance of other ensemble models in prediction and to improve the result. In this research, Support Vector Machine (SVM), Random Forest (RF) and Extreme Gradient Boosting (XGBoost) algorithms will be integrated to improve the prediction of cervical cancer. Also, previous studies reported issues of imbalanced datasets, however, this research used SMOTE and RUS techniques and has overcome issues of imbalanced datasets to obtain better results. Proper analysis of some papers reviewed are shown in Table 1.

Table 1. Tabular representation of strength and weaknesses of reviewed papers:

Ref. Paper	Methods	Strength of the Study	Weakness
[1]	K-Nearest Neighbor, Support Vector Machine and Random Forest Tree.	The results show the Random Forest algorithm delivered more promising results over SVM and KNN for four target variables Schiller, Biopsy, Hinselmann and Cytology respectively.	It was concluded that with the limited amount of data which also suffers from unbalancing brings about problem to the promising results drawn using the proposed model.
[8]	Random Forest, Complement Naive Bayes, Bernoulli Naive Bayes, and SVM	Four classifiers were evaluated for predicting a future cancer diagnosis where Random Forest achieved AUC of 0.70. This concludes that the approach is reliable.	Not extending patient histories through the integration of primary health records preceding referral to hospital.
[9]	K-Nearest Neighbor, Gaussian Naïve Bayes, Logistic Regression, Random Forest and Decision Tree (DT).	The findings demonstrate that Decision Tree algorithm was used and the study recorded an accuracy of 90%	The study did not focus on prediction duration even though the task needs to be fast
[11]	K Nearest Neighbor and Support Vector Machine	The results of their study indicate that the accuracy results obtained in the ensemble method increased by 1.72% compared to the average accuracy value in SVM and KNN.	The study focused on only two classes of abnormalities for the classification and prediction of cervical cancer.
	Decision Trees, Support Vector Machine, K-Nearest Neighbours.	The Fine Gaussian SVM The most effective classifier for categorizing Hinselmann, cytology, and biopsy The research used optimal characteristics to train various machine learning classifiers to predict cervical cancer among many risk variables.	Many datasets have been characterized by low sample size, outliers, imbalance and multiple risk factors.
[6]	Random forest, Support vector machine and AdaBoost	The study's results included a 92.57% accuracy, 91.25% positive predictive accuracy, and 92.14% negative predictive accuracy.	Data access control, generalization, building practical applications were among the challenges. The short comings of this study

Ref. Paper	Methods	Strength of the Study	Weakness
			include, the small sample size with the imbalanced input and target datasets.
[12]	Stacking-Integrated Machine Learning Approach, Random Forest, Logistic Regression.	This study shows that SIML enables the precise identification of high-risk females of developing cervical cancer. By maximizing the based on clinical data, behavioral patterns, and patient demographics.	The issue of imbalanced data was recorded in the study.
[13]	AdaBoost, Random forest and Support vector machine.	In this study the algorithms were integrated into many layers to generate the final stacked model. This classifier's accuracy, sensitivity, specificity, PPA, and NPA were 92.57%, 93%, 91.25%, 92.14%, and 90% respectively.	_
[14]	Decision Tree, Support Vector Machine and Multi-layer Perceptron	This study validated that machine learning can improve cervical cancer prediction. The study's findings demonstrated that the most pertinent predictors can be found using Decision Tree algorithms. Furthermore, it appears that raising patients' sociocultural standing and personal wellness may help avoid cervical cancer.	_
[15]	Random Forest, Custom Stacking Architecture	Explainable AI was utilized to improve interpretability. The model predictions were understood by the application of random forest, SHAP, and LIME.	Various issues must be addressed before deploying the classifiers in health care facilities like rigorous testing must be conducted, then comprehensive external validation.
[4]	Decision tree (DT), logistic regression (LR), support vector machine (SVM), and K-nearest neighbors (KNN).	The classification score of 86% has been accomplished using decision tree (DT), and random forest (RF) algorithms.	Limited datasets were recorded.
[16]	Logistic Regression (LR), Decision Tree (DT), Random forest (RF)	From the results obtained from this study, the voting method with SMOTE and PCA technologies helped classify cervical cancer data correctly for all target variables and raise the accuracy, sensitivity, and ROC_AUC of predictive models	In future work, the dataset used to detect cervical cancer can be improved and the efficiency of future prediction models can be increased by adding several

