Analysis of Stacked Ensemble Classification Models in Cervical Cancer Prediction using Machine learning

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Abstract –

Cervical cancer is an often-fatal disease that primarily affects women. Nevertheless, early detection of cervical cancer may lower death and other consequences. Cervical cancer risk factors may help in early detection. Unfortunately, the existing prediction models need clinical physiological and biochemical variables, resulting in a narrower spectrum of use. We suggested a study for early detection of cervical cancer utilizing a reduced risk feature set and three ensemble-based classification approaches to improve diagnostic accuracy. In the present study, SUML (stacked unified machine learning) is a sophisticated machine learning approach that combines different learning algorithms to increase prediction performance. The screening data were randomly divided into training data (80%), used to construct the algorithm, and testing data (20%), used to confirm the algorithms' accuracy. The random forest (RF) model and AdaBoost were utilized to discover predictive markers for developing cervical cancer. Three well-known machine learning algorithms were chosen, and their effectiveness in predicting cervical cancer was examined. Moreover, compared to prior benchmark studies for cervical cancer detection utilizing a decreased risk factors data set, the performance of the suggested models is significant in terms of accuracy.

Index Terms: Cervical Cancer , machine learning, Stacked Ensemble
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1. INTRODUCTION

Cervical cancer is one of the most common malignant tumors in women worldwide [1]. The 5-year survival rate for early-stage cervical cancer is high, ranging from 80% to 90% [2]. However, the cure rate goes down to 10% for stage 4 disease [3]. Cervical screening has, therefore, an important role in identifying the disease at an early stage and hence reduces the morbidity and mortality from the disease. The incidence and mortality from cervical cancer vary across different countries and tend to be lower in highly developed countries due to well-established screening and vaccination programs [4]. However, underdeveloped regions often do not have sufficient medical resources allocated to screening. This implies that there is an increased need to identify women at a high risk of developing cervical cancer to optimize the screening interval and hence make better use of medical resources [5].Currently, this cancer diagnosis involves two tests: First, the patient is required to undergo a cytology test called the pap smear or Papanicolaou's test [6]. In this test, cells are gently removed from the cervix and the surrounding regions with a tiny brush to be examined under a powerful microscope. Cell abnormalities and cancer cells can be easily identified using this method. The next step is to conduct a thorough colposcopy exam [7].

Several studies have found significant changes in the risk of contracting cancer at various age levels. This cancer can be easily prevented, yet most women are unaware of the aetiology, health risks, prevention and management of cervical cancer due to their background and education levels. Cervical cancer is rare in developed countries, and low-income nations account for almost 95% of cervical cancer mortality [8]. Another prominent reason is the HPV infection, which spreads through sexual contact. As a result, the age during first sexual contact, the number of sexual partners, and the use of contraceptives has all been linked to cervical cancer [9]. If these factors are managed, the occurrence of this malignant tumour can be minimized. Regular cervical cancer screening can prevent infections and is also an effective measure for clinical management of potential cancer patients [10]. There is also a pressing need to identify alternative approaches to diagnosing early-stage cancer.

Traditionally, hospitals use statistical methods to describe and analyze the dataset since the amount of data is small and the data are not too complicated. However, in the big data era, the number and complexity of data grow exponentially. It is difficult for statistical methods to accurately analyze and effectively mine massive amounts of internal data. With the rapid development of machine learning and data mining, researchers have applied various machine learning methods, such as random forest (RF), support vector machine (SVM), decision tree (DT), neural network (NN), etc., to the medical field, which have been shown to be capable of efficiently improving the accuracy of prediction.

