

Improvisation of Healthcare Security System with Incorporation of Machine Learning Algorithms

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Abstract: A World Health Organization (WHO) calls cancer a generic term for a large group of diseases that can have an impact on any aspect of the body. Sometimes it could be the cause of the loss of patients. If cancer is diagnosed and treated early, mortality can be minimized. The classification of patients due to their answers to a survey has been done to determine someone who has highly cervical cancer risk. We will give symptoms as input. The classification is done according to the symptoms. There are 858 entries in the collection, each having 33 characteristics and a biopsy result. In the dataset, the number of patients with a cervical cancer diagnosis is 55 and the number of healthy patients is 803. The dataset was randomly split into two groups: train and test. The training group is 66% of the main dataset so there are 565 records in the training dataset. The rest of the dataset has been assigned as a test dataset. The classification has been done by using various methods like Naive Bayes, Random Forest, SVM, and Decision Tree. Correctly classified instances and percentages, true positive and false positive classified instances rate for each class and confusion matrix have been presented for each method. And all of the results are discussed.

Index Terms - Cervical Cancer, Naive Bayes, Classification, Internet of Things, Random Forest Classification, Machine Learning.

1. Introduction

Cervical cancer develops as cells in a girl's cervix, which binds her uterus to her vagina, alter. Most cancers may affect the deeper tissues of the cervix and can spread to other parts of the body (metastasize), including the lungs, liver, bladder, vaginal region, and rectum. The majority of cervical cancers are caused by infection with the human papillomavirus (HPV), which can be prevented by a vaccine. Cervical cancer develops slowly, so it's usually possible to detect and treat it before it causes serious complications. Every year, fewer and fewer girls die as a result of improved screening through Pap tests. Women between the ages of 35 and 44 are the most likely to contract this type of infection. More than 15% of new cases are in women over 65, especially those who haven't been having frequent screenings. The proposed research study is about the implementation of Machine Learning (ML), which is closely connected to (and often overlaps with) predictive statistics and has many links to mathematical optimization.

2 Literature Survey

Amita Dessai, Moffy Vas, A computer tomography scan is used by radiologists to diagnose and monitor the progression of cancer in the body. Visual database interpretation may lead to a later cancer diagnosis, resulting in late cancer care, which only serves to raise cancer mortality rates. As a result, image recognition software can be used to detect cancer in its early stages. This article proposes a lung cancer detection algorithm that uses mathematical morphological operations to segment the lung area of interest, from which Haralick features are extracted and used by artificial neural networks for cancer classification.

According to Annette McWilliams, Parmida Beigi, Akhila Srinidhi, Stephen Lam, and Calum E. MacAulay, E -nostril measurements could distinguish lung cancer patients from high-hazard control subjects with a higher than 80 % classification accuracy. Topic intercourse and smoking popularity affected the group, as shown by the results below the curve (Ex-smoker adult males score 0.846, ex-smoker females score 0.816, current smoker man scores 0.745, and current smoker girl scores 0.725.)Two e-nostril systems could be set up to provide the same readings during the subject's exhaled breath, and the results could be measured in parallel. Conclusions: E-nostril generation should be used as a non-invasive screening technique to identify people at risk of lung cancer. The compounds found in the alveolar cavity are essential.

Ho Tak Lau, Adel Al-Jumaily, in this paper, an automatic skin cancer classification scheme is developed, and the relationship of skin cancer images through various types of neural networks is investigated using various preprocessing techniques. The images are fed into the device and processed through various image processing procedures to improve the image properties. The normal skin is then removed from the infected region, leaving only the cancer cell in the picture. These images can be used to extract useful information that can then be fed into the classification system for training and testing. In image science software, the recognition accuracy of the 3-layer back-propagation neural network classifier is 89.9%, and the auto-associative neural network is 80.8 percent.

