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A Search for Machinery Intelligence Towards Sustainable Health : An Improved Ensemble Cervical Cancer Diagnosis

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ABSTRACT

Health professionals identify cervical cancer as a potentially fatal condition. Patients' valuable lives are at risk due to the difficult late diagnosis and treatment. The formal screening for illness identification suffers in both developed and developing countries because of high medical costs, a lack of healthcare facilities, social norms, and the late onset of symptoms. Early detection of various different illnesses, including cervical cancer, is possible because to machine intelligence. It is also cost-effective and computationally cheap. Modern, time-consuming medical treatments are not necessary for the patients, and machine intelligence can help with early cervical cancer detection. The reliance on a single classifier's prediction accuracy is the issue with the present machine classification approaches for illness detection. Due to bias, over-fitting, improper treatment of noisy data, and outliers, the use of a single classification method does not guarantee the best prediction. In order to provide an appropriate diagnosis that addresses the patient's symptoms or problems, this research study presents an ensemble classification approach based on majority voting. A broad variety of classifiers, including Decision Tree (DT), Support Vector Machine (SVM), Random Forest (RF), K-Nearest Neighbor (KNN), Naive Bayes (NB), Multiple Perceptron (MP), and Logistic Regression (LR) classifiers, are experimented in the study. The study shows an increase in prediction accuracy of 94%, which is much higher than the prediction accuracies of individual classification methods tested on the same benchmarked datasets. As a result, the suggested paradigm offers health professionals access to a second opinion for early illness detection and treatment.

Keywords : Machine Learning Algorithms, Classifiers, Cervical Cancer, Ensemble Classification.

I. INTRODUCTION

Cancer is one of the fatal diseases of today. Specific abnormal behavior of affected cells characterizes the disease. Cancerous cells start damaging normal tissues, hence affecting their normal functions. 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. 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. Commonly used techniques for the detection of cervical cancer include Pap smear (Papanicolaou test), HPV DNA genotyping, HCII (Hybrid Capture II), hybrid capture and Southern blot hybridization assay. In this regard, the latest invention is biosensors that carry colossal potential because of low cost, speedy results, and ease of use. Each one of these techniques has its limitations. The Pap smear test's significant shortcomings include a high false negative rate, low sensitivity, and high cost. The southern blot hybridization assay test is time-consuming and has low sensitivity. HPV DNA genotyping requires a long time to perform the test and is relatively expensive. 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. Biomedical sensors suffer from several operational constraints, such as lack of electrode reusability, operational stability, and limited lifetime. These limitations of existing methods advocate the need for better strategies for the early detection of cervical cancer.

Reference 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, finance, large enterprises, government, military, and even space science. Machine learning techniques have been successfully used in the medical domain. Various machine learning solutions are appealing for multiple types of cancer, and cervical cancer is no exception. 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, 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 WORKS

Application of cyclodextrins in cancer treatment: Cancer is one of the major fatal diseases. Chemotherapy is a typical treatment method that uses a combination of drugs to either destroy cancer cells or slow down the growth of cancer cells. However, most of the cytotoxic chemotherapeutic drugs are water insoluble resulting in formulation difficulty. One promising strategy is to use cyclodextrins (CDs) which have been widely employed to enhance the solubility, bioavailability, stability and safety of drug molecules by forming non covalent inclusion complexes. The objective of this review is to explain the use of CDs in the different approaches for cancer treatment. Of specific interest is that CDs are shown to have anticancer activity both in vitro and in vivo. The use of CDs as anticancer agent and the possible mechanism to inhibit cancer cell growth are discussed. CDs/anti-neoplastic-drug complexes with improved solubility, increased stability and enhanced anti-cancer activity are described and possible future applications are discussed. Use and their advantages of CDs in the different drug delivery systems like

liposomes, conjugates, nanoparticles and SI RNA carriers for cancer treatment are detailed in this review.