Ref. Paper	Methods	Strength of the Study	Weakness
			essential attributes that support cervical cancer early detection. It could be possible to gather some data and add it to the dataset. For instance, if the HPV vaccine was administered and if the Pap smear was completed lately. To help with the development of a more accurate predictive model, this extra data can be gathered from clinics and patients. Additionally, incorporating a few key characteristics can enhance the predictive model for cervical cancer early detection.
[17]	K-Nearest Neighbor, Classification and Regression trees.	According to the study, following the training of the final prediction model verified, 87.21% of the predictions were made correctly.	_
[18]	Random forest, weighted voting ensemble, gradient boosting classifier, majority voting ensemble, k-nearest neighbor, multi-layer perceptron.	Two feature selection approaches were used to extract the most significant features. The proposed stacking architecture, applied for the first time on the cervical cancer dataset, used time elapse of 5.6 s and achieved an area under the curve score of 92.7% performing better than the methods used in previous works.	Concerning the limitations of this study, it should be reported that the size of the cancer dataset is limited and the optimal training requires a lot of malignant cases. Also, a detailed analysis of different Techniques for class balance are necessary because the danger of oversampling the minority class increases when overfitting. Therefore, a thorough examination of various data is needed.
[19]	Random Forest, Support Vector Machine, K-Nearest Neighbor and Decision Tree	Results in this study show that stacking using a blend of support vector machines, random forests, and bagging were used	New hybrid classification algorithms should also be developed in the future to get more reliable classification for multiple datasets and cross-datasets.

Ref. Paper	Methods	Strength of the Study	Weakness
[20]	Support Vector Machine, K-Nearest Neighbor, Decision Tree and Multilayer Perceptron	In this paper an approach using ensemble methods with SVM as the base classifier has been taken.	The accuracy obtained in this result can further be improved with nature inspired optimization algorithms and therefore will continue to exist as a potential future expansion of the work.

2.1 Research Gap

The knowledge gap of previous finding and how it can be bridged: The performance of the existing models for predicting cervical cancer in above literature review remains suboptimal in terms of accuracy, necessitating further study and improving ensemble machine learning models.

[1] applied K-Nearest Neighbor (KNN) and Decision Tree (DT) using class balancing technique and suggested that other machine learning methods can be applied in future to observe the performance of other ensemble models in prediction and to improve the result. In this research Support Vector Machine (SVM), Random Forest (RF) and Extreme Gradient Boosting (XGBoost) algorithms were integrated to improve the result and accuracy of the prediction of cervical cancer. Also, previous studies reported issues of imbalanced datasets, however, this research uses SMOTE and RUS techniques to overcome issues of imbalanced datasets to obtain better results.

3.0 METHODS AND MATERIAL

This explains how listed objectives in this study will be achieved. It describes the methodology involved in the research. Also, it explained method of data collection and its source. Datasets variables, data cleansing, the enhanced model, and model validation were also discussed.

3.1 Data Collection

This is an important stage in every research and especially when it involves cervical cancer prediction. In this research, a secondary source from the UCI Machine Learning repository was used for data collection, however, preprocessing data is crucial to ensure quality of the dataset.

3.1.2 Cervical Cancer Dataset

This research used a secondary dataset from the UCI Machine Learning Repository. The dataset is an electronic health record of patients. It provides valuable features that help in building robust predictive models to improve cervical cancer detection. The dataset was diverged into three sets; train set, test set and data validation to determine the model accuracy. Cervical cancer (factors) dataset were obtained from the UCI Machine Learning Repository website. A total of two thousand nine hundred and sixty nine (2,969) occurrence showing records of patients. These features include age, pregnancies, and smoking behaviors, use of contraceptives and sexually transmitted diseases (STDs). Target variables namely ‘biopsy’, ‘schiller’, ‘Hinselmann’ and ‘citology’ confirm if the person has cervical cancer or is healthy. The dataset were imbalanced hence, oversampling and under sampling methods were employed during pre-processing.

After the data collection, the dataset was fed into the model for training which helped the model to be familiar with the dataset. Furthermore, training datasets comprises of pairs of an input vector and corresponding result for prediction (Output), which is known as the target. After training the dataset, the second dataset was used for validation of the model to produce unbiased assessment of its performance on the trained dataset. This helps to identify any overfitting issues and to optimize the model's hyper parameters before it is used on unseen data. After training the model and learning from the dataset. The testing dataset gives an unbiased development of the final model. So, a test dataset fed to the model to evaluate its performance.