J. Geoffrey Chase, Tom Botterill, Thomas Lotz, Amer Kashif The internal stiffness of the breast can be inferred by the surface motion of a vibrated breast, causing a tumor to be seen. A computer vision system for properly sensing 3-D floor motion is described in this study. A version-based total segmentation is used to recognize the profile of the breast in each image, and the 3-d floor is reconstructed using the profiles as a guide. The floor movement is computed with the help of a current optical glide implementation custom designed for the application, then trajectories of factors at the 3-D floor are obtained by fusing the optical flow implementation custom designed for the application, and trajectories of points on the 3-D surface are obtained by fusing the optical glide with the drift with the surfaces that have been preserved. The machine outperforms and earlier marker-based system at measuring skin surface motion, according to data from human trials. The research study demonstrates that the scanner can identify a ten-millimeter tumor in a silicone phantom breast. Display the abstract. The DIET breast cancer screening device uses a vision-based 3-D floor activity capture system.

Azadeh Noori Hoshyar, Adel Al- Jumpily In several countries, especially Australia, skin cancer is on the rise. Early detection of skin cancers aids in the effective treatment of cancer; hence, cancer curability and survival are contingent on detecting cancer early. Automatic prognosis can help to improve diagnosis accuracy because scientific findings are restricted in their ability to diagnose cancer. The final goals of this paper are to study previous skin cancer detection studies and to evaluate automatic skin cancer detection. It includes an analysis of the literature on computerized skin cancer diagnosis as well as a step-by-step breakdown of the process. Discover the 17+ million people who have taken part in surveys around the world.

One of the most common alternatives to X-ray mammography as an imaging modality is ultra-wideband (UWB) radar for the early detection of breast cancer, according to Dallan Byrne, Martin O'Halloran, Edward Jones, and Martin Glavin. Several beam shaping

algorithms that take advantage of the dielectric contrast To detect cancerous Amplifications, a microwave frequency difference between normal and cancerous tissue has been identified. Since dielectric heterogeneity in the breast has a direct impact on a beamformer's ability to identify very small tumors, designing an efficient beamformer for this application is a major difficult task This paper examines and contrasts three data-independent beamforming algorithms, putting each one to the test on an anatomically accurate, MRI-derived breast model that includes recently published dielectric property data.

R.S.A. Raja Abdullah, A Munawar, S Adabi, Al Ismail, MI Saripan, R Mahmood, WNL Wan Mahadi, R.S.A. Raja Abdullah, R.S.A. Raja Abdullah, R.S.A. Raja Abdullah, R.S.A. Raja Abdullah, R.S.A. This paper describes the results of a preliminary study into the identification of breast cancer using a special form of bistatic radar known as forwarding Scattering Radar (FSR). For cancer diagnosis and localization, the proposed approach analyses the Doppler frequency in the obtained signal scattered from the tumor. Three architectures were investigated, each of which was determined by the mechanical action of the transmitter, receiver, or both. Also, as a feasibility assessment of using FSR for breast cancer diagnosis, this paper addresses an initial simulated outcome using CST Microwave Studio. It has been shown that cancer can be predicted by examining the peculiar characteristics of Radar Cross Section (RCS) for breast tissue and FSR tumors. An electromagnetic model of fatty tissue and a tumor was simulated and analyzed to obtain the RCS parameter, as well as compared to fatty tissue without a cancerous lesion to pinpoint the presence of tumor from its FSR characteristic. In FS RCS, the results indicate a large difference between these two models.

Write and save the material of the document as a separate text file before beginning to format it. Separate the text and graphic files before the text has been styled and formatted. Hard tabs should be avoided, and hard returns should be used only once per paragraph.

2.1 Referred Dataset for proposed WorkDescription

The proposed work deals with the study of sample data files from Patient_train.csv. There are 858 statistics in the dataset, each with 33 attributes and a biopsy result. The number of women diagnosed with cervical cancer in the dataset is 55, while the number of healthy patients is 803. This dataset was split into teaching and test companies at random. This dataset was split into teaching and test companies at random. The training dataset contains 565 statistics and it makes up 66 percent of the main data collection. Taking a look at the dataset has been delegated to the relaxing of the data collection. Several methods, such as Naive Bayes, Random Forest(RF), Support Vector

Machine(SVM), and Decision Tree(DT), were used to create the group.