Conclusively, the finding made after the above-mentioned literature is that the data set found at UCI repository had several missing values; therefore, previous studies have removed at least 2 features. Missing values were due to patient's concerns regarding their privacy. After removing 2 features due to huge missing value, SVM-PCA seemed to provide satisfactory performance. However, SMO and SMOTE-RF were amongst the best performing models. Another approach to deal with the imbalance in UCI cervical risk factor data set was using oversampling. Deep learning proved to be effective, especially where the Biopsy and possibly other screening results are absent. Age, first sexual intercourse, number of pregnancies, smoking, hormonal contraceptives, IUD, STDs, STDs: genital warts, or HPV infections were identified as the top key features. +e significant outcomes made by the machine learning classifiers motivate the need for further investigation and enhancement of the outcomes for the prediction of cervical cancer.

In this study, three ensemble-based classifiers SVM, Ada Boost, and RF are used to classify cervical cancer. In addition to the importance of correctly classifying cancerous and noncancerous cases, it is also essential to identify key risk factors that contribute to developing cancer. Furthermore, the Synthetic Minority Oversampling Technique (SMOTE) is used to balance the classes of the data as it suffers greatly from imbalanced problem.

The rest of the paper is organized as follows. We first briefly review the related literature in Section 2. Section 3 presents our material and methods framework. Section 4 presents experimental results which show that our method stands out as a state-of-the-art technique. Finally, we present a discussion and conclude the paper in Section 5.

2. RELATED WORK

In the early years, many researchers compared the Cox proportional hazard model with machine learning and deep learning methods for survival prediction problems.

Machine learning algorithms provide several tools for smart data analysis [11], with the recent digital revolution, many modern hospitals are now equipped with means for data capture, storage and sharing. Decision trees [12] have been used diagnosing cervical cancer, from experiments, a decision tree achieved accuracies of 92.54%, 92.80%, 94.41% and 90.44% for Biopsy, Cytology, Hinselmann, and Schiller tests respectively. Multilayer Perceptron (MLP), Bayes Net and k-Nearest Neighbour have also been used [13] to correctly classify cervical cancer instances, experiments showed that, Bayes Net achieved the highest classification accuracy, by classifying 97.26 instances correctly, followed by both k-Nearest Neighbour and MLP at 95.89%.

The effectiveness of Iterative Dichotomous (ID)3, C4.5 and Naïve Bayes in predicting cervical cancer were analysed [14], the results from the test set of each

model was averaged, Naïve Bayes got the highest accuracy score of 81%, followed by C4.5 at 72%, then ID3 at 69%. Medical diagnosis is sensitive, therefore apart from accuracy analysis, it is also important to get from a model how often it predicts a disease when the patient actually has the disease, and how many often it predicts no disease when a person actually does not have the disease. From existing literature, many models including the ones discussed in this section, only present their accuracy levels or scores but fail to present their sensitivity and specificity levels.

Many other studies have explored different methods to predict cervical cancer, data-based approaches such as support vector machines (SVM), linear regression (LR), principal component analysis (PCA), particle swarm optimization (PSO), artificial neural networks (ANN) and clustering algorithms [15-20] have been used.

3. METHODOLOGY

For classification taskAdaBoost is fast, efficient and difficult to over fit, especially for high-dimensional data, but it can only give label classification. SVM algorithm with linear kernel function can give hyperplane representing malware detection, but its effect depends on the quality of feature selection. RF model is the best model with the highest accuracy. We expect to do prediction of cervical cancer on the main content of the modeling is shown in Figure 1.

Dataset:

The dataset for the study has been collected from UCI repository, which is have 858 instances with 32 features [21]. The data was consisting missing values in it, as some women were not willing to disclose some of the information. And, also it was highly imbalanced, that is majority of the instances were non-cancerous. The dataset was consisting of four target variables Hinselmann, Schiller, Cytology and Biopsy each of which represents a type of cervical cancer examination.

Data Preprocessing:

Not all the data for each predictive feature were available. About 20%–30% of the clinical predictive data and about 0%– 15% of the behavioral data were missing. The missing part of the data had to be estimated by using the information available in the existing data to replace the missing data with values. However, due to a large number of missing data, conventional mean and median filling methods could not be used in this case, since these techniques cannot guarantee data authenticity because the filling values are mostly unreal values, which will affect the accuracy of model construction.Additionally, the data set also suffers from huge class imbalance. +e data set target labels were imbalanced with 35 for the Hinselmann, 74 for Schiller, 44 for Cytology, and 55 Biopsy out of the 858 records. SMOTE was used to deal with class imbalance.