The Warburg effect and the hallmarks of cancer: Whether cancer is one illness or a group of quite different diseases is a topic of ongoing dispute. The purpose of this study is to make a convincing case that the Warburg's effect may be the cause of the majority, if not all, of the characteristics of cancer. A reduction in ATP concentration results from the metabolic impairment of oxidative phosphorylation. Massive glucose absorption, anaerobic glycolysis, and an over-regulation of the Pentose Phosphate Pathway, which results in greater biosynthesis and enhanced cell division and local pressure, are all used to make up for the decreased energy production. This increased pressure gives the tumour its fractal structure, causes the fibroblasts to secrete collagen, and is essential for the progression of metastatic disease. The extracellular acidity and immune system activation are both influenced by the large extrusion of lactic acid. At least two carbonic anhydrase isoforms linked with cancer mediate the increased intracellular alkalosis and impaired CO2 levels within and outside of the cell as a result of the reduced oxidative phosphorylation.

Recent advances in cancer early detection and diagnosis: Role of nucleic acid based aptasensors: A difficult condition of great concern is cancer. Early and sensitive cancer diagnosis, together with the use of cancer biomarkers, can improve outcomes while enabling a better knowledge of how the disease develops and the creation of efficient therapeutic approaches. Apt sensors have showed considerable potential in the recognition and identification of cancer cells and associated biomarkers among the several detection techniques that are now available. In this review, we provide an overview of current breakthroughs in aptamer-based technologies for cancer exosome detection as well as optical and microfluidic apt sensors for early cancer diagnosis. Following an introduction to the aptamer manufacturing process and their various characteristics, a summary of the most recent optical apt sensors for cancer cell identification and detection is provided. The discussion of sensitive biomarker and cancer cell detection using microfluidic aptamer-based technology follows. Following that, a detailed discussion of modern fluorescence, colorimetric, and other methods for cancer exosome detection follows. We conclude by offering our viewpoint on the potential for suitable sensors to detect cancer in the future.

Human papillomavirus e6 bio sensing: Current progression on early detection strategies for cervical cancer: One of the major problems in the medical system is the prognosis of early cancer identification. The lack of early detection, risk factor cross-reaction, mobility, and quick and free labelling systems for cervical cancer has sparked heated medical disputes among specialists and researchers in treatment methods. Due to the hybridization of DNA duplex between the analyte target and DNA probes, the electrical bio sensing-based system shown believability in enhanced specificity and selectivity. Due to its outstanding performance, ease of use, speed, and potential for miniaturization, the electrical DNA sensor for cervical cancer has drawn far too much interest from researchers. This study examines the state of HPV E6 genobiosensing and its prospective significance for cervical cancer early detection strategies.

Biomarkers in cervical cancer screening: Cervical cancer incidence has significantly decreased in developed nations thanks to population-wide cytological screening programmes employing the Pap test. Despite their clear effectiveness, Pap-stained cytological sample-based screening techniques have a number of drawbacks. First, a number of ambiguous or somewhat abnormal test findings necessitate expensive follow-up procedures such as repeated testing or direct colposcopy and biopsy because some of the high grade lesions that necessitate rapid

treatment can be found among these ambiguous test results. A significant portion of the total expenditures associated with cervical cancer screening go into this work up of cytological tests that are just marginally aberrant or ambiguous. Improved triage of these samples might result in significant cost savings. Chronic infections with oncogenic human papilloma viruses cause cervical cancer. Although HPV infection is a necessary component, it is not enough to induce cancer. More over 90% of acute HPV infections cause low grade precursor lesions that spontaneously disappear within a few months, and less than 10% of these infections result in high grade lesions or invasive malignancy. The uncontrolled expression of the viral oncogenes E6 and E7 in infected basal and parabasal cells is a hallmark of progression. The identification of lesions with a high risk of progression in both primary screening and triage settings is anticipated to be improved by novel biomarkers that allow monitoring these crucial molecular processes in histological or cytological material. With an emphasis on the quality of clinical evidence that supports their use as new markers in sophisticated cervical cancer screening programmes, we will address prospective biomarkers for cervical cancer screening in this study.

