IEEE Access
Multidisciplinary | Rapid Review | Open Access Journal

Received December 15, 2020, accepted December 26, 2020, date of publication January 5, 2021, date of current version January 22, 2021.

Digital Object Identifier 10.1109/ACCESS.2021.3049165

An Enhanced Ensemble Diagnosis of Cervical Cancer: A Pursuit of Machine Intelligence Towards Sustainable Health

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The authors extend their appreciation to the Deanship of Scientific Research at King Faisal University, Saudi Arabia for funding this research work through KFU Nasher Track 2020 with research grant number 206127.

ABSTRACT Cervical cancer is a potentially life-threatening disease marked by health practitioners. The late diagnosis and treatment, being quite challenging, stake the precious lives of patients. In both developed and undeveloped states, the formal screening for disease identification suffers due to its medical cost, unavailable health facilities, society norms, and late appearance of symptoms. Machine intelligence is cost-effective, computationally inexpensive, and early diagnosis of several types of diseases, including cervical cancer. The patients are not required to pass through contemporary and tedious medical procedures, and early diagnosis of cervical cancer is quite handy with machine-intelligent solutions. The problem with the current machine classification methods for disease identification is the reliance on a single classifier's prediction accuracy. The adoption of single classification methods doesn't ensure the optimum prediction due to bias, over-fitting, mishandling of noisy data, and outliers. This research study proposes an Ensemble classification method based on majority voting for an accurate diagnosis addressing the patient's medical conditions or symptoms. The study experiments a wide range of available classifiers, namely Decision Tree (DT), Support Vector Machine (SVM), Random Forest (RF), K-Nearest Neighbor (KNN), Naive Bayes (NB), Multiple Perceptron (MP), J48 Trees, and Logistic Regression (LR) classifiers. The study records a significant enhancement in prediction accuracy of 94% that outperforms the prediction accuracies of single classification methods tested on the same benchmarked datasets. Thus, the proposed model bestows a second opinion to health practitioners for disease identification and timely treatment.

INDEX TERMS Cervical cancer, machine intelligence, classification algorithms, support vector machine, Naïve Bayes, random forest, decision trees, K-nearest neighbors, ensemble classification.

I. INTRODUCTION

Cancer is one of the fatal diseases of today [1]. Specific abnormal behavior of affected cells characterizes the disease. Cancerous cells start damaging normal tissues, hence affecting their normal functions [2]. Cancer also has a high potential of spreading to other parts of the body. Therefore, a failure to detect cancer at an early stage may lead to death in several cases. Depending on the type of cancer, there is generally a higher probability of survival if cancer is detected early [3]. Cervical cancer is one of the most common types of cancer in women, mostly caused by HPV (Human Papilloma Virus). Several studies have shown that early detection of cervical cancer can significantly impact patients' treatment and recovery [4], [5]. Commonly used techniques for the detection of cervical cancer include Pap smear (Papanicolaou test) [6], HPV DNA genotyping [7], HCII (Hybrid Capture II), hybrid capture [8], [9] and Southern blot hybridization assay [10]. In this regard, the latest invention is biosensors that carry colossal potential because of low cost, speedy results, and ease of use [11], [12]. Each one of these techniques has its limitations. The pap smear test's significant shortcomings include a high false negative rate [13], low sensitivity, and high cost [13]. The southern blot hybridization assay test is time-consuming and has low sensitivity [14]. HPV DNA genotyping requires a long time to

The associate editor coordinating the review of this manuscript and approving it for publication was Ioannis Schizas.

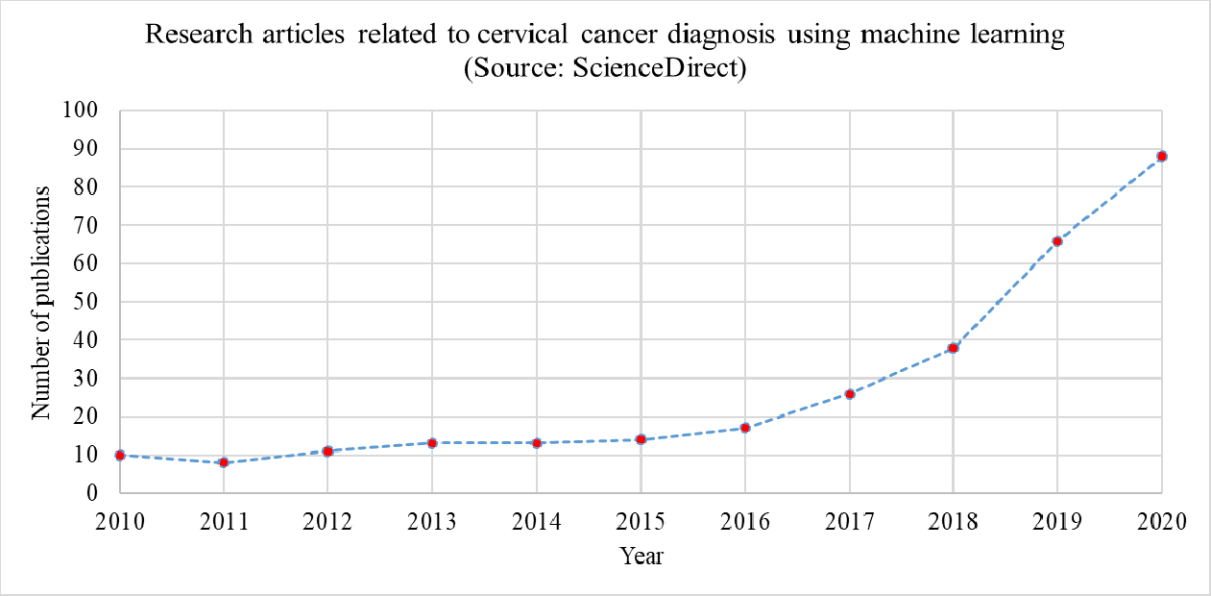

FIGURE 1. Research trend related to the adoption of machine learning for cervical cancer diagnosis.

perform the test and is relatively expensive [15]. HCII hybrid capture is one of the most advanced techniques for the early detection of cervical cancer. However, its main limitation is its ability to detect only 13 strains of HPV [16]. Biomedical sensors suffer from several operational constraints, such as lack of electrode reusability, operational stability, and limited lifetime [17]. These limitations of existing methods advocate the need for better strategies for the early detection of cervical cancer.

Reference [18] defines machine learning as "computational methods using experience to improve performance or to make accurate predictions." Machine learning techniques are quite applicable across a broad spectrum of domains such as personal [19], finance [20], large enterprises [21], government [22], military [23], and even space science [24]. Machine learning techniques have been successfully used in the medical domain [25], [26]. Various machine learning solutions are appealing for multiple types of cancer [27]–[29], and cervical cancer is no exception [30], [31]. The existing approaches used for the detection of cervical cancer mostly focus on a single classifier. As Ensemble techniques can usually produce better results in specific problems [32], this work proposes to use Ensemble techniques for cervical cancer detection from two publicly available datasets. The work approach utilizes several classifiers, including Decision Tree, Support Vector Machine, Random Forest, K-Nearest Neighbor, Naive Bayes, Multiple Perceptron, J48 Trees, and Logistic Regression. The majority voting mechanism classifies the target attribute. The rest of the paper is organized as follows. Section 2 presents a critical analysis of recent works related to cervical cancer identification. Section 3 elaborates on the methodology in this work. Section 4 presents the results, and section 5 concludes the research.