There are many ways to do resampling to an imbalanced dataset, such as SMOTE and Bootstrap Method. We will use SMOTE (Synthetic Minority Oversampling Technique) that will randomly generate new replicates of our undersampling data to balance our dataset.Now the data is already balanced as we can see from the counter of each sentiment categories before and after the resampling with SMOTE.

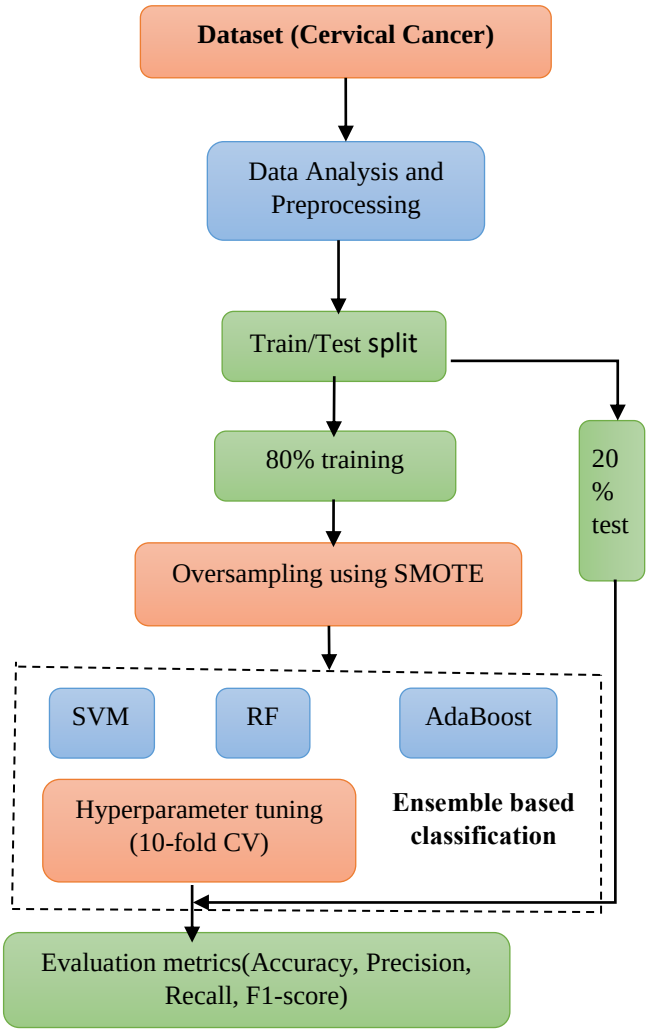


Figure 1: Cervical cancer prediction framework using machine learning

Splitting Dataset:

We splitted our dataset into 80:20 portion respectively for the training and test set.

StackedEnsemble-Based Classification Methods.

Three ensemble-based classification techniques such as Random Forest, Support vector machine, and Ada Boost were used to train the model. the description of these techniques is discussed in the section below.

We do not really know what is the best model that fits our data well. Because of that, we will need to try every classification model available and find the best models using the Confusion Matrix and F1 Score as our main metrics, and the rest of the metrics as our support. First, we should do some cross validation techniques in order to find the best model.

Random forest

The random forest classifier was chosen due to its superior performance over a single decision tree with respect to accuracy. It is essentially an ensemble method based on bagging. The classifier works as follows: Given *D*, the classifier firstly creates *k* bootstrap samples of *D*, with each of the samples denoting as D_i . A D_i has the same number of tuples as *D* that are sampled with replacement from *D*. By sampling with replacement, it means that some of the original tuples of *D* may not be included in D_i , whereas others may occur more than once. The classifier then constructs a decision tree based on each D_i . As a result, a "forest" that consists of *k* decision trees is formed.