III. METHODOLOGY

Proposed system:

In the suggested approach, an ensemble classification method based on majority voting is used to make a precise diagnosis that takes into account the patient's symptoms or circumstances. A broad variety of classifiers, including Decision Tree (DT), Support Vector Machine (SVM), Random Forest (RF), K-Nearest Neighbor (KNN), Naive Bayes (NB), Multiple Perceptron (MP), and Logistic Regression (LR) classifiers, are experimented in this work. The study reports an increase in prediction accuracy of 94%, which is much higher than the prediction accuracies of single classification methods evaluated on the same benchmarked datasets.

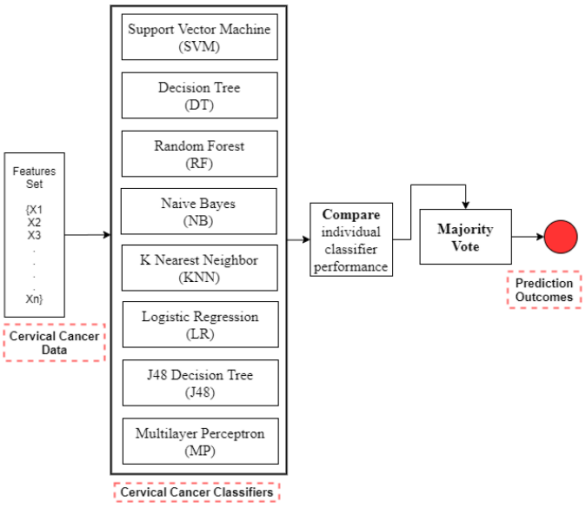


Figure 1 : Block diagram

IV. IMPLEMENTATION

The project has implemented by using below listed algorithm.

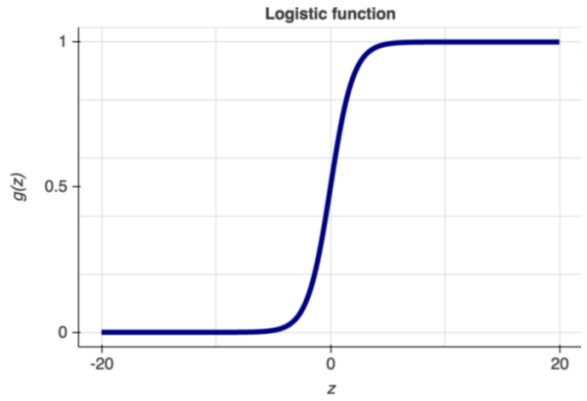
Logistic regression

Logistic regression is a Machine Learning classification algorithm that is used to predict the probability of a categorical dependent variable. In logistic regression, the dependent variable is a binary variable that contains data coded as 1 (yes, success, etc.) or 0 (no, failure, etc.). In other words, the logistic regression model predicts P(Y=1) as a function of X.

Step1: Logistic regression hypothesis

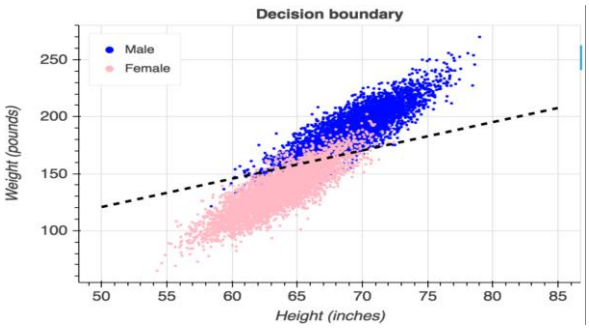
The logistic regression classifier can be derived by analogy to the logistic *regression* the function **g(z)** is the logistic function also known as the *sigmoid function.*

The logistic function has asymptotes at 0 and 1, and it crosses the y-axis at 0.5.



