Project Report

on

PERFORMANCE EVALUATION OF BREAST CANCER DIAGNOSIS USING VARIOUS MACHINE LEARNING ALGORITHMS

Submitted by

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Under the Supervision of
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CERTIFICATE

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ABSTRACT

Breast cancer affects most women worldwide, and it is the second most common cause of death among women. However, if cancer is detected early and treated properly, it is possible to be cured of the condition. There are around 2000+ new cases of breast cancer in men each year, and about 2,30,000 new cases in women every year. Diagnosis of this disease is crucial so that woman can get it treated faster Early detection of breast cancer can dramatically improve the prognosis and chances of survival by allowing patients to receive timely clinical therapy. Machine Learning (ML) techniques can help in the detection of breast cancer. We can use these techniques to make tools for doctors that can be used as an effective mechanism. Furthermore, precise benign tumor classification can help patients avoid unneeded treatment.

Machine learning techniques can bring a large contribution to the process of prediction and early diagnosis of breast cancer, became a research hotspot and has been proved as a strong technique. In this study, four machine learning algorithms: Support Vector Machine (SVM), Logistic Regression, Naïve Bayes and K-Nearest Neighbors (KNN) are applied for numerical dataset, after obtaining the results, a performance evaluation and comparison is carried out between these different classifiers.

These techniques are coded in python and use NumPy, pandas, matplotlib, seaborn libraries. Finally, both image and numerical test data will be used for prediction

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CHAPTER 1

INTRODUCTION

1.1 DOMAIN SPECIFIC

Thousands of females fall victim to breast cancer every year. The human body comprises millions of cells each with its unique function. When there is unregulated growth of the cells it is termed as cancer. In this, cells divide and grow uncontrollably, forming an abnormal swelling tissue part called a tumor. Tumor cells grow and invade digestive, nervous, and circulatory systems disrupting the bodies' normal functioning. Though every single tumor is not cancerous. Cancer is classified by the type of cell that is affected and more than 200 types of cancers are known. This study is focused on Breast cancer.

The cancer that develops in the breast cells is called breast cancer. This type of cancer can be seen in the breast ducts or the lobules. Cancer can also occur in the fatty tissue or the fibrous connective tissue within the breast. These cancer cells become uncontrollable and end up invading other healthy breast tissues and can travel to the lymph nodes under the arms.

As per the National Breast Cancer Foundation, "Breast cancer is the most commonly diagnosed cancer in women". Breast cancer is the second largest cause of cancer death among women. Women generally approach clinics with a mild to serious pain in their breasts. After the examination of the breasts, the doctors usually suggest an ultrasound scan. The proceedings after the scan are more painful. Some women feel that the pain is intensely increased only after clinical proceedings. It is because of the painful process that is followed to detect whether the lymph node is malignant or benign.

Malignant cancers are cancerous. These cells keep dividing uncontrollably and start affecting other cells and tissues in the body. They spread to all other parts of the body, and it is hard to cure this type of cancer. Chemotherapy, radiation therapy and immunotherapy are types of treatments that can be given for these types of tumors. Benign cancer is noncancerous. Unlike malignant, this tumor does not spread to other parts of the body and hence is much less risky that malignant. In many cases, such tumors don’t really require any treatment. Breast Cancer has always had a high mortality rate and according to statistics, its alone accounts for about 25% of all new cancer diagnoses and 15% of all cancer deaths among women worldwide.

1.2 OBJECTIVE OF THE PROPOSED PROJECT WORK

Breast cancer is a disease which we hear about a lot nowadays. It is one of the most widespread diseases. There are around 2000+ new cases of breast cancer in men each year, and about 2,30,000 new cases in women every year. Diagnosis of this disease is crucial so that woman can get it treated faster. It is best for a correct and early diagnosis.

The main objective of this research is to help doctors analyze the huge data sets of cancer data and find patterns with the patient’s data and that cancer data available. With this analysis we can predict whether the patient might have breast cancer or not.