2. Proposed System Requirement Specification

2.2 Description

For cancer diagnosis, there is no automatic method available.

- In the medical sector, there is no such thing as automatic. The procedure for detecting cervical cancer.[1]
- The death rate is that as a result of cancer.
- Signs are used to diagnosing cancer using a manual procedure.

2.2.1 Proposed Work Scope

When a comprehensive overview of all aspects of the software package to be developed is required before the project can begin, a software specifications specification (SRS) is firm the groundwork. It's important to note that a formal SRS isn't always written. Time spent on an SRS is often better spent on other software engineering tasks.

- To be able to comprehend the issue sentence.
- To know what are the hardware and software requirements of the proposed system.
- To have an understanding of the proposed system.
- To do planning various activities with the help of a planner.
- Designing, programming, testing, etc.

3. Proposed System

3.1 Description

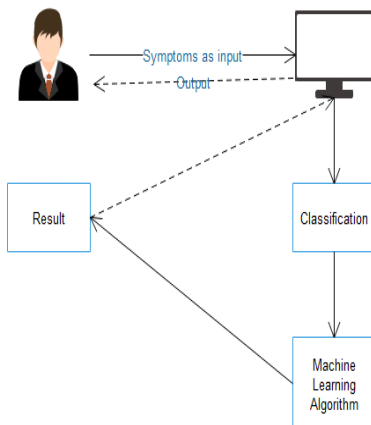


Fig. 4.1 Proposed System Architecture

In this Figure 4.1, the User gives symptoms as an input to the system. The system should work on the given input. First of all, with the help of the database, classification of the symptoms should be done. After the classification of the symptoms, the algorithm should be applied to the given symptoms. After applying the algorithm, the system should determine the patient is suffering from cancer or not.

5. IMPLEMENTATION

5.1 Data Pre-processing

```

Data Preprocessing

In [0]: # Imputing the missing values from the given dataset
# we will impute the categorical variables with 0 or 1 and continuous variables with median value

data['Number of sexual partners'] = data['Number of sexual partners'].fillna(data['Number of sexual partners'].median())
data['Number of sexual partners'].isnull().any()

# data['Number of sexual partners'].value_counts()

Out[96]: False

In [0]: # Imputing the missing values from First sexual intercourse

data['First sexual intercourse'] = data['First sexual intercourse'].fillna(data['First sexual intercourse'].median())
data['First sexual intercourse'].isnull().any()

# data['First sexual intercourse'].value_counts()

Out[97]: False
    
```

Fig. 5.1 Data Pre-Processing

5.1.1 Dataset Understand

```

Importing the Dataset

In [8]: data = pd.read_csv("kag_risk_factors_cervical_cancer.csv")

In [4]: data.head(4)

Out[4]:
   Age  Number of sexual partners  First sexual intercourse  Num of pregnancies  Smokes  Smokes (years)  Smokes (packs/year)  Hormonal Contraceptives  Hormonal Contraceptives (years)  STDs: Time since first diagnosis  STDs: Time since last diagnosis  DxCancer  DxCIN
0  18.0      4      15      1      0      0      0      0      0      0      ?      ?      0.0  0.0
1  15.0      1      14      1      0      0      0      0      0      0      ?      ?      0.0  0.0
2  34.0      1      ?      1      0      0      0      0      0      0      ?      ?      0.0  0.0
3  52.0      5      16      4      1      37      37      1      3      0      ?      ?      1.0  0.0

4 rows x 36 columns
    
```