II. RELATED WORK

Cervical cancer has been marked as the third most life-threatening disease in females worldwide [33]. This disease is mainly caused by HPV that creates a tumor in the infected region [34]. Health practitioners suggest timely screening and vaccination cure the disease. HPV infection is the root cause of this disease in almost 99.7% of cervical cancer cases. Besides, it is one of the frequent cancers in females that arose to an estimated 528,000 cases recorded in 2012 [35]. The current cancer research demands timely diagnosis and accurate identification of disease.

Figure 1 presents an exciting research trend that describes the employment of machine learning adoption for cervical cancer diagnosis. It is viable that machine intelligence exploits on a large scale to identify cervical cancer with time. In the last five years, based on this disease's seriousness and its timely identification, there is a significant increase in machine intelligence research towards cervical cancer prediction. Hence, machine learning applications are compelling and influential in the early diagnosis of cervical cancer related to the biomedical field [36]. Such intelligent applications of machine learning much help to provide a second opinion to health practitioners. Here, we give the prevailing solutions of cervical cancer diagnosis employed using machine intelligence, Table 1 presents an overview of machine intelligence solutions for the prediction of cervical cancer. Most cervical cancer diagnosis solutions rely on the pap-smear test, cervical image analysis, and general disease symptoms. Different research scenarios apply a variety of classification algorithms. Most of the existing research adopted a single classifier used at particular datasets of cervical cancer patients and evaluates the performance of a single classification against the other classifiers. A few cited works can be noticed that

adopted ensemble classification with different strategies to enhance individual classifiers' prediction accuracy. The pre-processing, feature selection, and dimension reduction also significantly contributed to optimizing classification methods' prediction accuracy. Thus, this research study proposes a new ensemble classifier that integrates individual weak classifiers' prediction outcomes with the majority voting to produce a robust ensemble classification model.

III. METHODOLOGY

The optimal identification of cervical cancer is very much dependent on the individual classifier's performance. In the literature, we have seen that the classifier's performance positively correlates with the orientation of data samples in outliers and missing attribute values. It is also evident that some classifiers outperform some smaller or medium-sized data points. Still, their performance degrades at larger data points, especially when the data points have larger standard deviations. Since an optimum diagnosis of cervical cancer is essential for health practitioners to suggest the best possible treatments, the early and accurate detection of the disease requires a robust and resilient solution. This study adopts an ensemble classification method based on a significant voting policy to adopt the best classification outcomes for cervical cancer prediction. The study adopts a wide range of available classifiers, namely Decision Tree (DT), Support Vector Machine (SVM), Random Forest (RF), K-Nearest Neighbor (KNN), Naive Bayes (NB), Multiple Perceptron (MP), J48 Trees, and Logistic Regression (LR) classifiers.

The figure presents the proposed framework for cervical cancer prediction. As a holistic picture, cervical cancer is predicted by integrating different classifiers' classification outcomes through a majority voting scheme to produce an optimal result.

Let us consider a feature set $S = \{X_1, X_2, X_3, X_4, \ldots\ldots X_n\}$ of n data points $\forall n \leq N$, where N is the total number of available features in S. let us apply feature reduction filter F on $S \forall S_F = \{X_1, X_2, X_3, X_4, \ldots\ldots X_m\}$. We consider (Xj, Yj) points $\forall j \leq N$.

$$f(Yj) = Sign(Q^T Xj + b) \tag{1}$$

$$Xi = Yi(Q^T Xi + b) \tag{2}$$

$$Q^T Xi + b \geq 1 \text{ if Yi} = 1 \tag{3}$$

$$Q^T Xi + b \leq -1 \text{ if Yi} = -1 \tag{4}$$

Equations (1) through (4) describe the linear association of supported vector points whose distance of interest from the hyperplane becomes,

$$d = \frac{y(Q^T X + b)}{\|w\|} \tag{5}$$

The margin that separates the points,

$$m = \frac{2}{\|w\|} \tag{6}$$

For decision tree classification, we take,

$$Entropy = -\sum_{1}^{n} p_i \log(p_i) \text{ with Gini index} = 1 - \sum_{1=1}^{n} p_i^2.$$

Here the entropy helped us find the spread of data with the required Gini index between 0 and 1. For the sake of random forest implementation, we consider the classification problem of classifying Xn data points $\forall n \leq N$, such that the majority vote classified the Xn points into required target output classes. Naïve Bayes classification considered Xn data points with n inputs such that,

$$P(y\,|X) = \frac{P(X\,|y) * P(y)}{P(X)} \tag{7}$$

For Xn data points, the KNN calculates,

$$d(X, Y) = d(Y, X) = \sqrt{(x_1 - y_1)^2 + (x_2 - y_2)^2 + \ldots..(x_n - y_n)^2} \tag{8}$$

The logistic regression implements the classification by calculating the cost function,

$$Cost(c) = (^{-1}/_{s}) \sum_{j=1}^{s} (y_j \log(\overline{y_j}) + (1 - y_j) \log(1 - \overline{y_j})) \tag{9}$$

For multiplayer perceptron, we have chosen an appropriate learning rate. We also tested different weights for gradient descent. We observed that logistic sigmoid is a proper replacement of step function for simple perceptron process. Besides, we also noted that the range of logistic function between 0 and 1 helped the descent to learn faster. Depending on the noise in Xn data points, we scaled the training patterns employing different k-fold cross validations to achieve unbiased outcomes.

Figure 3 presents the methodological steps in analyzing cervical cancer data to classify the disease. Let's us consider n data points defined as D = {D1, D2, D3, Di}, i <= N. For the sake of achieving best classification, it is important to remove the outliers and noisy attributes from Xn data points such that n <= N.

We apply the k-fold cross-validation and segment the Di data points into an aggregate of training, test, and validation segments for i <= N. Later, we analyze Di instances with the chosen classifiers, namely SVM, DT, RF, NB, KNN, J48, MP, and LR classifiers for each Di in D. We then define a filter DF to analyze the individual performance of classifiers for i <= N. Finally, ensemble classification outcomes are achieved by a Majority Voting Filter to CLFy (y <= 8).

IV. RESULTS AND DISCUSSION

For cervical cancer diagnosis, this research employs two publicly available cervical cancer datasets. The first dataset, "Cervical Cancer Behavior Risk Dataset," was contributed by [75]. This dataset contains 20 attributes, including the class attribute. The second dataset, "Cervical cancer (Risk Factors) Dataset," was contributed by [76] and experimented with by several researchers [37], [51], [77]–[79]. The dataset contains 36 attributes and 858 subjects. The contributor reported several missing values since the respondents left some

TABLE 1. An overview of machine intelligence solutions for cervical cancer identification.