Machine learning algorithms will help with this analysis of the data sets. These techniques will be used to predict the outcome. In this study, four machine learning algorithms: Support Vector Machine (SVM), Logistic Regression, Naïve Bayes, and K-Nearest Neighbors (KNN) will be used for numerical dataset and CNN(Convolutional Neural Networks) for image dataset. .The main objective is to analyze the performance of various algorithms in prediction of breast cancer.

This prediction can help doctors prescribe different medical examinations for patients based on the cancer type. This helps save a lot of time as well as money for the patient.

1.3 PROBLEM STATEMENT

In today’s scenario, we have too much delay and inaccuracy in the diagnosis results provided by clinical centers. There are many cases where patients are given wrong inputs regarding their diagnosis and face false-positive or false-negative results which results in either poring the money unnecessarily or even pays for the death due to delay of treatment.

In order to achieve these disadvantages of traditional methodology, Our system proposes an easy approach for clinical examination for breast cancer diagnosis prediction. Using Machine learning and Deep learning algorithms the classifier will be training by the dataset and the classifier will classify the new record values to either benign or malignant tumors. Higher accuracy results will be obtained than traditional methods, which also reduces the patient’s waiting time and increases the life rate of people.

1.4 PROJECT FEATURES

This project scheme was developed to reduce the amount of work for the physicians and other doctors so that they don’t have to conduct many tests on the patients. It also helps minimize the amount of time and money spent by the patients undergoing these tests. As everything is digitalized and based on data analysis, it takes less amount of time to get results. Based on the results, further action can be taken. It also helps researchers in the medical as well as IT sector to understand how different algorithmscan predict different outcomes.

This scheme normally requires a huge amount of data about different patient histories and the cancer details. This data has been collected by many doctors for a long period of time and will be used to do the analysis. This reduces the computational time required to gather all the data necessary.

CHAPTER 2

LITERATURE SURVEY

2.1 DOMAIN SPECIFIC

Literature survey is a very important step in the software development process. Before building any new tool, we need to check the time factor, economy, and company strength. When these things are fulfilled, at that point following stages is to figure out which working framework and language can be utilized for building up thedevice. A lot of help is required for building the tool, internal as well as external. Senior programmers can help and provide this support to the developers from various sources like research papers, books, or online websites. Before building the framework, the above thought are considered for building up the proposed framework.

2.1.1 Machine Learning

Machine Learning is a subcategory of Artificial Intelligence which allows systems to automatically learn and understand data from experience without the system being programmed to do so. It helps software applications become better at predicting outcomes for various types of problems. The basic idea of ML is to take in input dataand use different algorithms to help it predict outcomes and update these outcomes when new data is available as input.

The procedures used with machine learning are like that of data mining and predictivemodeling. Both require scanning through huge amounts of data to search for any typeof pattern in the data and then modify the program accordingly.

Machine Learning has been seen many a times by individuals while shopping on theinternet. They are then shown ads based on what they were searching for earlier on. Thishappens because many of these websites use machine learning to customize the ads based on user searches and this is done in real time. Machine learning has also been used in other various places like detecting fraud, filtering of spam, network security threat detection, predictive maintenance and building news feeds.

Machine Learning methods:

- Supervised learning – Here both the input and output is known. The training dataset also contains the answer the algorithm should come up with on its own. So, a labeled dataset of fruit images would tell the model which photos were of apples, bananas, and oranges. When a new image is given to the model, it compares it to the training set to predict the correct outcome.
- Unsupervised learning – Here input dataset is known but output is not known. A deep learning model is given a dataset without any instructions on what to do with it. The training data contains information without any correct result. The network tries to automatically understand the structure of the model.
- Semi-supervised learning – This type comes somewhere between supervised and unsupervised learning. It contains both labelled and un-labelled data.
- Reinforcement learning – In this type, AI agents are trying to find the best way to accomplish a particular goal. It tries to predict the next step which could possibly give the model the best result at the end.