3.2 Architecture of the Ensemble Model

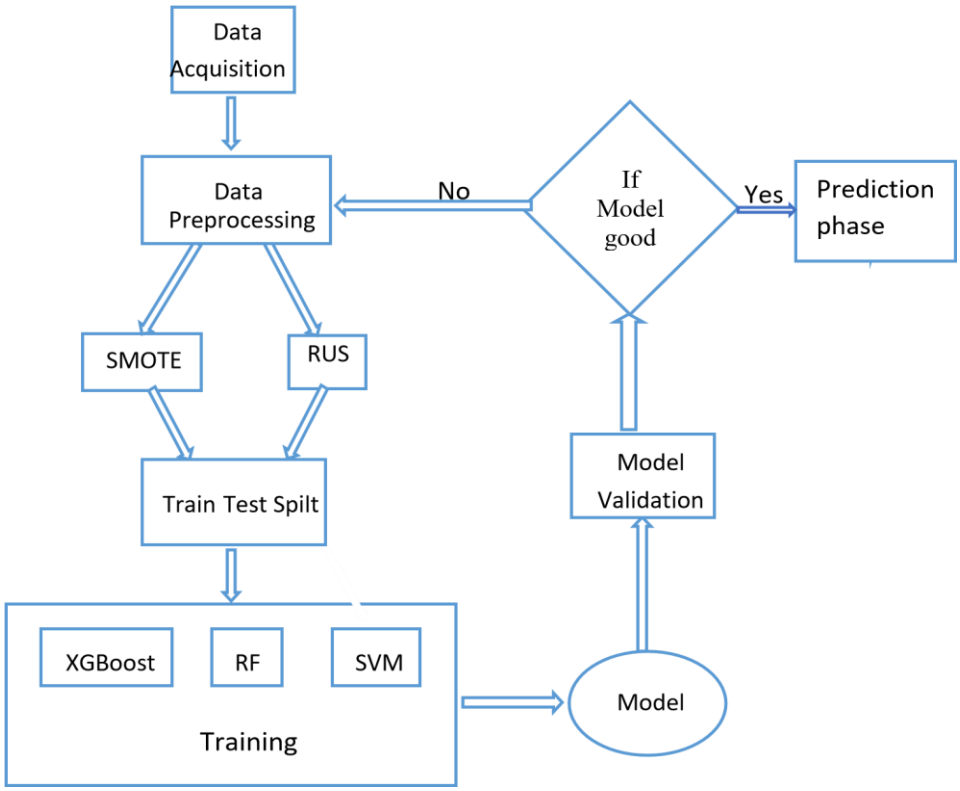

Figure 1. Architecture of the Model

Figure 1 can also be explained in the following algorithm:

Algorithm 1: Architecture of the Model

Step i: Collecting the dataset, which served as the foundation for the developed model.

Step ii: Clean and prepare a dataset for modeling by applying feature extraction Feature extraction in identifying and describing the features that are relevant to cervical cancer. This step involved handling scaling features, removing duplicate values. The Synthetic Minority Over-sampling Technique, or SMOTE, creates instances of the minority class in order to address the problem of data imbalance. Additionally, the dataset for the Support Vector Machine model is subjected to random under sampling. RUS technique reduces number of samples, which can be useful when SVM struggles with large datasets. Oversampling method is implemented by duplicating the random datapoints while undersampling is implemented by removing random datapoints

Step iii: The dataset is divided into two portions: typically, 70% for training and 30% for testing. This separation aids in evaluating performance of the model on unseen data.

Step iv: Training the models (XGBoost, Random Forest, and SVM) using the preprocessed data. Each model is trained with subsets of the data due to SMOTE and random under sampling. Stacking Ensemble Method was used to enhance the three algorithms robustness against overfitting so as to have high accuracy.

Step v: Evaluate the trained models on the 30% of dataset set aside for testing. Their performance is assessed using confusion matrix to evaluate how well they generalize to unseen data.

3.2.1 Confusion Matrix

Confusion Matrix, which is composed of TP, TN, FP, and FN, is designed to provide an overview of anticipated outcomes. Several evaluation metrics are usually applied in Machine Learning and data analysis, which includes the following:

3.2.2 Accuracy

Means proportion of accurately anticipated outcomes to the total observations represented in equation 1.

$$Accuracy = (tp + tn)/(tp + tn + fp + fn) \quad (1)$$

True positives, or TPs, indicate that a diseased person is expected to be ill. True negatives, or healthy people correctly classified as healthy, are represented by the symbol TN. False positive, or FP, refers to the erroneous classification of a healthy individual as ill. False negatives, or FNs, characterize a sick individual as healthy. This indicates that the most crucial component that must be as minimal as possible is FN. Another crucial component that needs to be as high as possible is TP. Hence accuracy is important in making correct prediction of cervical cases so as to have effective and efficient treatment

3.2.3 Precision

It is proportion of correctly predicted positive outcomes to the total predicted positive outcomes represented in equation 2.

$$Precision = tp/(tp + fp) \quad (2)$$

The precision is important in measuring how many real positive predictions there are out of all the positive forecasts.