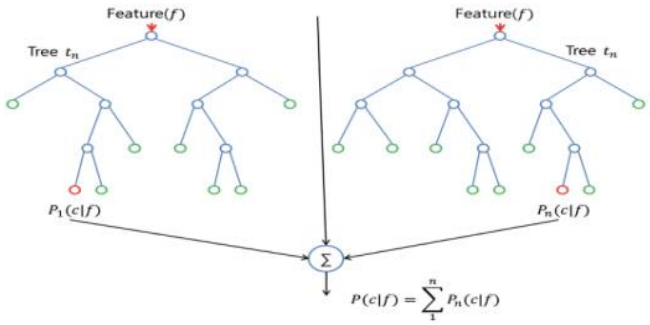


Figure 2: Tree structure of Random Forest model

To classify an unknown tuple, *X*, each tree returns its class prediction counting as one vote. The final decision of X's class is assigned to the one that has the most votes. The decision tree algorithm implemented in scikit-learn is CART (Classification and Regression Trees). CART uses Gini index for its tree induction. For *D*, the Gini index is computed as:

$$Gini(D) = 1 - \sum_{i=1}^{m} p_i^2 \qquad (1)$$

Where p_i is the probability that a tuple in *D* belongs to class C_i . The Gini index measures the impurity of *D*. The lower the index value is, the better *D* was partitioned.

Support vector machine:

Support vector machine (SVM) is a method for the classification of both linear and nonlinear data. If the data is linearly separable, the SVM searches for the linear optimal separating hyperplane (the linear kernel), which is a decision boundary that separates

data of one class from another. Mathematically, a separating hyper plane can be written as: $W \cdot X+b=0$, where W is a weight vector and $W=w_1,w_2,...,w_n$. X is a training tuple. b is a scalar. In order to optimize the hyperplane, the problem essentially transforms to the minimization of $\|W\|$, which is eventually computed as:

$$\sum_{i=1}^{n} \alpha_i y_i x_i \quad (2)$$

where α_i are numeric parameters, and y_i are labels based on support vectors, X_i .

$$\sum_{i=1}^{n} w_i x_i \geq 1 \quad (3)$$

If y_i= -1 then

$$\sum_{i=1}^{n} w_i x_i \geq -1 \quad (4)$$

If the data is linearly inseparable, the SVM uses nonlinear mapping to transform the data into a higher dimension. It then solves the problem by finding a linear hyperplane. Functions to perform such transformations are called kernel functions. The kernel function selected for our experiment is the Gaussian Radial Basis Function (RBF):

$$K(X_i, X_j) = e^{-\gamma \|X_i - X_j\|^2/2} \quad (5)$$

where X_i are support vectors, X_j are testing tuples, and γ is a free parameter that uses the default value from scikit-learn in our experiment. Figure shows a classification example of SVM based on the linear kernel and the RBF kernel on the next page.

AdaBoost.

It is an ensemble technique to build a meta classifier by combining several weak classifiers using progressive learning. AdaBoost uses the concept of boosting data sampling technique; adaptive sampling was used to assign high weights to the misclassified events. the misclassified samples will be selected in the next iteration to better train the model, and the final prediction was made using weighted voting.

AdaBoost has reduced error rate, has a better effect on the prediction as compared to bagging [24], and uses decision tree stumps. Initially, all the samples in the data set have equal weights. Let x be the number of samples in the data set, and let y be the target. the target is a binary class represented by 0 and 1. the first decision tree stump will use some records from the data set, and predictions will be performed. After the initial prediction, the weights to the sample will be updated. More weights will be assigned to the data samples that were misclassified. the samples with the high weights will be selected in the next iteration. the process will be continued, unless the error rate is completely reduced, or a certain target level is achieved.