Study	Concept (Research motivation)	Classification Method						Remarks
		SVM	NB	RF	KNN	DT	Others	
[37]	Synthetic Minority Oversampling Technique (SMOTE) to balance the datasets	×	×	✓	×	✓	Decision Jungle algorithm	The boosted decision tree classifier outperformed the other classifiers
[38]	ANN classification for cervical cancer identification	×	×	×	×	×	Artificial Neural network	Comparative analysis of different ANN architectures
[39]	Chung Shan Medical University Hospital Tumor Registry	✓	×	×	×	✓	Extreme learning machine	C5.0 model was found to be most useful in this study
[30]	Review article that incorporates multiple existing approaches	✓	×	×	✓	×	CHAMP digital image software	SVM, KNN, and CHAMP digital image software were reported significant
[40]	Two distinct datasets with multi-features	×	×	×	×	×	The dynamic multi-template deformation model	The proposed model was reported significant
[41]	Feature selection with mutual information and random subset selection	✓	×	×	×	×	Image segmentation with thresholding	The sequential floating forward selection was reported outperforming
[42]	Early detection of cervical cancer based on features set	×	✓	✓	×	✓	Logistic regression	Random forest outperformed the other classifiers
[43]	Clinical text, named entity recognition	×	×	×	×	×	Clinical entity finder, a rule-based tool	Clinical entity finder with NegEx depicted excellent classification
[44]	Ensemble classification based on voting policy	✓	×	✓	✓	✓	Multi-Layer Perceptron	The proposed ensemble classifier performed better than the other classifiers
[45]	Multiple overlapping cells in cervical images	×	×	×	×	×	Automatic segmentation method	Superpixel generation and triangle thresholding
[46]	Comparative analysis of machine learning algorithms for cervical cancer prediction	✓	×	✓	×	✓	Rpart	C5.0 and Random Forest performed better than other algorithms
[47]	Two-level cascade integration	×	×	×	×	✓	LR classifier	The combination of cascade classifiers bestowed significant accuracy
[48]	Pap smear images of the cervical region	×	×	×	✓	×	5-fold cross-validation	KNN performed significantly on particular datasets
[49]	Microscopic biopsy images	×	×	×	✓	×	K-Means	The combination of K-Means and KNN produced better results
[50]	Graph-partitioning-based method	×	×	×	×	×	Multiscale convolutional network	The combination of both algorithms outperformed on particular datasets
[51]	Diagnosis of cervical cancer based on patients' symptoms datasets	×	✓	×	✓	×	Multi-Layer Perceptron	KNN has been reported as the best classifier
[52]	Validation with neural network method	×	×	×	×	×	Fuzzy C-Means	Both algorithms produced promising outcomes
[53]	Comparative analysis of cervical cancer prediction algorithms	✓	✓	✓	✓	✓	High dimension biopsy samples of patients	Naïve Bayes has been reported as best classifier
[54]	Superpixel method in combination with DL approach	×	×	×	×	×	Convolution neural networks (CNN)	CNN and Superpixel method performed excellently on particular images
[55]	Comparative analysis of three cervical cancer prediction algorithms	✓	×	✓	×	×	XGBoost	XGBoost and Random forest performed better than the SVM classifier
[56]	Joint optimization with hybrid functions	×	×	×	×	×	Segmentation of cytoplasm	Both approaches significantly address the relevant issues of cancer detection
[57]	SMOTE has been employed for imbalance datasets	×	×	✓	×	×	Principle component analysis	SMOTE contributed generously towards the enhancement of research outcomes
[58]	Joint level optimization	×	×	×	×	×	Scene segmentation	Unsupervised segmentation achieved a useful Jaccard index
[59]	Automatic thresholding	×	×	×	×	×	The multiscale unsupervised hierarchical approach	Binary classification outperformed on given datasets
[60]	Segmentation thresholding	×	×	×	×	×	Mahalanobis distance classifier	A combination of both methods achieved significant accuracy on data specimens
[61]	Elastic segmentation algorithm	×	×	×	×	×	Voting scheme of classification	Canny edge detection in integrations with Elastic and Voting schemes produced excellent outcomes
[62]	Nucleus and cytoplast contour detector (NCC)	×	×	×	×	×	Maximal gray-level-gradient-difference (MGLGD)	The gradient vector flow and edge detection performed better on specimen datasets
[63]	Morphological operation	×	×	×	×	×	Watershed transformation	The combination of both approaches outperformed on particular data
[64]	Radiating gradient vector flow (RGVF)	×	×	×	×	×	K-Means	RGVF snake approach with K-Means performed effectively
[65]	Supervised cell-image	×	×	×	×	×	Integrated framework	The local Fourier transform method with

TABLE 1. *(Continued.)* **An overview of machine intelligence solutions for cervical cancer identification.**

	segmentation						approach	supervised segmentation outperformed on specimen datasets
[66]	Nuclei segmentation algorithm	×	×	×	×	×	HSV color space with adaptive thresholding	The concave point-based overlapped method with HSV scheme produced the desired outcomes
[67]	Morphological image reconstruction	×	×	×	×	×	Watershed Transform	Gradient vector and ACM predicted the required test sets
[68]	A seed-based region growing algorithm	×	×	×	×	×	A pseudo coloring technique	Both methods produced excellent segmentation of desired regions
[69]	Gaussian filter for noise suppression	×	×	×	×	×	Two-group object enhancement approach	The combination of these methods showed promising results
[70]	Meta-heuristic algorithm	×	×	×	✓	×	Genetic algorithm scheme	The proposed approach achieved excellent outcomes of this research
[71]	Empirical rule-based method	×	×	×	×	×	Fuzzy C-Means algorithm	Both methods performed better on pap-smear images
[72]	Edge enhancement nucleus and cytoplast contour (EENCC) detector	×	×	×	×	×	Trim-meaning filter	Edge enhancement and trim filtering outperformed on a given set of images of cervical cancer
[73]	Efficient second-order neural network	×	×	×	×	×	Levenberg Marquardt with adaptive momentum	The optimized Levenberg–Marquardt produced better outcomes on particular datasets
[74]	Pixel level classification	✓	×	×	×	×	The novel feature screening method	The pixel-level classification and screening method outperformed on specimen datasets