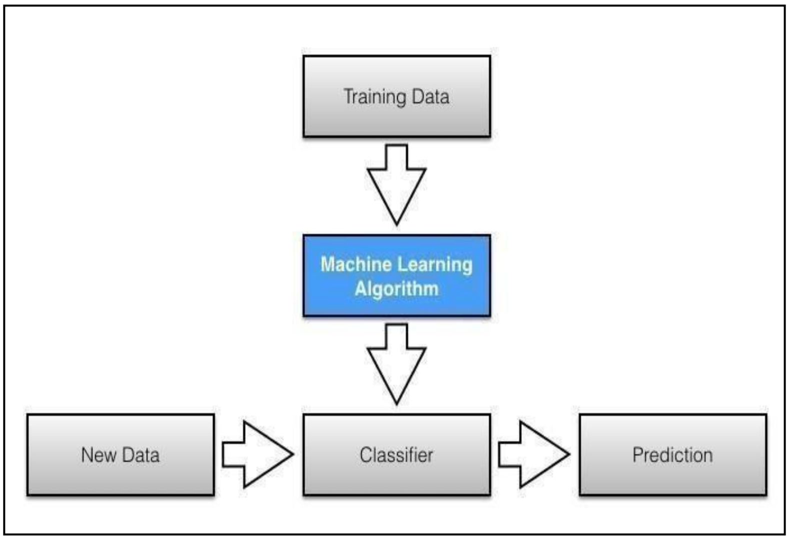


Fig 2.1 ML Architecture

Advantages of ML:

- It gives fast and real-time predictions of problems.
- Efficiently utilizes the resources.
- Helps in automation of different tasks.

- It is used a lot in different sectors of life like business, medicine, sports etc.
- Helps interpret previous behavior of model.

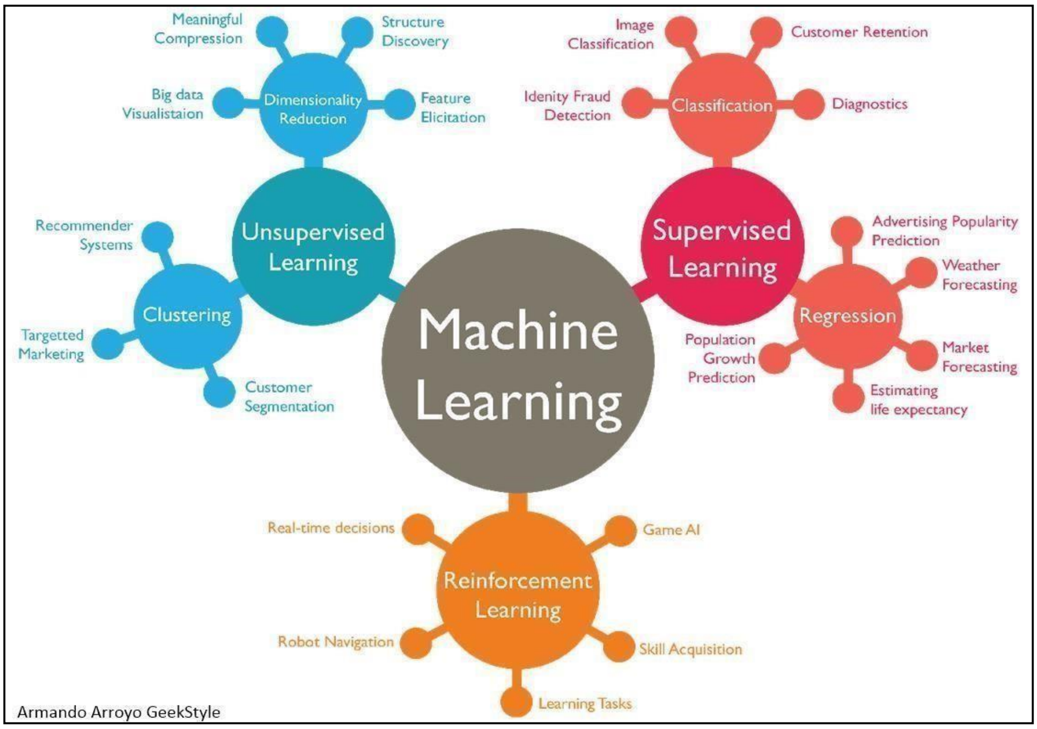


Fig 2.2 Places ML is used.