AdaBoost contains two main steps, combination and step forward using sequential iterative approach. All the instances in the training set have equal weights in the first iteration. However, in subsequent iterations, the weights are changed based on the error rates. the instances with error have increased weights. For the binary class classificationproblem containing T training samples is represented in the following equation:

$$\{(x_i, y_i)\}_{i=1,}^{T} with\ y_i \epsilon \{0,1\} \quad (6)$$

Let C be the linear combination of weak classifiers. +e combination of the classifiers is represented as

$$C(x) = \sum_{n=1}^{N} w_n c_n(x) \quad (7)$$

where N is the number of weak classifiers, w represents the weights, and C (x) represents weak classifiers. In every next iteration, the classifier is trained based on the performance of the classifier in previous iteration.

$$C(x)_t = C(x)_{t-1} + w_n c_n(x) \quad (8)$$

where $C(x)t$ represents the classifier in t iteration. $C(x)t$-1 is the performance of the classifier at t - 1 iteration.

The weights can be calculated using the following equation:

$$w_n = \frac{1}{2} ln\left(\frac{1-\epsilon_n}{\epsilon_n}\right) \quad (9)$$

n represents the error rate of the weak classifier.

Model Building: We are using K-Fold Cross Validation (CV) on our early dataset (before resampling) because the CV itself is not affected by the imbalanced dataset as it splits the dataset and takes into account every validation. If we use the CV on the balanced dataset that we got from resampling we should be able to get similar result.

4. RESULTS AND DISCUSSIONS

The model was implemented in Python language 3.8.0 release using Jupyter Notebook environment. Ski-learn

library was used for the classifiers along with other needed built-in tools, while separate library (XGBoost 1.2.0) was used for XGBoost ensemble. There is K-fold cross validation with K=10 for partitioning the data into training and testing. Five evaluation measures such as accuracy, sensitivity (recall), specificity (precision), positive predictive accuracy (PPA), and negative predictive accuracy (NPA) were used.

Exploratory Data Analysis:

For EDA we consider the initial data, which consisted of 858 rows and 36 columns, had many null values. These missing values were represented using the "?" symbol. Initially, this symbol was replaced with "NaN" for ease of processing. Most patients were diagnosed as non-cancerous after the biopsy test and only 6.4% had cervical cancer, as per Figure 3.

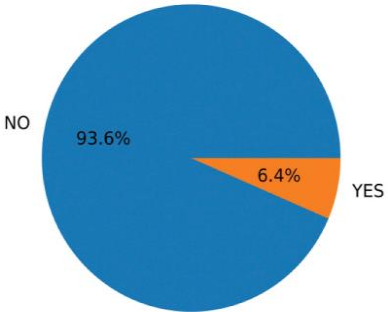
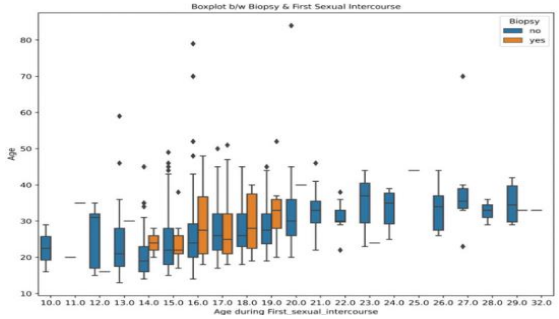
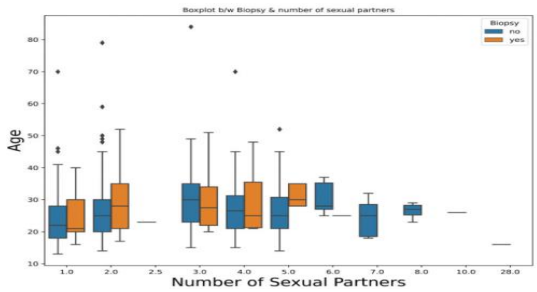


Figure 3: The percentage of biopsy positive and biopsy negative results.

After univariate analysis, multivariate analysis was performed. Figure 4a shows a box plot to understand the relationship between age and age during first sexual intercourse on biopsy results. From the figure, it can be inferred that sexual intercourse at a young age (14–19 years) can result in a positive biopsy result.