Step (1b): Logistic regression decision boundary

Since our data set has two features: height and weight, the logistic regression hypothesis is the following:



Random forest classifier

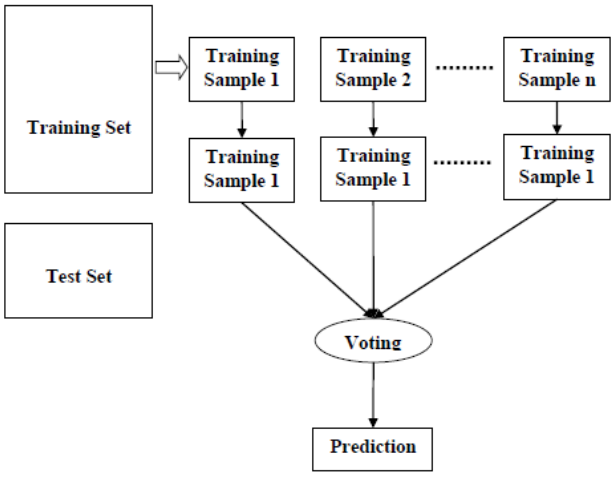
A supervised learning approach called random forest is employed for both classification and regression. But it is mostly employed for categorization issues. As is common knowledge, a forest is made up of trees, and a forest with more trees will be more sturdy. Similar to this, the random forest method builds decision trees on data samples, obtains predictions from each one, and then uses voting to determine the optimal option. Because it averages the results, the ensemble technique is superior than a single decision tree in that it lessens over-fitting.

Working of Random Forest Algorithm

We can understand the working of Random Forest algorithm with the help of following steps –

- **Step 1** – First, start with the selection of random samples from a given dataset.
- **Step 2** – Next, this algorithm will construct a decision tree for every sample. Then it will get the prediction result from every decision tree.
- **Step 3** – In this step, voting will be performed for every predicted result.
- **Step 4** – At last, select the most voted prediction result as the final prediction result.

The following diagram will illustrate its working –



Naive Bayes algorithm

Bayes' Theorem provides a way that we can calculate the probability of a piece of data belonging to a given class, given our prior knowledge. Bayes' Theorem is stated as:

P (class data) = (P (data class) * P(class)) / P(data)

Where P (class data) is the probability of class given the provided data.

Step 1: Separate by Class

This means that we will first need to separate our training data by class. A relatively straightforward operation.

We can create a dictionary object where each key is the class value and then add a list of all the records as the value in the dictionary.

Step 2: Summarize Dataset

We need two statistics from a given set of data.

- We'll see how these statistics are used in the calculation of probabilities in a few steps. The two statistics we require from a given dataset are the mean and the standard deviation (average deviation from the mean).

The mean is the average value and can be calculated as:

- mean = sum(x)/n * count(x)

Where *x* is the list of values or a column we are looking.

Step 3: Summarize Data By Class

We require statistics from our training dataset organized by class.

Above, we have developed the *separate_by_class ()* function to separate a dataset into rows by class. And we have developed *summarize dataset ()* function to calculate summary statistics for each column.

We can put all of this together and summarize the columns in the dataset organized by class values.

Step 4: Gaussian Probability Density Function

Calculating the probability or likelihood of observing a given real-value like X1 is difficult.

One way we can do this is to assume that X1 values are drawn from a distribution, such as a bell curve or Gaussian distribution.

A Gaussian distribution can be summarized using only two numbers: the mean and the standard deviation. Therefore, with a little math, we can estimate the probability of a given value. This piece of math is called a Gaussian Probability Distribution Function (or Gaussian PDF) and can be calculated as:

- f(x) = (1 / sqrt(2 * PI) * sigma) * exp(-((x-mean)^2 / (2 * sigma^2)))

Where *sigma* is the standard deviation for *x*, *mean* is the mean for *x* and *PI* is the value of pi.

Support vector classifiers algorithm

Support Vector Machine or SVM algorithm is a simple yet powerful Supervised Machine Learning algorithm that can be used for building both regression and classification models. SVM algorithm can perform really well with both linearly separable and non-linearly separable datasets. Even with a limited amount of data, the support vector machine algorithm does not fail to show its magic.