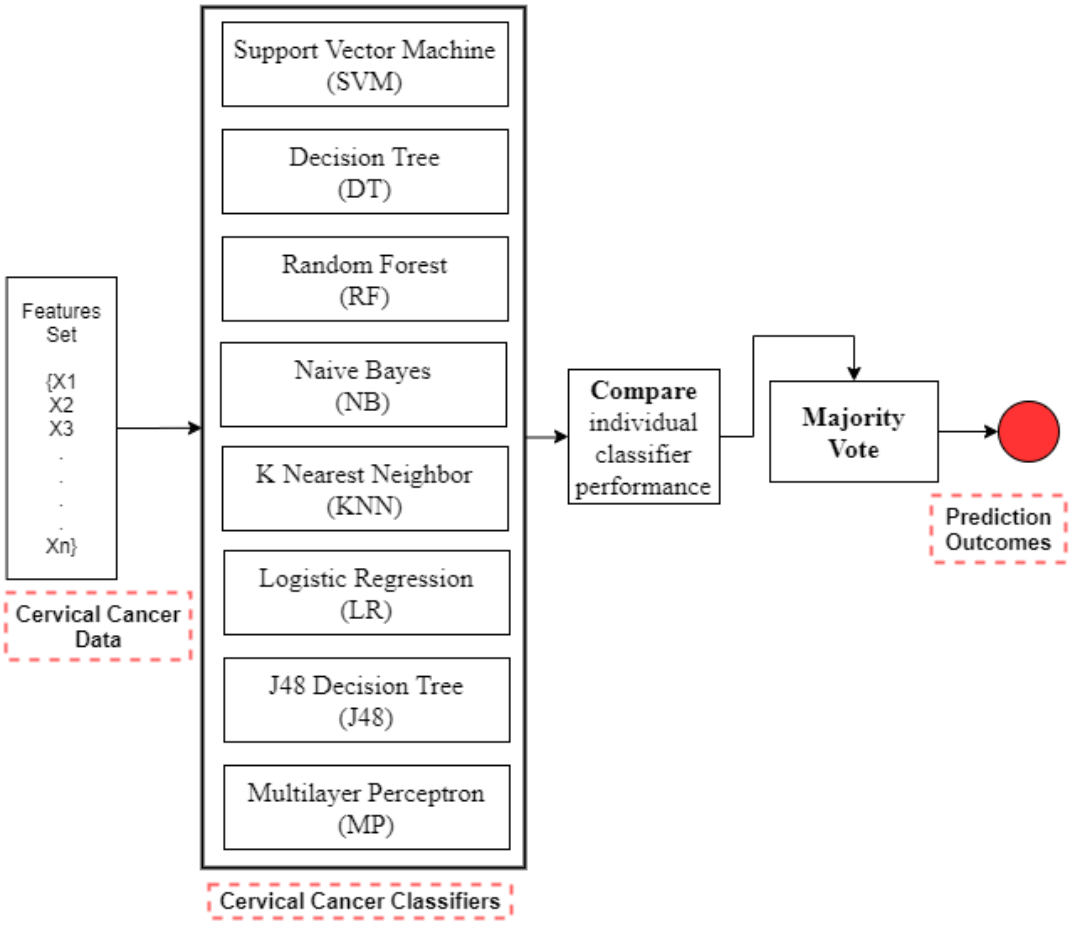

FIGURE 2. **The proposed framework for cervical cancer prediction.**

queries unanswered. Since machine intelligence algorithms' performance significantly correlates with data quality, this research performed necessary preprocessing to accommodate the missing information. We applied an unsupervised

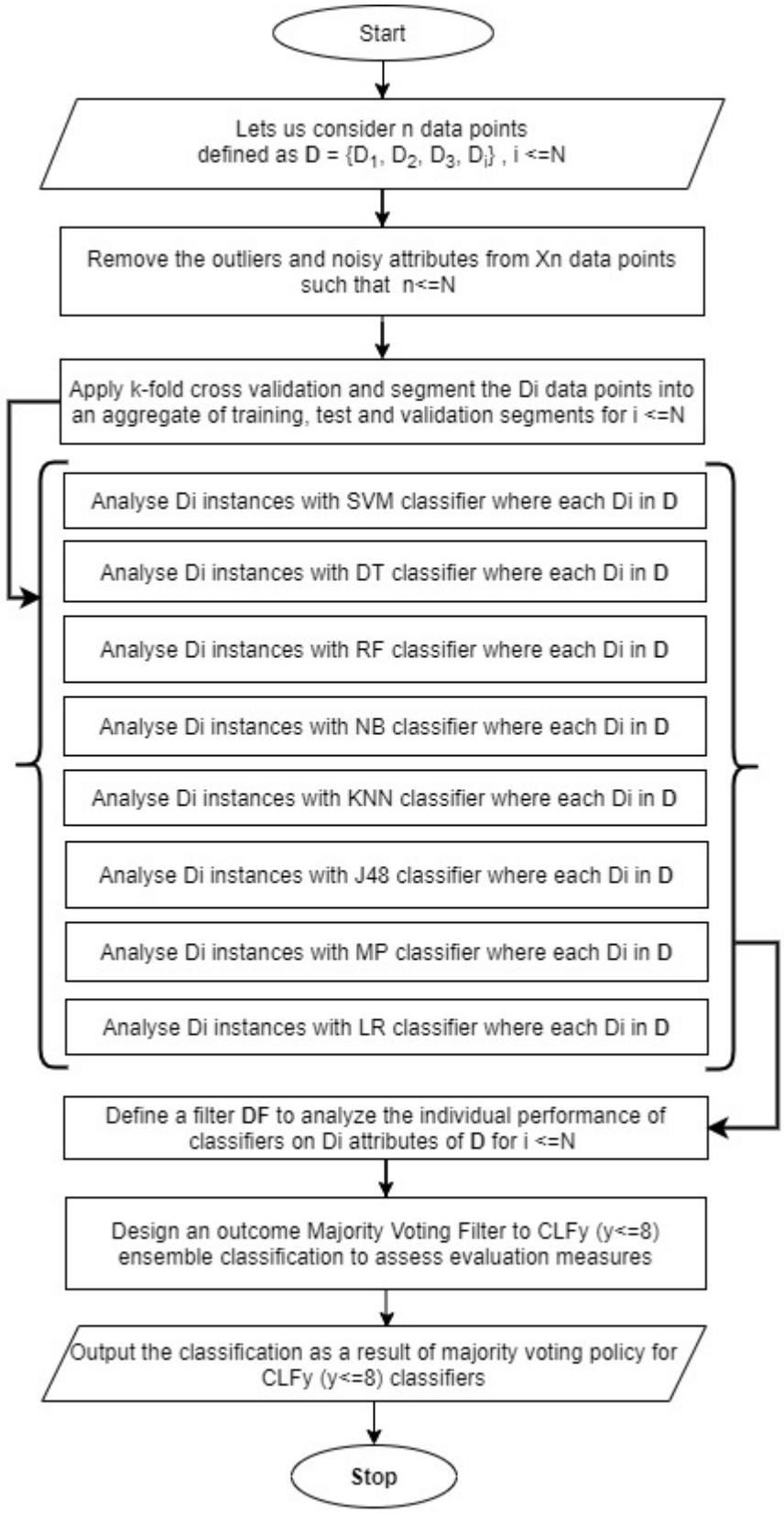

FIGURE 3. The sequence of steps of the methodology.

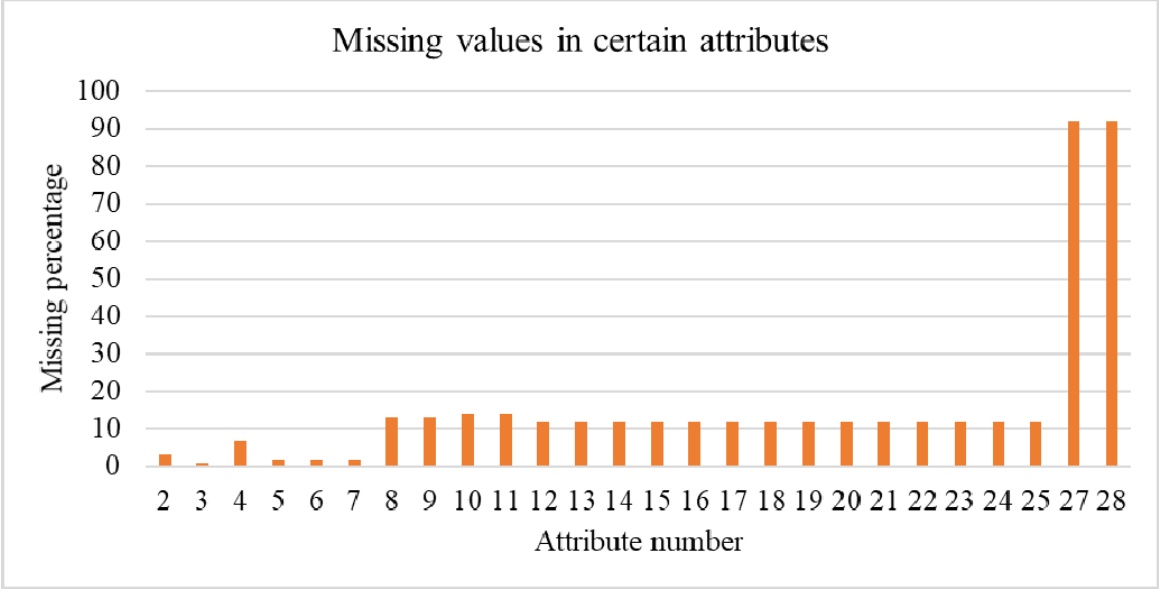

FIGURE 4. Percentage of missing data in specific attributes of the dataset.

filter that replaces the missing nominal and numeric attributes with modes and medians and skipped the class attribute.