(a)



(b)

Figure 4: Multivariate analysis using box plots**.**

In Figure 4b, a box plot is used to understand the relationship between age, the number of sexual partners and the biopsy result. The figure shows that the chances of getting diagnosed with cervical cancer increase when the number of sexual partners increases.

Prediction Performance of the Sampling Method

Table 1 described the comparative performance scores of different sampling methods using RF. Each sampling model had been verified internally and externally.

Table 1: Prediction performance of random forest algorithm on different sampling models.

Approach	**Acc**	**Pre**	**Sen**	**Spe**
Undersampling	0.375	0.152	0.167	0.741
Oversampling	0.608	0.159	0.909	0.639
SMOTE	**0.842**	**0.189**	**1.000**	0.62

In the external validation of Figure 5, SMOTE-based RF performed best among all classifiers with an accuarcy of 0.842 and had the highest score in three of our four performance metrics. The precision were 100%, higher than 70% as related to undersampling and over sampling approaches respectively. SMOTE was therefore selected as the imbalance data processing algorithm for the final model.

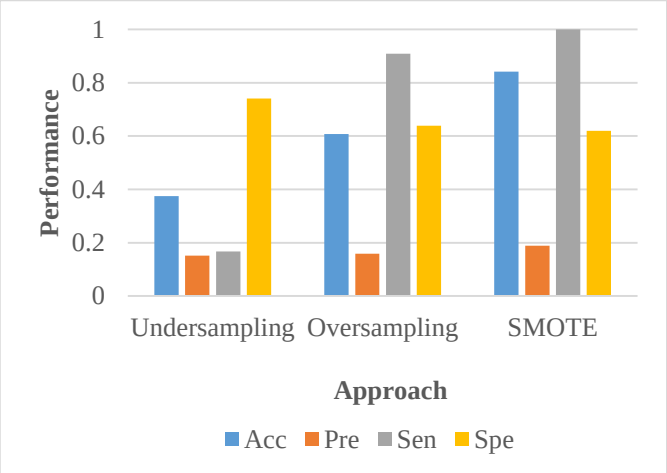


Figure 5: Performance of random forest algorithm on different sampling models.

Comparison with Existing Studie

The study used three ensemble techniques AdaBoost, extreme SVM, and Random Forest. Furthermore, the proposed study is the pioneer in using bioinspired algorithm for feature selection and optimization for cervical cancer diagnosis. To explore the significance of our proposed study, the outcome of the study was compared with the benchmark studies.

Table 2: Comparison of the proposed study with benchmark studies.

Target class	Authors	Accuracy	Sensitivity	Specificity	PPA	NPA
Hinselmann	Authors in [23]	97.6	96.65	98.54	98.48	96.78
	Authors in [24]	93.97	100	89.96	84.97	100
	Proposed work	98.21	100	98.65	98.65	97.84
Biopsy	Authors in [23]	96.06	94.94	97.76	97.58	94.91
	Authors in [24]	94.13	100	90.21	86.07	100
	Proposed work	95.57	100	91.25	92.14	100

The criteria for the benchmark studies selection were based on data set used for the diagnosis of cervical cancer [25, 26]. Also, Table 2 contains the comparison of the proposed technique with the benchmark studies in the literature. However, some of the outcomes in the previous studies were achieved with the reduced features.

5. CONCLUSION

This paper looks at ensemble algorithms for detecting cervical cancer, including Random Forest, AdaBoost, and SVM. The data set was from the University of California, Irvine's machine learning library. The target variables are the cervical cancer diagnostic test. Experiments were carried out independently for each target class. Imputing missing values and class balancing using SMOTE are examples of data preparation. Experiments were carried out using chosen characteristics and selected features utilizing SMOTED data to compare the performance of the models. The algorithms were then integrated into many layers to generate the final stacked model. This classifier's accuracy, sensitivity, specificity, PPA, and NPA were 95.57%, 100%, 91.25%, 92.14%, and 100%, respectively.

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