Step 1: Load Pandas library and the dataset using Pandas

Step 2: Define the features and the target

Step 3: Split the dataset into train and test using sklearn before building the SVM algorithm model

Step 4: Import the support vector classifier function or SVC function from Sklearn SVM module. Build the Support Vector Machine model with the help of the SVC function

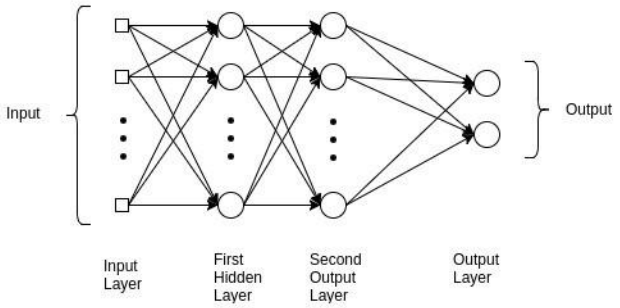
Step 5: Predict values using the SVM algorithm model

Step 6: Evaluate the Support Vector Machine model

Multi linear perceptron:

There may be more than one linear layer in the multilayer perceptron (combinations of neurons). If

we use the straightforward example of a three-layer network, the input layer will be on the top, the output layer will be at the bottom, and the middle layer will be referred to as the hidden layer. The input layer receives our input data, and the output layer receives our output. To make the model more complicated and better suit our purpose, we may increase the number of hidden layers as much as we'd want.



The most prevalent neural network model is the feed-forward network. To approximate some function f is its objective (). By constructing a mapping, y = f(x;), and learning the optimal parameters for it, the MLP may determine the best approximation to a classifier, such as y = f(x) that translates an input x to an output class y. The MLP networks are made up of several linked together functions. A three-function or three-layer network would have the formula f(x) = f(3)(f(2)(f(1)(x))). Each of these layers is made up of units that convert a linear sum of inputs using an affine transformation. Every layer is denoted by the formula y = f(WxT + b). Where x is the input vector, which can also be the output of the preceding layer, f is the activation function (discussed below), W is the set of parameter, or weights, in the layer, and b is the bias vector. Because every unit in a layer is linked to every other unit in the layer before it, an MLP has many completely connected layers. Each unit in a fully linked layer has its own set of weights since its properties are independent of those of the other units in the layer.

Each input vector in a supervised classification system has a label, or ground truth, specifying its class, or the class label is provided with the data. For each input, the network's output provides a class score or prediction. The loss function is established to gauge the classifier's effectiveness. If the anticipated class does not match the actual class, the loss will be considerable; otherwise, it will be minimal. When the model is being trained, the issue of overfitting and under fitting might occasionally arise. Our model works admirably on training data in this example, but not on testing data. An optimization technique is needed in order to train the network, and for this, a loss function and an optimizer are necessary. The values for the set of weights, W, that minimizes the loss function will be discovered using this technique.

Initializing the weights at random values and iteratively adjusting them to achieve a reduced loss is a common tactic. By going in the direction indicated by the gradient of the loss function, this refinement is accomplished. Additionally, it's crucial to provide a learning rate that specifies how much the algorithm advances with each iteration.

K-NEAREST NEIGHBOUR:

This k-Nearest Neighbors tutorial is broken down into 3 parts:

Step 1: Calculate Euclidean Distance.
Step 2: Get Nearest Neighbors.
Step 3: Make Predictions

Step 1: Calculate Euclidean Distance.

He first step is to calculate the distance between two rows in a dataset.

Rows of data are mostly made up of numbers and an easy way to calculate the distance between two rows or vectors of numbers is to draw a straight line. This makes sense in 2D or 3D and scales nicely to higher dimensions

Euclidean Distance = sqrt(sum i to N (x1_i – x2_i)^2)

Where *x1* is the first row of data, *x2* is the second row of data and *i* is the index to a specific column as we sum across all columns.