2.1.2 Convolutional Neural Networks

It is a Deep Learning algorithm which can take in an input image ,assign importance to various aspects in the image and be able to differentiate one form to the other.

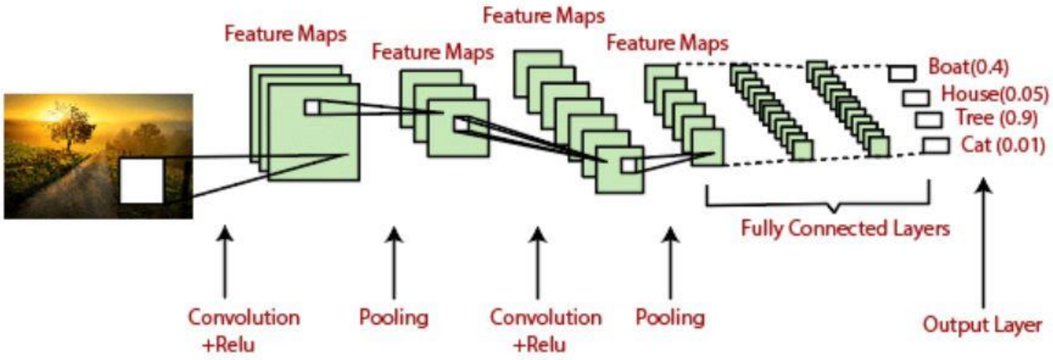


Fig2.3 CNN

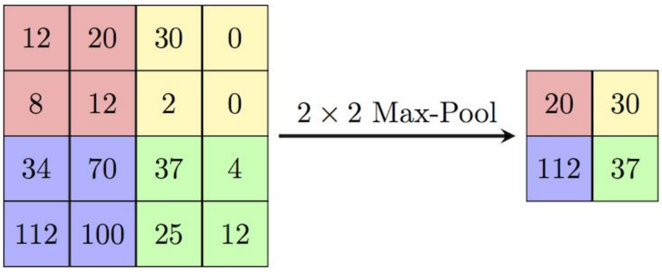
How does CNN work on images?

Template matching: It is a technique used in digital image processing to find out for small parts of an image which will match the template image.

Convolution filters: image filtering is the process of modifying an image by changing its shades or color of pixels.

We usually use 3*3 or 5*5 filter and pass through image extract features from image.

Pooling layer: It is used to reduce the dimensions of the feature maps. So, that number of computations can be reduced.



12	20	30	0
8	12	2	0
34	70	37	4
112	100	25	12

20	30
112	37

The probability of having existence of feature is highest that's why maximum value is taken.

Padding layer: Padding is relevant to CNN as it refers to the amount of pixels ,adding 0s around image when it is being processed by the kernel or filter.

Padding and pooling: There is no learning.

Flattening: It refers to the_converting of high dimensional data into 1-D for inputting it to the next layer. We flatten the output of convolutional layers to create a single long feature vector.

A classification layer computes the cross-entropy loss for classification and weighted classification tasks with mutually exclusive classes.

2.2 EXISTING SYSTEM

Traditionally, the diagnosis of breast cancer and the classification of the cancer as malignant or benign was done by various medical procedures like:

- **Breast exam** – The doctor would check the breasts and lymph nodes in the armpits to check if there are any lumps or abnormalities.
- **Mammogram** – These are like X-ray of the breast. They are used to check whether there is breast cancer or not. If any issues are found, the doctor mayask

the patient to take a diagnostic mammogram to check for further abnormalities.