3.2.4 Recall

Equation 3 shows the percentage of correctly predicted positive observations to all observations.

$$Recall = tp/(tp + fn) \quad (3)$$

Quantifies the proportion of real positive cases that the ensemble model accurately recognized.

3.2.5 F1 Score

Represents the mean of recall and precision. The closer to 1, the better the execution or performance as shown in equation 4.

$$F1\ Score = 2((precision * recall)/(precision + recall)) \quad (4)$$

The F1-score is a statistic that balances precision and recall, calculated as the harmonic mean of the two.

Prediction Phase:

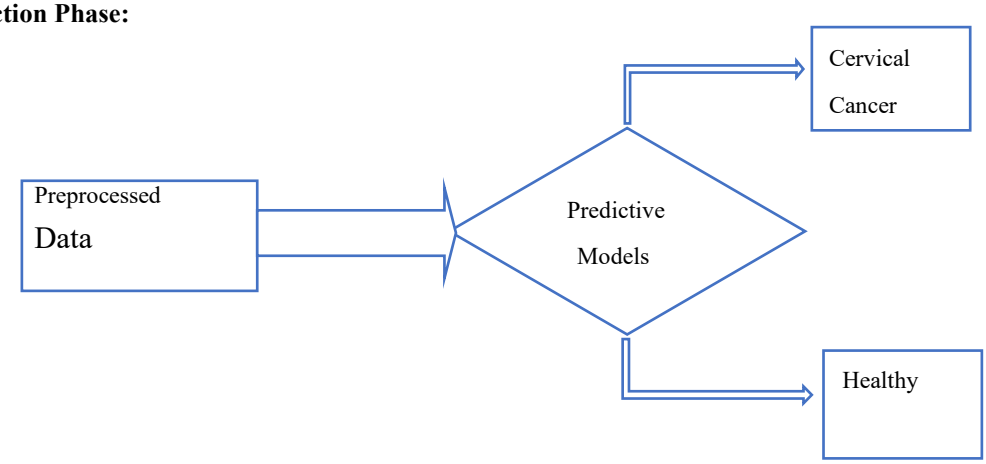

Figure 2. Prediction phase

Algorithm 2: Prediction Phase
Figure 2 can also be explained in the following algorithm:

Step i: Collect data that has been preprocessed, which in this case would be condition that you want to classify as either cervical cancer or healthy as shown in Figure 2.

Step ii: Utilize the trained machine learning model using majority voting to predict whether the condition is cervical cancer or healthy.

Step iii: From Figure 2 the model will output predictions classifying them as either "Cervical cancer" or "healthy" based on the patterns it learned during training.
Step vi: If a model performs well and meets the criteria for training, move on to the Prediction Phase (Deployment) as shown in Figure 2. However, if a model doesn't meet the expectations, return to the data preprocessing stage, make necessary adjustments, and retrain the model until it learns effectively from the dataset.

3.2 Implementation

This study was implemented using Python Programming language for the following reasons or tools. Python is a well-liked programming language for machine learning. Python's benefits include readability and simplicity. Python has a variety of strong libraries and frameworks. These libraries offer a different of tools for Machine Learning.

Here are the general system requirements for using Google Collaboratory (Collab):

i. Device: Google Collab is accessible via a PC, laptop, tablet, or even a smartphone using a current web browser.
ii. Internet Connection: Google Collab cannot be accessed or used without a reliable internet connection.
iii. Web Browser: Google Collab performs best when using Google Chrome version 42 or later.
iv. The python libraries that were used are Numpy 1.23.0, Scikit-learn and Matplotlib 3.10

4.0 RESULTS AND DISCUSSION

Table 2 presents the outcomes acquired from the experiment carried out on the individual machine learning algorithms and the improved ensemble machine learning algorithms.