With Euclidean distance, the smaller the value, the more similar two records will be. A value of 0 means that there is no difference between two records

Step 2: Get Nearest Neighbours:

Neighbors for a new piece of data in the dataset are the *k* closest instances, as defined by our distance measure.

To locate the neighbors for a new piece of data within a dataset we must first calculate the distance between each record in the dataset to the new piece of data. We can do this using our distance function prepared above.

Once distances are calculated, we must sort all of the records in the training dataset by their distance to the new data. We can then select the top *k* to return as the most similar neighbors.

We can do this by keeping track of the distance for each record in the dataset as a tuple, sort the list of tuples by the distance (in descending order) and then retrieve the neighbor

Step 3: Make Predictions

The most similar neighbours collected from the training dataset can be used to make predictions.

In the case of classification, we can return the most represented class among the neighbours.

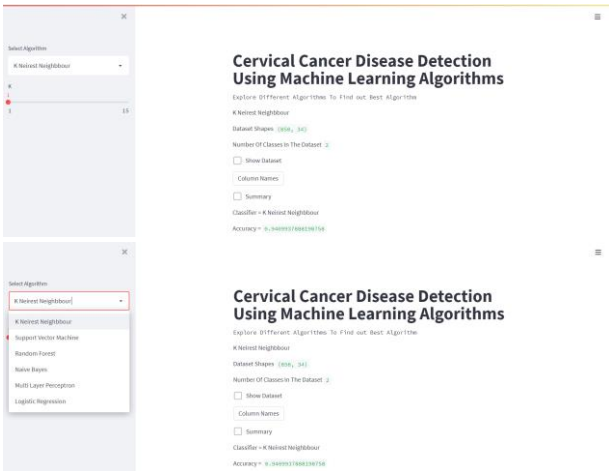
We can achieve this by performing the *max()* function on the list of output values from the neighbours. Given a list of class values observed in the neighbors, the *max()* function takes a set of unique class values and calls the count on the list of class values for each class value in the set.

V. RESULTS AND DISCUSSION

The following screenshots are depicted the flow and working process of project.

Home Page:

This is the home page of this application. KNN Algorithm giving accuracy 94%:



SVM:

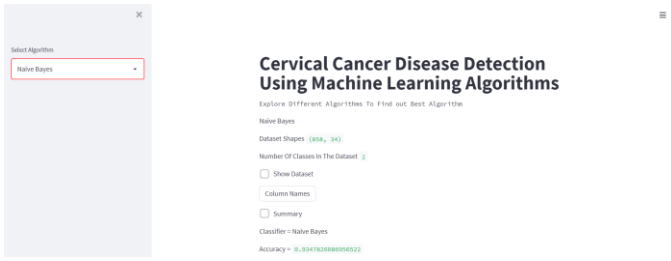
SVM Algorithm giving accuracy 90%

Random Forest:

Random Forest Algorithm giving accuracy 96%

Naïve Bayes:

Naïve Bayes Algorithm giving accuracy 93%



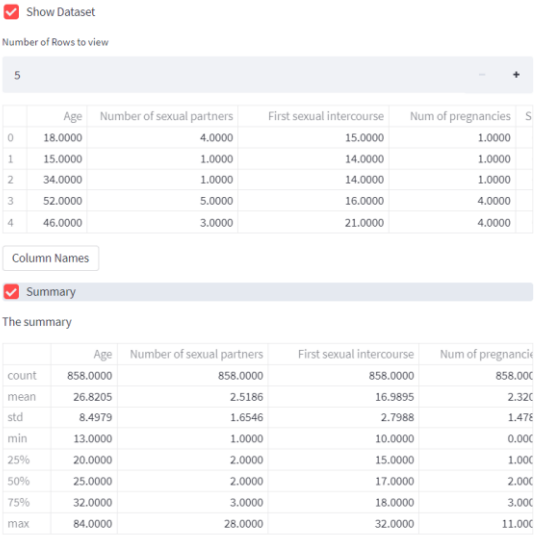
Multi-Layer Perceptron:

MLP Algorithm giving accuracy 95%

Logistic Regression:

Logistic Regression Algorithm giving accuracy 94%.