Figure 4 presents the percentage of missing data related to specific attributes in the dataset. It is explicit that attribute numbers 27 and 28 contain 92% missing values. These attributes relate to the time of first and last diagnosis performed with certain subjects. Attribute numbers 8 to 25 have about 12% missing information. Such features represent the data against queries that were not answered by the subjects due to privacy reasons. The noise in the data directly impacts machine learning and information mining predictive systems' performance. It has been reported in the literature that preprocessing is a crucial phase that consumes about 60% of the overall project time in cleaning the data, i.e., smoothing, normalization, and correlation aspects. The fundamental classification and prediction measures require a well-preprocessed set of inputs for excellent outcomes.

Table 2 shows the rank wise selection of attributes concerning merit (significance of feature set correlated with the class attribute). This feature selection bases on 10-fold cross-validation (stratified with a single seed and with no missing data) of correlated traits and supervised selection of features (with missing data). We can see that the rank of attributes in both scenarios is almost similar.

Figure 5 describes the attributes ranking achieved using two criteria, i.e., cross-validation with a single seed and with no missing data, and supervised the selection of features with missing data. Since both measures have shown almost the same attributes' merits, we have opted for the attributes mentioned above for performance analysis of different classification algorithms.

A. PERFORMANCE EVALUATION OF DIFFERENT CLASSIFIERS

For the performance evaluation of different classifiers, we adopted the following metrics,

a) True Negative (TN): The subject with no disease and the prediction correctly predicts the same.
b) False Positive (FP): The subject with no disease, but the prediction incorrectly predicts that it carries the disease.
c) False Negative (FN): The subject carries the disease, but the prediction incorrectly predicts that the subject has no disease
d) True Positive (TP): The subject carries the disease and the prediction correctly predicts the same.

For the evaluation of the accuracy of the classification, the values from the confusion matrix are used. Evaluation metrics, i.e., specificity, sensitivity F1 score, precision, and Recall, are calculated.

a) Specificity: It correctly predicts the individual with no heart disease

$$Specificity = \frac{TN}{TN + FP} \times 100\% \tag{10}$$

b) Sensitivity: It correctly predicts the individual with heart disease

$$Sensitivity = \frac{TP}{TP + FN} \times 100\% \tag{11}$$

c) F1-Score:

$$F1 - Score = \frac{2TP}{2TP + FP + FN} \times 100\% \tag{12}$$

d) Precision:

$$\text{Precision} = \frac{TP}{PP} \times 100\% \tag{13}$$

TABLE 2. Selection of attributes using cross-validation and supervised criteria.

Att. #	Attribute name	Correlated attributes merit (with no missing data)	Supervised attributes merit (with missing data)
34	Schiller	0.733 +- 0.013	0.7332
33	Hinselmann	0.547 +- 0.024	0.54742
35	Citology	0.327 +- 0.015	0.32747
29	Dx: Cancer	0.161 +- 0.021	0.1609
31	Dx: HPV	0.161 +- 0.023	0.1609
32	Dx	0.157 +- 0.016	0.15761
20	STDs: genital herpes	0.128 +- 0.013	0.13052
23	STDs: HIV	0.114 +- 0.018	0.1277
12	STDs	0.124 +- 0.041	0.11415
30	Dx: CIN	0.113 +- 0.018	0.11317
26	STDs: Number of diagnosis	0.098 +- 0.017	0.09745
13	STDs (number)	0.096 +- 0.018	0.09622
17	STDs: vulvo-perineal condylomatosis	0.092 +- 0.018	0.09255
14	STDs: condylomatosis	0.09 +- 0.018	0.09016
9	Hormonal Contraceptives (years)	0.079 +- 0.019	0.079
6	Smokes (years)	0.062 +- 0.018	0.06148
10	IUD	0.059 +- 0.014	0.05923
1	Age	0.056 +- 0.013	0.05596
4	Num of pregnancies	0.044 +- 0.013	0.04346
18	STDs: syphilis	0.038 +- 0.001	0.03831
11	IUD (years)	0.032 +- 0.012	0.03225
27	STDs: Time since first diagnosis	0.03 +- 0.015	0.02981
5	Smokes	0.029 +- 0.012	0.02872
7	Smokes (packs/year)	0.026 +- 0.012	0.02466
28	STDs: Time since last diagnosis	0.018 +- 0.001	0.02022
8	Hormonal Contraceptives	0.021 +- 0.011	0.01802
16	STDs: vaginal condylomatosis	0.02 +- 0.016	0.01791
25	STDs: HPV	0.013 +- 0.002	0.01265
19	STDs: pelvic inflammatory disease	0.012 +- 0.006	0.00894
24	STDs: Hepatitis B	0.008 +- 0.003	0.00894
21	STDs: molluscum contagiosum	0.007 +- 0.005	0.00894
3	First sexual intercourse	0.008 +- 0.003	0.00726
2	Number of sexual partners	0.008 +- 0.003	0.00143
15	STDs: cervical condylomatosis	0 +- 0	0
22	STDs: AIDS	0 +- 0	0

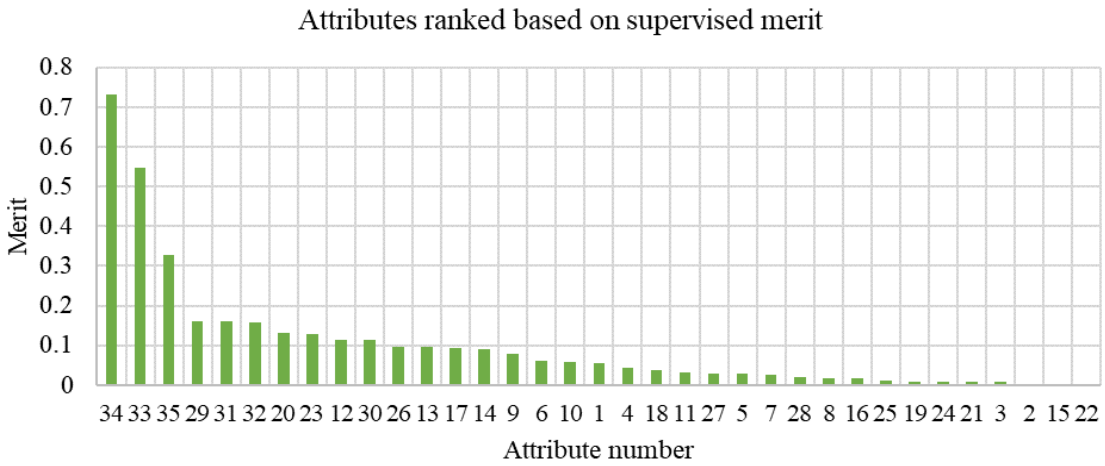

FIGURE 5. Ranking attributes based on correlated and supervised ranking criteria.

e) Recall:

$$\text{Recall} = \frac{TP}{AP} \times 100\% \tag{14}$$

where, PP is the number of predicted positives, and AP is the number of actual positives. We achieve the following statistics by employing the above evaluations metrics. In below tables, the terms F1 to F10 refer to 10-fold cross validation.