Table 2: Results of individual algorithms and ensemble model

Model	Accuracy	Precision	Recall	F1-Score	ROC-AUC
Random Forest	0.94	0.72	0.85	0.78	0.93
Extreme Gradient Boosting	0.93	0.70	0.84	0.77	0.92
SVM	0.92	0.68	0.83	0.75	0.91
Ensemble Model	0.95	0.97	0.96	0.94	0.94

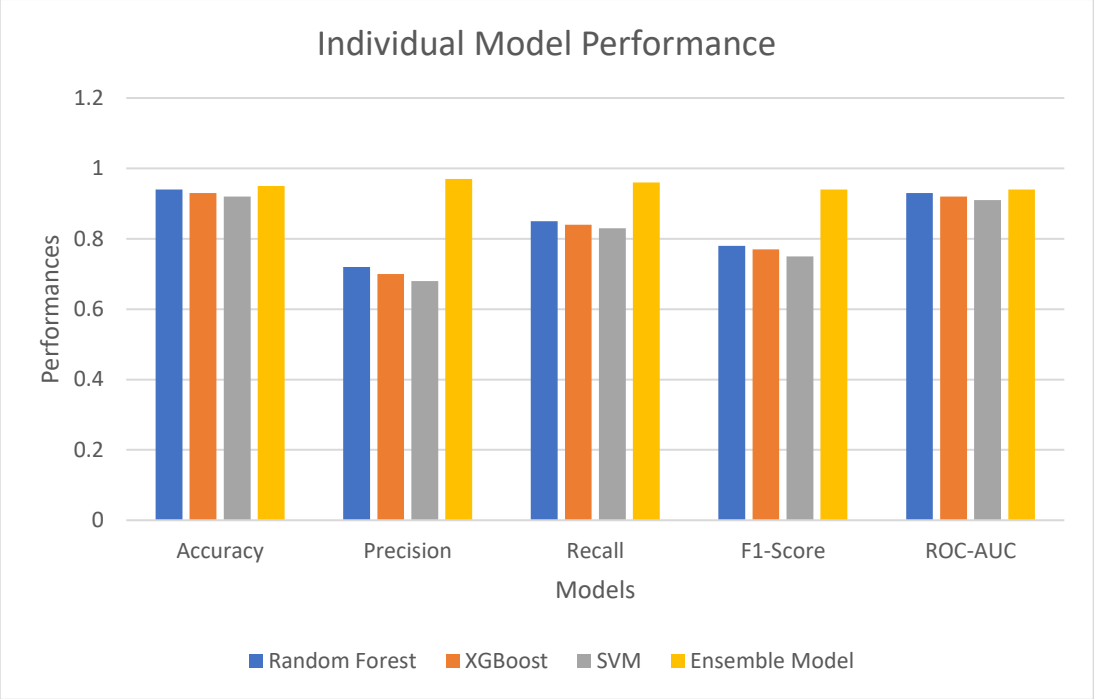

Figure 3. Performance of Individual Models and Ensemble Model

As shown in table 3, the improved ensemble machine learning approach has higher f1-score, roc-auc, accuracy, recall and precision as presented in table 3. This means the improved model correctly predicts a high proportion of actual positive cases (good sensitivity).

Table 3. Comparison between the ensemble and existing results

Model	Accuracy	Precision	Recall	F1-Score	ROC-AUC
Existing [1]	0.86	0.90	0.97	0.95	--
Ensemble	0.95	0.97	0.96	0.97	0.94