Data-set and summary:



Show Dataset

Number of Rows to view

5

	Age	Number of sexual partners	First sexual intercourse	Num of pregnancies	S
0	18.0000	4.0000	15.0000	1.0000	
1	15.0000	1.0000	14.0000	1.0000	
2	34.0000	1.0000	14.0000	1.0000	
3	52.0000	5.0000	16.0000	4.0000	
4	46.0000	3.0000	21.0000	4.0000	

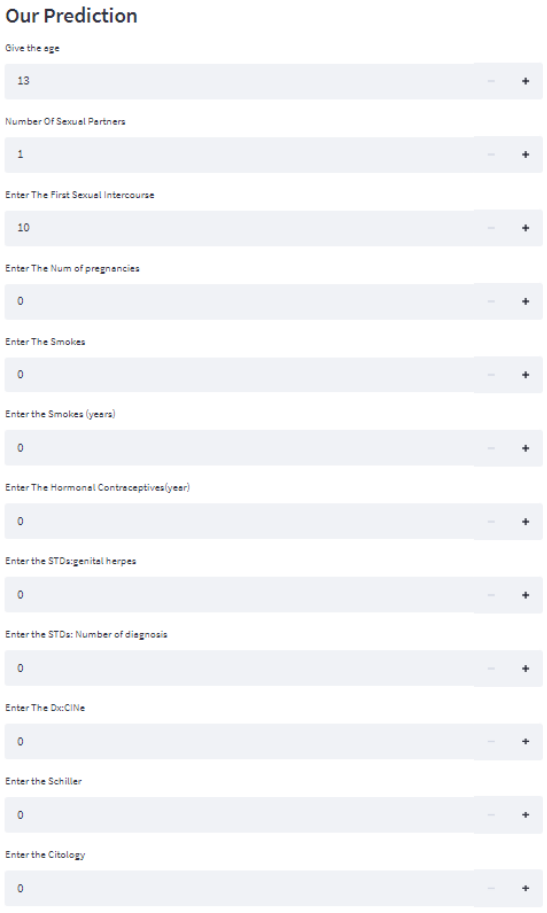
Column Names

Summary

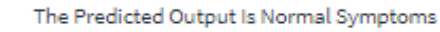
The summary

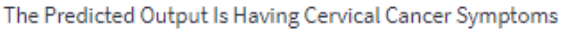
	Age	Number of sexual partners	First sexual intercourse	Num of pregnanci
count	858.0000	858.0000	858.0000	858.00
mean	26.8205	2.5186	16.9895	2.32
std	8.4979	1.6546	2.7988	1.47
min	13.0000	1.0000	10.0000	0.00
25%	20.0000	2.0000	15.0000	1.00
50%	25.0000	2.0000	17.0000	2.00
75%	32.0000	3.0000	18.0000	3.00
max	84.0000	28.0000	32.0000	11.00

Prediction:



Results:





VI.CONCLUSION

To preserve the subjects' priceless lives, the health 4.0 requirements need an accurate and reliable cervical cancer detection. Despite the difficulties and problems, machine intelligence-based solutions now available are regarded as reliable. However, the effectiveness of various categorization systems for the detection of cervical cancer is also a problem. Different classifiers provide distinctly different results when used to the same datasets because the specific classification algorithms are sensitive to the nature of the data. Based on a major voting procedure to accept

the best classification outcomes for cervical cancer prediction, this research study proposed an ensemble classification approach for cervical cancer diagnosis. The study included a variety of classifiers, including Decision Tree (DT), Support Vector Machine (SVM), Random Forest (RF), K-Nearest Neighbour (KNN), Naive Bayes (NB), Multiple Perceptron (MP), and Logistic Regression (LR). When compared to other classifiers, the suggested ensemble classifier performed better than individual classifiers, achieving the greatest accuracy at 94%. The findings of this study can be used by medical professionals to give cervical cancer patients a knowledgeable and trustworthy second opinion to better treat the condition.

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