1) PREDICTION ACCURACY

Table 3 presents the statistics related to 10-fold cross-validation using different classifiers. The aggregate prediction

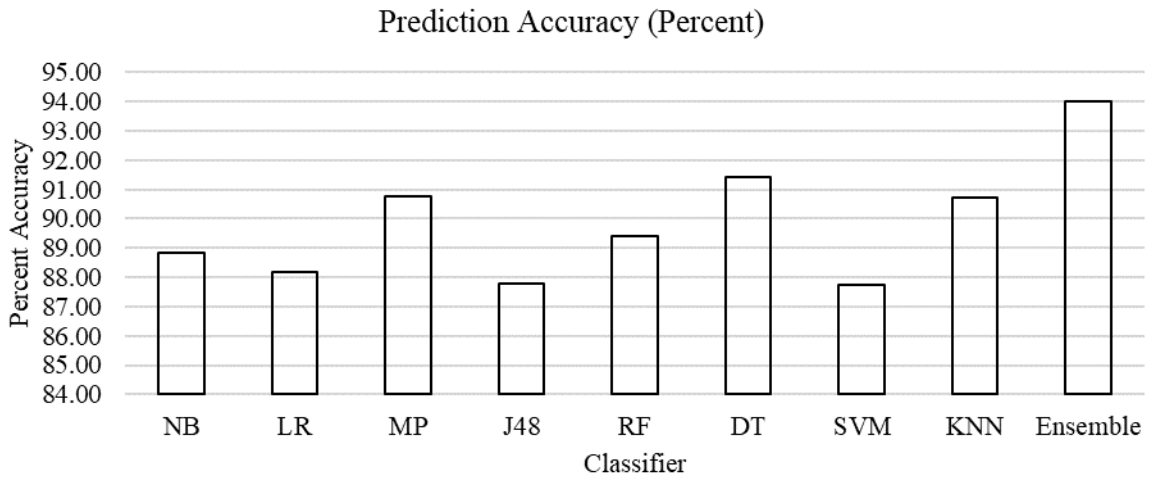

FIGURE 6. The outperformance of Ensemble classifier in terms of prediction accuracy.

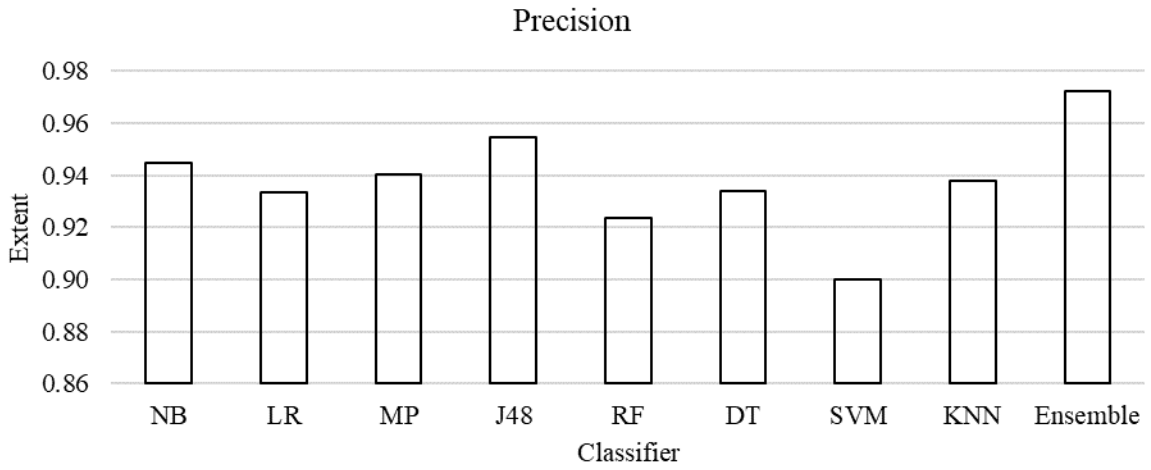

FIGURE 7. Performance measure in terms of precision.

TABLE 3. Prediction accuracy (percent).

Classifier	F1	F2	F3	F4	F5	F6	F7	F8	F9	F10	Average
NB	97	93	95	75	100	86	86	86	86	86	88.83
LR	97	93	96	88	100	86	86	71	71	94	88.19
MP	99	98	93	93	96	100	86	71	86	86	90.75
J48	94	98	93	94	95	75	100	71	71	86	87.79
RF	94	93	93	98	88	100	86	86	86	71	89.39
DT	91	97	99	93	93	98	88	100	71	86	91.43
SVM	94	97	98	98	93	94	95	75	63	71	87.74
KNN	93	99	93	94	98	88	100	71	86	86	90.70
Ensemble	94	97	98	98	93	94	95	100	86	86	93.99

accuracy has been highlighted in the last column. It is explicit that the Ensemble classifier has performed better than the individual classifiers.

Figure 6 previews the performance measure of different classifiers. Ensemble classifiers produce 94% accuracy as compared to the other individual classifiers. Decision tree

TABLE 4. Performance evaluation in terms of precision measure.

Classifier	F1	F2	F3	F4	F5	F6	F7	F8	F9	F10	Average
NB	0.98	0.97	1.00	0.83	1.00	1.00	0.83	0.83	1.00	1.00	0.94
LR	0.98	0.97	1.00	1.00	1.00	1.00	0.83	0.80	0.80	0.95	0.93
MP	1.00	1.00	0.96	0.97	1.00	1.00	0.83	0.80	1.00	0.83	0.94
J48	0.99	1.00	0.97	0.99	1.00	1.00	1.00	0.80	0.80	1.00	0.95
RF	0.98	0.96	0.97	1.00	0.86	1.00	0.83	0.83	1.00	0.80	0.92
DT	0.96	0.96	0.99	0.96	0.97	1.00	0.86	1.00	0.80	0.83	0.93
SVM	0.99	0.98	0.99	1.00	0.97	0.99	1.00	0.75	0.63	0.71	0.90
KNN	0.96	0.99	0.96	0.97	1.00	0.86	1.00	0.80	0.83	1.00	0.94
Ensemble	0.98	0.96	0.99	1.00	0.97	0.99	1.00	1.00	0.83	1.00	0.97

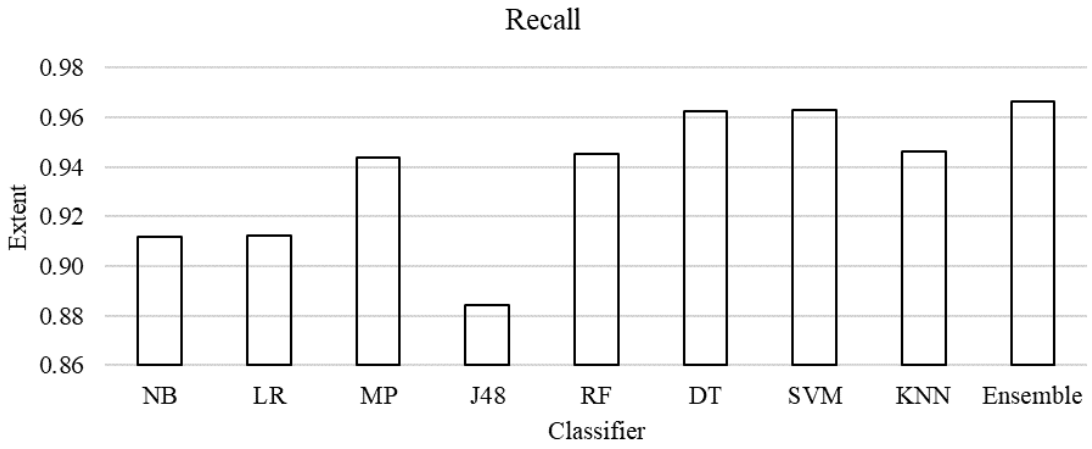

FIGURE 8. Performance measure in terms of Recall.

classifier, multi-perceptron, and K-nearest neighbor glimpsed a comparable prediction accuracy on the given datasets.