- **Breast ultrasound -** Ultrasound uses sound waves to produce images to determine whether a new breast lump is a solid mass or a fluid-filled cyst.
- **Removing a sample of breast cells for testing (biopsy) –** This is probably the only definite way of checking if a patient has breast cancer. The doctor uses a specialized needle device guided by X-ray or any other test to take samples of tissues from the area to be checked.
- **MRI of the breasts -** An MRI machine uses a magnet and radio waves to create pictures to see the interiors of the breast tissues.
- Blood tests, CT scans and PET scans are also done to check for breast cancer.

Disadvantages:

- Time consuming.
- Not completely accurate.
- Very expensive.

2.3 LITERATURE REVIEW

The work in this paper is focusing on various models for predicting the time of breast cancer tumor recurrence. Methods include screening the database from GLOBOCAN, CDC, and WHO health repository highlights the lethality of breast cancer, taking thousands of lives each year. However, a timely prediction of cancer can help patients to consult the doctor on time. In the past, various studies have successfully predicted the nature of the tumor to be benign or malignant and if the breast cancer tumor will reoccur or not but, no time-based models have been studied. With the help of Machine Learning, this study shows various prediction models that can be used to predict tumor reoccurrence time as accurately as 1 year. Among the 198 patients analyzed, 40% of the total patients were predicted to have breast cancer tumors reoccurring within 1st year of the diagnosis. The proposed machine learning techniques use various classification models such as Spectral clustering, DBSCAN, and k-means along with prediction models like Support Vector Machines (SVM), Decision trees, and Random Forest. The results demonstrate the ability of the model to predict the time taken by the tumor to reoccur or the time taken by the patient for full recovery with the best accuracy of 78.7% using SVM. This population-based study performed on multivariate real attributed characteristics data can therefore provide the patients a reasonable estimate about their recovery time or the time before which they should consult the doctor.[1]

Priyanka Khanna, Mridu Sahu, Bikesh Kumar Singh, Vikrant Bhatia proposed a model integrating pre-trained Convolutional neural network (CNN) with machine learning for prognosticating pathologic complete response (PCR) using breast cancer dynamic contrast-enhanced magnetic resonance imaging (DCE-MRI) prior to commencement of neoadjuvant chemotherapy (NACT). For predicting pathologic complete response (PCR)using dynamic contrast-enhanced magnetic resonance imaging (DCE-MRI) for breast cancer prior to the start of neoadjuvant chemotherapy,they presented a hybrid model integrating a pre-trained Convolutional neural network (CNN) with machine learning (NACT). In this retrospective study, 64 patients receiving NACT for invasive breast cancer are examined. Deep learning-based pre-trained CNN models ResNet-50 and ResNet-18 were used to extract features from patient visit 1 MRI images (before the initiation of NACT). Mann-Whitney U tests is used to assess features and their relevance(significance level $p<0.05$ and confidence interval is 95%). Furthermore, features extracted and features selected were independently given as an input to different machine learning classifiers for the prediction of response of NACT. Classification performance was assessed under different data division protocols using accuracy, specificity, sensitivity, and area under the receiver operating characteristic curve (AUROC). The proposed model employing DCE-MRI images acquired before starting chemotherapy hasconsiderable accuracy in classifying PCR and non-PCR patients. The efficacy of the prediction model can improve considerably on the back of a larger dataset.[2]

The work on this paper proposes and suggests a unique feature selection method based on the Eagle Strategy (ESO) Optimization, Gravitational Search Optimization (GSO) algorithm, and their hybrid algorithm. They chose this infection as their subject of investigation since the number of women with breast cancer is increasing rapidly on a global scale. After lung cancer, which affects more women than any other kind of cancer, breast cancer is the second leading cause of cancer mortality. The goal of this study is to categorize breast cancer into two groups using the benchmark feature set (Wisconsin Diagnostic Breast Cancer (WDBC)) and to choose the fewest features (feature selection) to achieve maximum accuracy. This work also provides a hybrid technique for finding important features that combines two algorithms, ESO and the GSO algorithm, while reducing insignificant characteristics (features) and complexity Thus, this work presented a new approach for classifying breast cancer tumors. In this research, they coupled soft computing methodologies—our implemented algorithms are applied for the first time to this problem—with artificial intelligence-based machine learning strategies to create a prediction model. The efficacy of the suggested technique was evaluated using WDBC breast cancer data sets, and the findings show that our proposed hybrid algorithm performs very well in breast cancer classification. They havebeen able to attain astonishing results withaccuracy up to 98.9578%, sensitivity up to 0.9705 specificity up to 1.000, precision up to1.000, F1-score up to 0.9696, and an AUC up to 0.9980(close to maximum, i.e., 1.0000). The study's goal is to incorporate our findings into a valid clinical prediction system, allowing visual science specialists to make more accurate and effective judgments in the future. Furthermore, the suggested technology might be used to detect a wide range of diseases.[3]