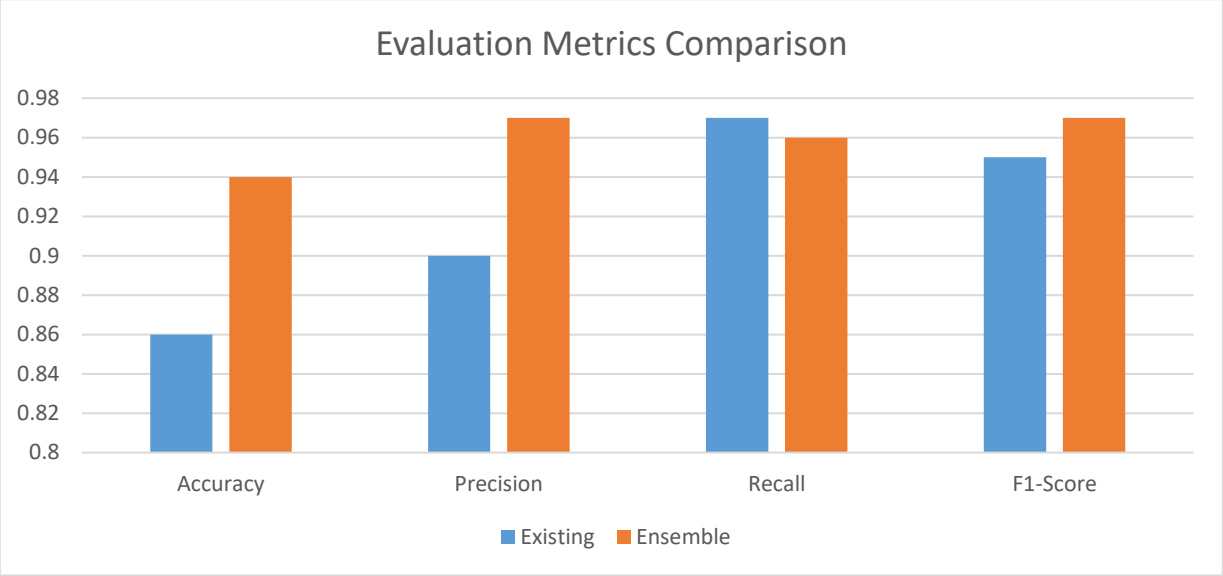

Figure 4: Comparison of Performance Evaluation Metrics

Figure 4 displayed the comparison of performance evaluation metrics of both the ensemble and existing methods. From figure 3, it can be deduced that our improved model has performed wonderfully well by exceeding or outperforming the existing method. The model achieved accuracy of 94% as against the 86% found in the existing literature, we achieved 97% precision against 90%. Likewise, f1-score, we have 97% to 95% in the literature. It was only in the recall metric that we have 96% against 97% found in the existing study.

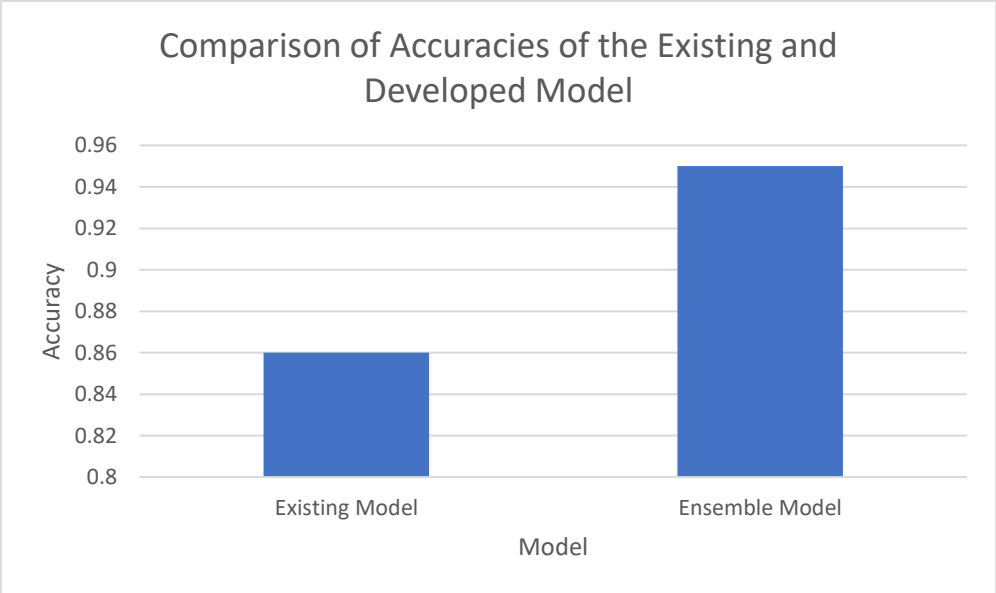

Figure 5: Comparison of accuracies of the existing and developed model

4.1 Confusion Matrix

Confusion Matrix are useful for measuring the performance of classification algorithms, as they give a more detailed explanation of accuracy and errors of the model. From the confusion matrix, different evaluation metrics such as accuracy, precision, recall, and F1 score can be calculated. Figure 5 is a confusion matrix of results acquired from the ensemble Machine Learning techniques.