2) PRECISION

Similarly, we calculated the precision measure of classification algorithms for the identification of cervical cancer.

Table 4 describes the performance evaluation statistics against 10-fold cross-validation performed on cervical cancer datasets. The average precision has been calculated for each classifier. We can see that the Ensemble classifier achieved the highest precision as compared to other individual classifiers.

Figure 7 presents the Ensemble classifier's outperformance by achieving a precision factor of 0.97, significant than the J48 classifier that gained a precision of 0.95. We can observe that Naïve Bayes, multi-perceptron, and K-nearest neighbor held a comparable precision executed on cervical cancer datasets. The support vector classifier performed the least as compared to other classifiers in these experiments.

3) RECALL

We evaluated the performance of different classifiers using the "Recall" as a factor for performance evaluation of classifiers; we achieved the following stats, Table 5 describes the performance evaluation statistics in the context of "Recall" against 10-fold cross-validation performed on cervical cancer datasets. From the aggregate score, it can be observed that the ensemble classifier has better segregated cervical cancer patients from non-cancerous subjects.

Figure 8 glimpses the excellence of ensemble classifier with a recall factor of 0.97, significant than the support vector machine and decision tree classifiers that gained a comparable Recall factor of 0.96. We can observe that multi-perceptron and K-nearest neighbor held a relative precision. Simultaneously, the J48 classifier performed the least compared to Naïve Bayes and logistic regression classifiers in these observations.

4) F-MEASURE

The performance measure of classification was also evaluated using another measure known as "F-measure." We achieved the following observation based on the outcomes of the experiment, Table 6 describes the performance evaluation measures related to "F-Measure" against 10-fold cross-validations. We performed these validations with random

TABLE 5. Performance evaluation in terms of Recall.

Classifier	F1	F2	F3	F4	F5	F6	F7	F8	F9	F10	Average
NB	0.99	0.95	0.95	0.83	1.00	0.80	1.00	1.00	0.80	0.80	0.91
LR	0.99	0.95	0.96	0.83	1.00	0.80	1.00	0.80	0.80	0.99	0.91
MP	0.99	0.98	0.96	0.95	0.96	1.00	1.00	0.80	0.80	1.00	0.94
J48	0.95	0.98	0.95	0.95	0.95	0.67	1.00	0.80	0.80	0.80	0.88
RF	0.96	0.96	0.95	0.98	1.00	1.00	1.00	1.00	0.80	0.80	0.95
DT	0.94	1.00	1.00	0.96	0.95	0.98	1.00	1.00	0.80	1.00	0.96
SVM	0.95	0.97	0.97	0.96	0.95	0.95	0.94	0.98	0.98	0.98	0.96
KNN	0.96	1.00	0.96	0.96	0.98	1.00	1.00	0.80	1.00	0.80	0.95
Ensemble	0.96	1.00	0.99	0.98	0.97	0.96	0.95	1.00	1.00	0.86	0.97

TABLE 6. Performance evaluation in terms of F-Measure.

Classifier	F1	F2	F3	F4	F5	F6	F7	F8	F9	F10	Average
NB	0.98	0.96	0.97	0.83	1.00	0.89	0.91	0.91	0.89	0.89	0.92
LR	0.98	0.96	0.98	0.91	1.00	0.89	0.91	0.80	0.80	0.97	0.92
MP	0.99	0.99	0.96	0.96	0.98	1.00	0.91	0.80	0.89	0.91	0.94
J48	0.97	0.99	0.96	0.97	0.97	0.80	1.00	0.80	0.80	0.89	0.91
RF	0.97	0.96	0.96	0.99	0.92	1.00	0.91	0.91	0.89	0.80	0.93
DT	0.95	0.98	0.99	0.96	0.96	0.99	0.92	1.00	0.80	0.91	0.95
SVM	0.97	0.98	0.99	0.99	0.96	0.97	0.97	0.86	0.77	0.83	0.93
KNN	0.96	0.99	0.96	0.97	0.99	0.92	1.00	0.80	0.91	0.89	0.94
Ensemble	0.97	0.98	0.99	0.99	0.96	0.97	0.97	1.00	0.91	0.89	0.96

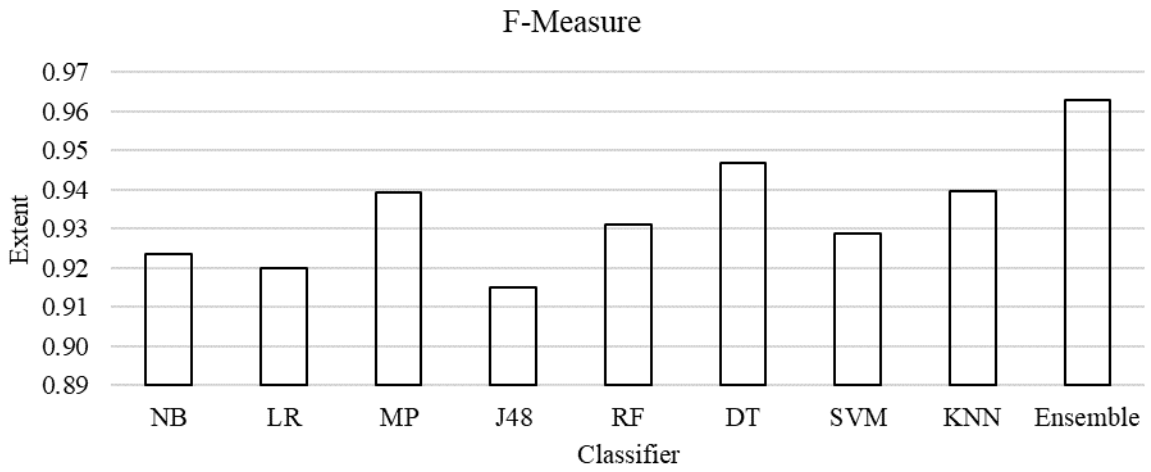

FIGURE 9. Performance evaluation in the context of F-Measure.

sampling to ensure that the procedure adopts an unbiased criterion for all the instances to be sampled randomly. The average score depicts the ensemble classifier achieving a better "F-measure" factor for cervical cancer subjects.

Figure 9 presents the "F-Measure" scores of different classifiers. The ensemble classifier achieved an F-Measure score of 0.96, significant than the decision tree classifier that gained an F-Measure of 0.95. The F-Measure values of multi-perceptron and K-nearest neighbor held a comparable

TABLE 7. Performance evaluation in terms of area under ROC curve.