Fig. 5.1.1 Dataset

5.1.1 Data Quality

```
In [6]: data.info()

<class 'pandas.core.frame.DataFrame'>
RangeIndex: 861 entries, 0 to 860
Data columns (total 36 columns):
 #   Column              Non-Null Count  Dtype
---  ---
 0   Age                 858 non-null   float64
 1   Number of sexual partners 858 non-null   object
 2   First sexual intercourse 858 non-null   object
 3   Num of pregnancies    858 non-null   object
 4   Smokes              858 non-null   object
 5   Smokes (years)      858 non-null   object
 6   Smokes (packs/year) 858 non-null   object
 7   Hormonal contraceptives 858 non-null   object
 8   Hormonal contraceptives (years) 858 non-null object
 9   IUD                 858 non-null   object
10   IUD (years)         858 non-null   object
11   STDs                858 non-null   object
12   STDs (number)       858 non-null   object
13   STDs:condylomatosis 858 non-null   object
14   STDs:cervical condylomatosis 858 non-null object
15   STDs:vaginal condylomatosis 858 non-null object
16   STDs:vulvo-perineal condylomatosis 858 non-null object
17   STDs:syphilis       858 non-null   object
18   STDs:pelvic inflammatory disease 858 non-null object
19   STDs:genital herpes 858 non-null   object
20   STDs:molluscum contagiosum 858 non-null object
21   STDs:AIDS           858 non-null   object
22   STDs:HIV            858 non-null   object
23   STDs:Hepatitis B    858 non-null   object
24   STDs:HPV            858 non-null   object
25   STDs: Number of diagnosis 858 non-null float64
26   STDs: Time since first diagnosis 858 non-null object
27   STDs: Time since last diagnosis 858 non-null object
28   Dx:Cancer           858 non-null   float64
29   Dx:CIN              858 non-null   float64
```

Fig. 5.1.2 Data Information

```
In [10]: data.isnull().sum()

Out[10]:
Age 3
Number of sexual partners 3
First sexual intercourse 3
Num of pregnancies 3
Smokes 3
Smokes (years) 3
Smokes (packs/year) 3
Hormonal Contraceptives 3
Hormonal Contraceptives (years) 3
IUD 3
IUD (years) 3
STDs 3
STDs (number) 3
STDs:condylomatosis 3
STDs:cervical condylomatosis 3
STDs:vaginal condylomatosis 3
STDs:vulvo-perineal condylomatosis 3
STDs:syphilis 3
STDs:pelvic inflammatory disease 3
STDs:genital herpes 3
STDs:molluscum contagiosum 3
STDs:AIDS 3
STDs:HIV 3
STDs:Hepatitis B 3
STDs:HPV 3
STDs: Number of diagnosis 3
STDs: Time since first diagnosis 3
STDs: Time since last diagnosis 3
Dx:Cancer 3
Dx:CIN 3
Dx:HPV 3
Dx 3
Hinselmann 3
Schiller 3
Cytology 3
```

Fig. 5.1.2 Data Missing Values

```
In [8]: # Imputing values for categorical variables

data = pd.get_dummies(data = data, columns = ['Smokes', 'Hormonal Contraceptives', 'IUD', 'STDs',
                                             'Dx:Cancer', 'Dx:CIN', 'Dx:HPV', 'Dx', 'Hinselmann', 'Cytology', 'Schiller'])

data.isnull().sum()

Out[122]:
Age 0
Number of sexual partners 0
First sexual intercourse 0
Num of pregnancies 0
Smokes (years) 0
Smokes (packs/year) 0
Hormonal contraceptives (years) 0
IUD (years) 0
STDs (number) 0
STDs:condylomatosis 0
STDs:cervical condylomatosis 0
STDs:vaginal condylomatosis 0
STDs:vulvo-perineal condylomatosis 0
STDs:syphilis 0
STDs:pelvic inflammatory disease 0
STDs:genital herpes 0
STDs:molluscum contagiosum 0
STDs:AIDS 0
STDs:HIV 0
STDs:Hepatitis B 0
STDs:HPV 0
STDs: Number of diagnosis 0
STDs: Time since first diagnosis 0
STDs: Time since last diagnosis 0
Biopsy 0
Smokes_0.0 0
Smokes_1.0 0
Hormonal contraceptives_0.0 0
Hormonal contraceptives_1.0 0
IUD_0.0 0
```