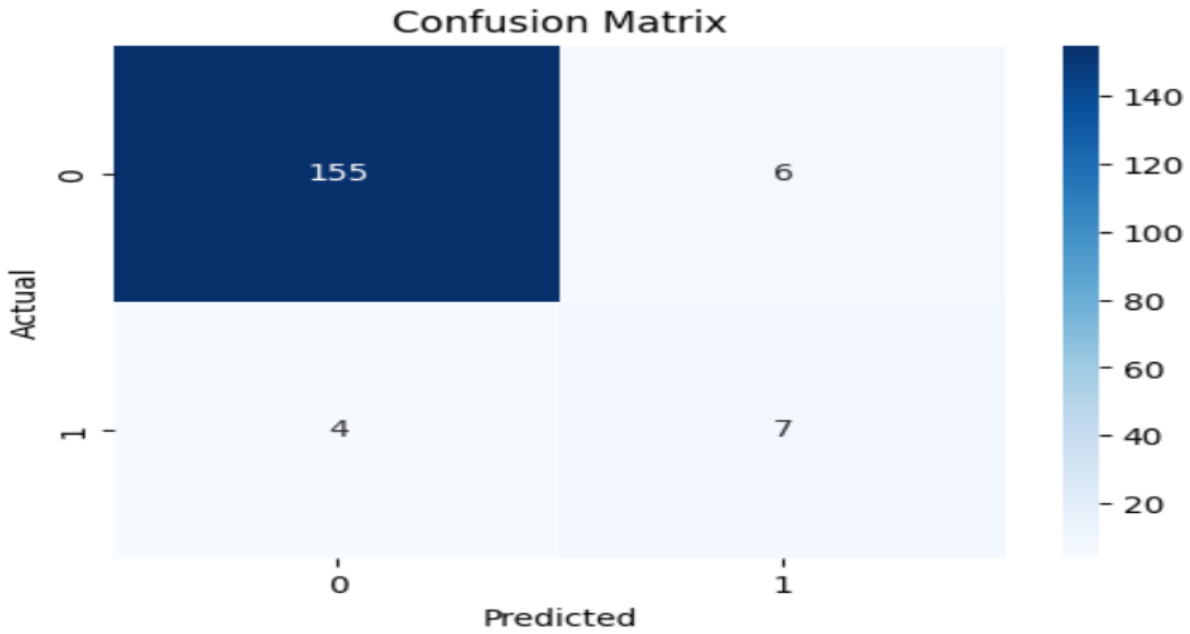

Figure 6. Confusion Matrix

As presented in confusion matrix in Figure 5, ensemble model has correctly made 155 true positive prediction and correctly made 7 true negative prediction; although, failed to make 4 false positive prediction and 6 false negative prediction. Hence, the ensemble model performed very good prediction.

4.2 Receiver Operating Characteristic (ROC) Curve

The ensemble Machine Learning approach ROC-AUC is 0.94 as shown in Figure 7, indicating excellent discriminative ability. ROC-AUC evaluates the model's capacity to differentiate between positive and negative cases across different threshold values. A high ROC-AUC demonstrates that the model performs well irrespective of the decision threshold, giving a robust evaluation of the model's overall achievement.