Classifier	F1	F2	F3	F4	F5	F6	F7	F8	F9	F10	Average
NB	0.97	0.96	0.99	0.92	1.00	0.80	0.90	1.00	0.90	1.00	0.94
LR	0.97	0.96	0.98	1.00	1.00	1.00	1.00	0.90	0.65	0.96	0.94
MP	0.99	1.00	0.76	0.96	0.99	1.00	1.00	0.90	1.00	0.90	0.95
J48	0.88	0.99	0.81	0.88	0.98	0.92	1.00	0.80	0.70	0.90	0.88
RF	0.79	0.75	0.97	0.99	1.00	1.00	1.00	0.90	0.90	0.90	0.92
DT	0.60	0.92	1.00	0.75	0.96	0.99	0.75	1.00	0.65	0.75	0.84
SVM	0.88	0.83	0.91	0.99	0.81	0.88	0.98	0.50	0.50	0.50	0.78
KNN	0.61	1.00	0.75	0.97	0.99	0.75	1.00	0.65	0.75	0.90	0.84
Ensemble	0.97	0.92	0.94	1.00	0.96	0.98	0.99	1.00	0.90	1.00	0.97

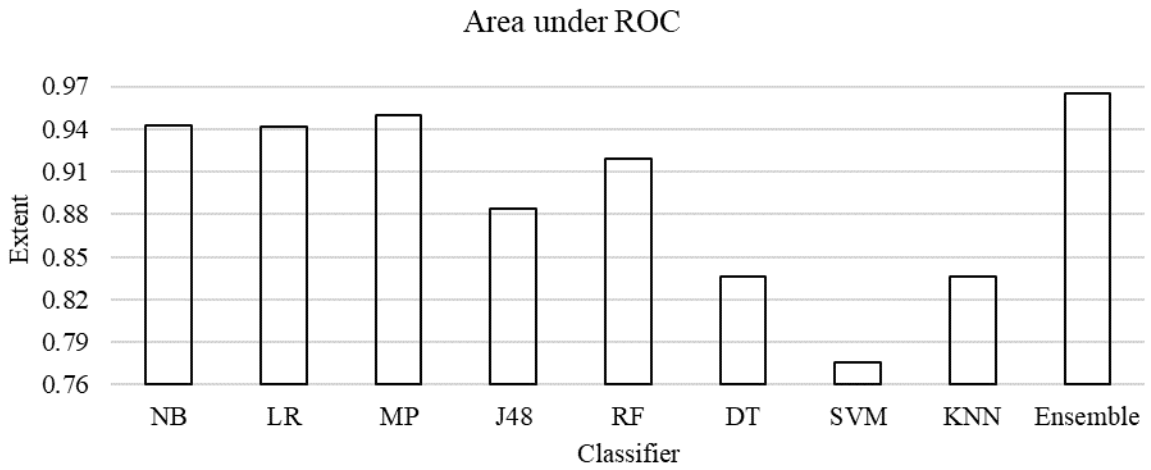

FIGURE 10. Performance evaluation in terms of areas of classifiers under ROC curves.

precision. Simultaneously, the J48 classifier performed the least compared to Naïve Bayes and logistic regression classifiers in these observations.

5) AREA UNDER ROC (RECEIVER OPERATING CHARACTERISTIC) CURVE

We also calculated the areas under different classifiers' ROC curve to ensure the outperformance of ensemble classification for cervical cancer identification and diagnosis. We noticed the following stats, Table 7 presents the performance evaluation of different classifiers against the areas under the ROC curves of classifiers. These areas were calculated for 10-fold cross-validations performed on cervical cancer datasets. Here, again we preferred the random sampling to diminish the probability of unbiased outcomes of subjected instances. We can notice that ensemble classification performed better than the other classifiers.

Figure 10 portrays the areas under the ROC curves of different classifiers. The ensemble classifier performed excellent, achieving an aggregate score as an area of 0.97. This evaluated score was found significantly better than the multi-perceptron that gained an area of 0.95. The areas under the curve for Naïve Bayes and logistic regression were quite comparable. In comparison, the K-nearest neighbor performed the least compared to J48 and decision tree classifiers in these observations.

6) ROC CURVE ANALYSIS

The receiver operating characteristic curve analysis is also considered a good evaluation measure to identify different classification methods' performance on input data. We adopted the ROC curve analysis for the performance evaluation of all classifiers in this study. We achieved the following analysis, Figure 11 describes the receiver operating characteristic curve analysis of classification methods in this research. The ROC curve has been drawn against the true positive rate and the false-positive rates. The ensemble curve is shown in red color that portrays an optimal area under the curve compared to other individual classifiers' curves. The ensemble curve is more inclined towards the left extreme corner, i.e., the highest true positive rate values and the least false-positive rates. The classifier J48 is comparable to

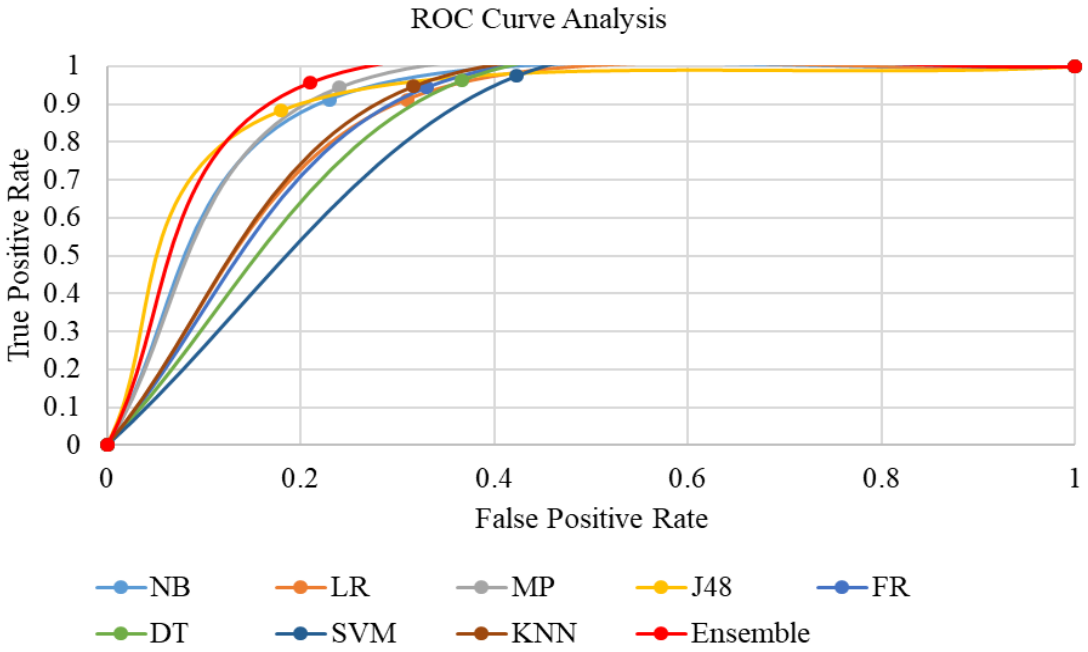

FIGURE 11. ROC curve analysis of different classifiers.

the ensemble curve, while other classifiers' ROC curves are viably below the ensemble and J48 classifiers. The SVM classifier performed the least as compared to different individual classifiers in ROC curve analysis.

V. CONCLUSION

The health 4.0 standards require efficient and robust cervical cancer diagnosis to save the precious lives of subjects. Despite the challenges and issues that hinder the timely identification of disease, the current machine intelligent solutions are considered robust. Still, the performance of individual classification methods for cervical cancer identification is also an issue. The particular classification methods are sensitive to the nature of data, and a variety of classifiers generates quite different results when exploited to the same datasets. This research study presented an ensemble classification method for cervical cancer diagnosis based on a significant voting policy to adopt the best classification outcomes for cervical cancer prediction. The study adopted a wide range of available classifiers, namely Decision Tree (DT), Support Vector Machine (SVM),0Random Forest (RF),0K-Nearest Neighbor (KNN), Naive Bayes (NB), Multiple Perceptron (MP), J48 Trees, and Logistic Regression (LR) classifiers. The performance evaluation of the proposed ensemble classifier outperformed individual classifiers' performance by attaining the highest accuracy at 94% compared to other classifiers. Health practitioners can adopt this research's outcomes to provide an expert and confident second opinion to cervical cancer subjects to treat the disease better.

CONFLICT OF INTEREST

The authors have no conflict of interest in this research.

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