Fig. 5.1.2 Accurate Data

5.1.2 TP and FP Rate

```
In [0]: # compiling the model
model.compile(optimizer = 'adam', loss = 'binary_crossentropy', metrics = ['accuracy'])

# feeding training data to the model
train_history = model.fit(x_train, y_train, batch_size = 150, epochs = 35, validation_split = 0.2, verbose = 2)

Train on 411 samples, validate on 103 samples
Epoch 1/35
- 1s - loss: 0.0527 - acc: 0.9976 - val_loss: 0.0568 - val_acc: 1.0000
Epoch 2/35
- 0s - loss: 0.0522 - acc: 0.9976 - val_loss: 0.0566 - val_acc: 1.0000
Epoch 3/35
- 0s - loss: 0.0520 - acc: 1.0000 - val_loss: 0.0565 - val_acc: 1.0000
Epoch 4/35
- 0s - loss: 0.0519 - acc: 1.0000 - val_loss: 0.0564 - val_acc: 1.0000
Epoch 5/35
- 0s - loss: 0.0518 - acc: 1.0000 - val_loss: 0.0563 - val_acc: 1.0000
Epoch 6/35
- 0s - loss: 0.0531 - acc: 0.9976 - val_loss: 0.0561 - val_acc: 1.0000
Epoch 7/35
- 0s - loss: 0.0517 - acc: 1.0000 - val_loss: 0.0560 - val_acc: 1.0000
Epoch 8/35
- 0s - loss: 0.0515 - acc: 1.0000 - val_loss: 0.0559 - val_acc: 1.0000
Epoch 9/35
- 0s - loss: 0.0513 - acc: 1.0000 - val_loss: 0.0558 - val_acc: 1.0000
Epoch 10/35
- 0s - loss: 0.0512 - acc: 1.0000 - val_loss: 0.0557 - val_acc: 1.0000
Epoch 11/35
- 0s - loss: 0.0511 - acc: 1.0000 - val_loss: 0.0555 - val_acc: 1.0000
Epoch 12/35
- 0s - loss: 0.0510 - acc: 1.0000 - val_loss: 0.0554 - val_acc: 1.0000
Epoch 13/35
- 0s - loss: 0.0509 - acc: 1.0000 - val_loss: 0.0553 - val_acc: 1.0000
Epoch 14/35
```