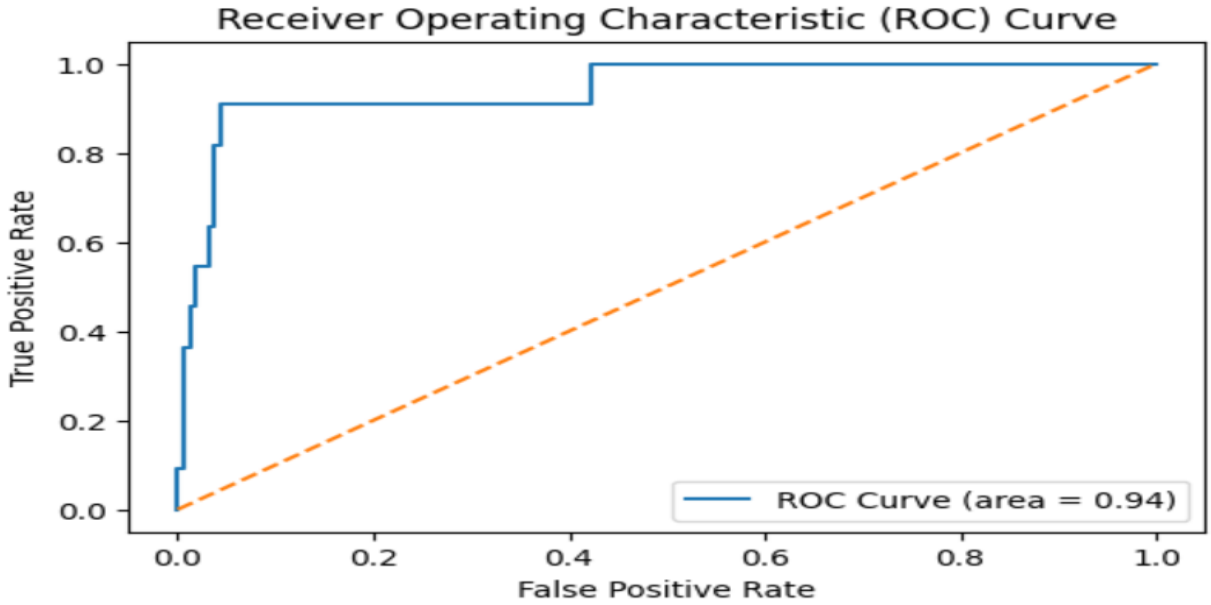

Figure 7. ROC Curve

As demonstrated by the performance of the ensemble model in Figure 7 the improved ensemble approach demonstrates significant improvements in accuracy and ROC-AUC and other evaluation metrics, indicating its potential for effectively predicting cervical cancer. However, the analysis between precision and recall highlights areas for further refinement. By focusing on threshold tuning, advanced feature engineering, hyper parameter optimization, and ensuring the model's integration into clinical workflows, the model can be enhanced to provide reliable and accurate predictions. Continuous learning and adaptation will help maintain its relevance and accuracy, ultimately contributing to better treatment outcomes and advancing the early prediction of cervical cancer. Also, higher precision and recall in the improved model indicates that it has higher number of true positives in contrast with the existing model which reduces unnecessary follow-up tests and potential anxiety for patients.

McNemar's Test

$$chi\text{^}2 = frac\{(b - c)\text{^}2\}\{b + c\} \quad (5)$$

This follows a chi-square distribution with 1 degree of freedom. For exact p-values (better for smaller s), we use a binomial test on the discordants, assuming under H_0 that b and c are equally likely (p=0.5). In Python (using SciPy), this is computed as `binomtest (max(b, c), s, p=0.5, alternative='two-sided').pvalue`.

1. Conservative case (least significant, largest p-value): Maximum s=35, so b=24, c=11 (b - c =13).
   - Exact p-value (binomial test): ≈0.041.
   - Chi-square approximation: $\chi^2 = 13^2 / 35 \approx 4.83$, $p \approx 0.028$.
2. Most significant case (smallest p-value): Minimum s=13, so b=13, c=0.
   - Exact p-value: ≈0.00024.
   - Chi-square: $\chi^2 = 13^2/13 = 13$, $p \approx 0.0003$.

In all possible scenarios, the p-value is <0.05 (ranging from ~0.0002 to 0.041). Therefore, we reject H_0 and conclude that the ensemble model's improvement in accuracy is statistically significant at $\alpha=0.05$.

5.0 CONCLUSIONS

In this study, several Machine Learning algorithms, including Random Forest (RF), Extreme Gradient Boosting (XGB), and Support Vector Machine (SVM), were used in an ensemble machine learning strategy to predict cervical cancer. The ensemble model was developed through the use stacking. According to the analysis, the accuracy and ROC-AUC of the ensemble model were much higher than those of the previous model [1]. In particular, the ensemble method produced results with ROC-AUC of 0.94, accuracy of 0.95, precision of 0.97, recall of 0.96, and F1-score of 0.97.

This study aimed to enhance ensemble Machine Learning approach for the prediction of cervical cancer disease. The ensemble model combined the strengths of various algorithms to overcome the individual limitations of these algorithms so as to get higher accurate prediction of the disease. Feature extraction was also applied to address data imbalance which also enhanced the performance of the model. The ensemble Machine Learning model demonstrates a remarkable enhancement in overall accuracy, as evidenced by the high ROC-AUC. However, the higher precision indicates an increased rate of true positives, which could reduce unnecessary follow-up tests and stress for patients. The high recall is advantageous for ensuring that most cervical cancer cases are detected, which is crucial for early intervention and treatment. The results indicate that the model is successful in categorizing positive cases, thereby enhancing the overall reliability of the predictions.

5.1 Contribution to knowledge

This study has a positive impact in Machine Learning and public health by providing a more reliable and interpretable model in order to predict cervical cancer early, undoubtedly contributing to better health and positive outcome of treatment for women globally. Also, previous studies reported issues of imbalanced datasets, however, this research used feature extraction, SMOTE and RUS techniques to overcome issues of imbalanced datasets thereby obtaining a better result.

5.2 Recommendations

Explore more sophisticated ensemble methods like stacking to capture complex patterns in the data more effectively. Collaborate with healthcare professionals to integrate the model into clinical workflows. Implement a continuous learning framework over time, add new data to the model and retrain it. This will guarantee that the model stays accurate and applicable as medical knowledge and patient demographics evolve.

5.3 Suggestion for Future Work

Future work should focus on advancing to Deep Learning to overcome limitation of utilizing a feature extraction in machine learning algorithms technique and adding a lot more medical images to the dataset.

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AUTHORS CONTRIBUTION

Fatima Isa Jibrin (Methodology; Data curation; Writing - original draft; Resources)

Dr. Lawan Jibrin Muhammad (Supervision, Project administration, Writing - review & editing)

CONFLICT OF INTEREST

The authors declare no conflict of interest

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