Fig. 5.1.3 TP and FP Rate

5.1.3 Data Visualization

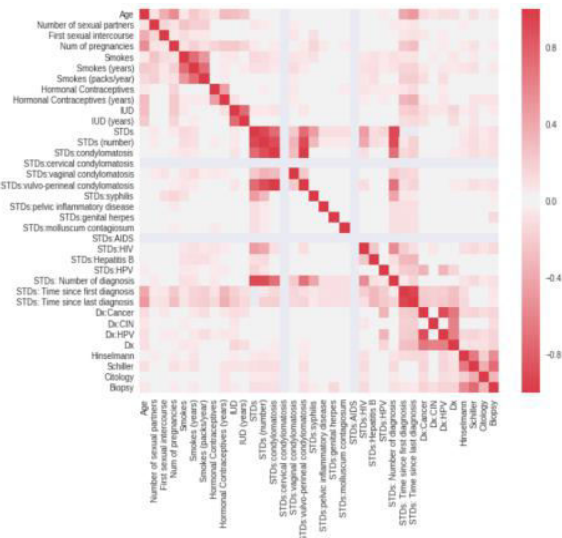


Fig. 5.1.3 Data Visualization

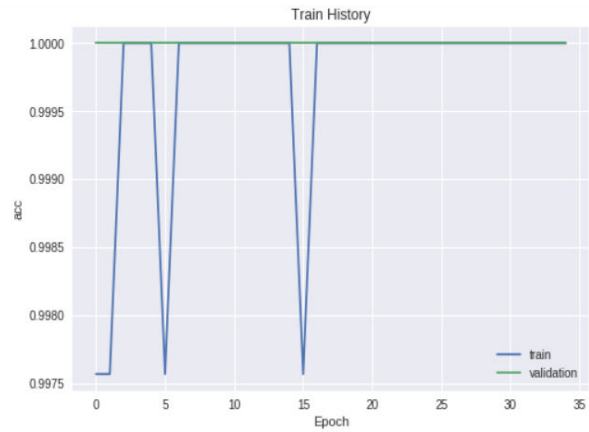


Fig. 5.1.4 Accurate Data Normalization

5.2 Data Processing

5.2.1 Data Normalization

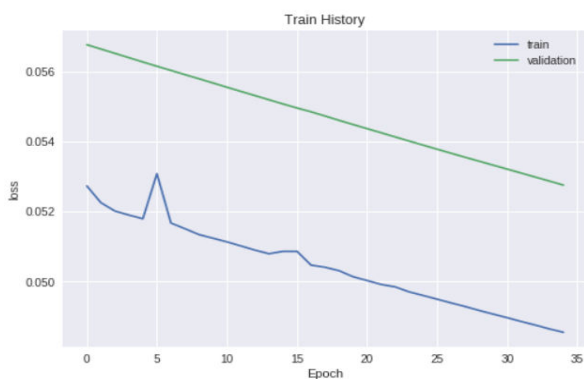


Fig. 5.1.4 Loss Data Normalization

5.2.2 Algorithm Used

Random Forest (RF)

Random forests or random decision forests are an ensemble learning method for classification, regression, and other tasks that operates by constructing a multitude of decision trees at training time and outputting the class that is the mode of the classes (classification) or mean/average prediction (regression) of the individual trees. For regression tasks, the mean or average prediction of the individual trees is returned. Random decision forests address the problem of decision trees overfitting their training set. Random forests outperform decision trees in most cases, though they are less accurate than gradient-enhanced trees. Data features, on the other hand, might have an impact on their performance.

Decision Tree (DT)

A decision tree is a decision-making aid that employs a tree-like model of decisions and their potential results, such as chance event outcomes, resource costs, and utility. It is one method of displaying an algorithm that consists solely of conditional control statements. Decision trees are a prominent technique in machine learning and are often used in operations research, particularly in decision analysis, to assist determine the best method for achieving a target. Decision trees are a prominent method in machine learning and are often used in operations research, notably in decision analysis, to assist determine the method most likely to achieve an objective.

Naive Bayes (NB)

Naive Bayes (NB) is a simple supervised function and is a special form of discriminate analysis. Because it's a generative model, it returns probabilities. It's the polar opposite of one Rule's categorization technique. To make a decision, each attribute weighs in equally and independently. Naive Bayes is a straightforward method for building classifiers, which are models that give class labels to problem cases represented as vectors of feature values, with the class labels selected from a limited strategy. Naive Bayes is a straightforward method for building classifiers, which are models that give class labels to problem cases represented as vectors of feature values, with the class labels selected from a limited prepare. The Naive Bayes classifier is used to solve binary and multi-class classification problems, particularly in the field of document classification, where text is typically utilized as input.

Support Vector Machine (SVM)

Support Vector Machine (SVM) is a relatively simple **Supervised Machine Learning Algorithm** used for classification and/or regression. It is more commonly used for classification, but it may also be quite effective for regression. SVM finds a hyperplane that divides the various types of data. This hyper-plane is nothing more than a line in two-dimensional space. SVM selects acute points/vectors that aid in the formation of the hyperplane. These numerous instances are known as support vectors, and the resulting set of rules is known as the Support Vector Machine. This preference boundary or hyperplane serves as a separator. In SVM, we plot each data item in the dataset in an N-dimensional space, where N is the number of features/attributes in the data. Next, find the optimal hyperplane to separate the data. So by this, you must have understood that inherently, SVM can only perform binary classification (i.e., choose between two classes). However, there are various techniques to use for multi-class problems.

5.3 Mathematical Background

Let 'S' be the system Where $S = I, O, P, Fs, Ss$
 Where,
 I = Set of input
 O = Set of output
 P = Set of technical methods
 Fs = Set of Failure nation
 Ss = Set of Success nation
 Identify the enter statistics $I1, I2, \dots, in$
 I = (Input Symptoms)
 Identify the symptoms as $O1, O2, \dots, on$
 O = (Symptoms detection)
 Identify the Process as P

P = (Cancer detection from symptoms)
 Identify the Failure state as Fs
 Fs = (If cancer not detected, Delay in processing)
 Identify the Success state as Ss
 P = (Cancer detected).

6. Proposed System Architecture

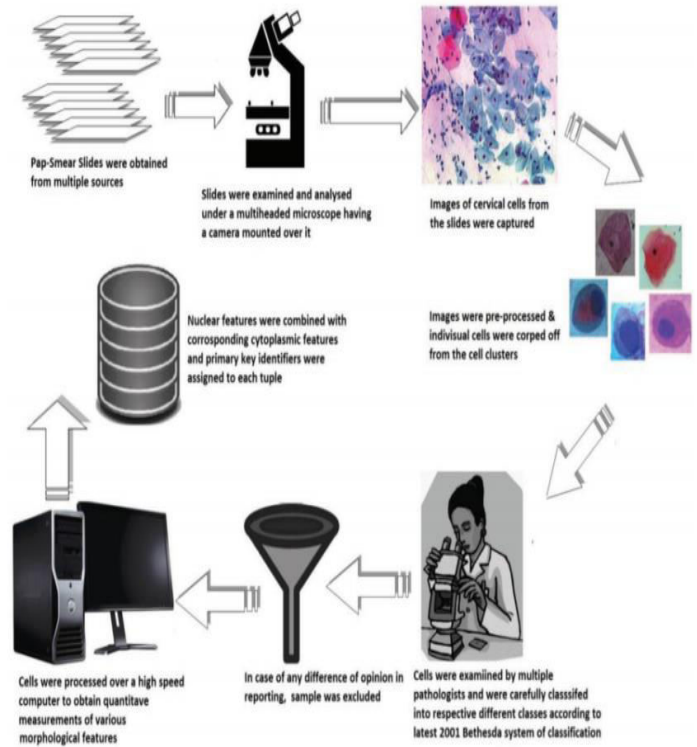


Fig. 6.1 Block diagram of various steps showing how the digital database was prepared

Figure 6.1 shows the block diagram of how the clinical data was transformed into a digital database. For profiling of the cells so obtained, as open-source software "CellProfiler" was used which evaluated the cells based on 39 morphological features (figure-6.1). These profiled cell measures were then placed in a spreadsheet so that each tuple represented a cervical cell. Various other properties of the database were also integrated so that digital data could be easily correlated with the corresponding clinical case. A detailed analysis of morphological features is a prerequisite for any automated cervical screening system as such the features set chosen for quantitative evaluation have to be such that they should be precisely measurable in a specific time with good accuracy. When opposed to manual interpretation by cytopathologists, which is subjective, lengthy, and frequently prone to human mistakes, computer approaches based on various image processing algorithms allow easy and proficient formulization of morphological traits.

7. Future Enhancement

- WHO's Global Strategy to Accelerate the Elimination of Cervical Cancer, launched today, outlines three key steps: vaccination, screening, and treatment. By 2050, successful adoption of all three might cut new occurrences of the illness by more than 40% and deaths by 5 million.
- Today's announcement is significant since it is the first time that 194 nations have pledged to eliminate cancer, after the passage of a resolution at the World Health Assembly this year.
- Meeting the following targets by 2030 will place all countries on the path toward elimination:
 1. By the age of 15, 90 percent of females had been properly vaccinated against HPV.
 2. 70% of women screened using a high-performance test by age 35 and again by 45.
 3. 90% of women identified with cervical disease receive treatment (90% of women with pre-cancer treated and 90% of women with invasive cancer managed).

8. CONCLUSION

The Proposed technical research examines the suitability of Nave Bayes(NB), Support Vector Machine(SVM), and Random Forest(RF) machine learning methods for detecting cervical cancer in the mentioned dataset. According to the research, if the gadgets identify cancer, the user should receive a message that cancer has been found. If no indications of cancer are present at the time, the result should be cancer not detected. As a result, the suggested study uses machine learning algorithms to predict cervical cancer detection in the mentioned sample data file. Hybrid machine learning methods can be used to improve the job in the future.

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