In this study Mohammed Amine Naji, Sanaa El Filali, Kawtar Aarika, EL Habib Benlahmar, Rachida Ait Abdelouhahid, Olivier Debauche applied five machine learning algorithms: Support Vector Machine (SVM), Random Forest, Logistic Regression, Decision tree (C4.5) and K-Nearest Neighbours (KNN) on the Breast Cancer Wisconsin Diagnostic dataset, after obtaining the results, a performance evaluation and comparison is carried out between these different classifiers. The main objective of this research paperis to predict and diagnosis breast cancer, using machine- learning algorithms, and find outthe most effective whit respect to confusion matrix, accuracy and precision. It is observedthat Support vector Machine outperformed all other classifiers and achieved the highest accuracy (97.2%). All the work is done in the Anaconda environment based on python programming language and Scikit-learn library.[4]

Breast cancer is one of the regularly found cancer in India. In this paper the data mining techniques are used to provide the analysis for the classification and prediction algorithms. The algorithms used here are KNN classification algorithm and KNN prediction algorithm. The algorithms are used to find whether the tumor is either benign or malignant. Data sets are taken from the Wisconsin University database to find the success rate and the error rate. This is used to compare with the original success rate andthe error rate.[5]

Information in digital mammogram images has been shown to be associated with the risk ofdeveloping breast cancer. Longitudinal breast cancer screening mammogram examinations may carry spatiotemporal information that can enhance breast cancer risk prediction. No deep learning models have been designed to capture such spatiotemporal information over multiple examinations to predict the risk. Saba Dadsetan, Dooman Arefan, Wendie A. Berg, Margarita L.Zuley, Jules H. Sumkin, Shandong Wu proposed a novel deep learning structure, LRP-NET, to capture the spatiotemporal changes of breast tissue over multiple negative/benign screening mammogram examinations to predict near-term breast cancer risk in a case-control setting. Specifically, LRP-NET is designed based on clinical knowledge to capture the imaging changes of bilateral breast tissue over four sequential mammogram examinations. They evaluated proposed model with two ablation studies and compare it to three models/settings, including 1) a“loose” model without explicitly capturing the spatiotemporal changes over longitudinal examinations, LRP-NET but using a varying number of sequential examinations, and a previous model that uses only a single mammogram examination. On a case-control cohort of 200 patients, each with four examinations, experiments on a total of 3200 images show that the LRP-NET model outperforms the compared models/settings.[6]

Generative adversarial networks (GAN) can learn from a set of training data andgenerate new data with the same characteristics as the training data. Based on the characteristics of GAN, this paper developed its capability as a tool of disease prognosis prediction and proposed a prognostic model PregGAN based on conditional generative adversarial network (CGAN). The idea of PregGAN is to generate the prognosis prediction results based on the clinical data of patients. PregGAN added the clinical data as conditions to the training process. Conditions were used as the input to the generator along with noises. The generator synthesized new samples using the noises vectors and the conditions. In order to solve the mode collapse problem during PregGAN training, Wasserstein distance and gradient penalty strategy were used to make the training process more stable. Results: In the prognosis prediction experiments using the METABRIC breast cancer dataset, PregGAN achieved good results, with the average accurate (ACC) of 90.6% and the average AUC (area under curve) of 0.946. Conclusions: Experimental results show that PregGAN is a reliable prognosis predictive model for breast cancer. Due to the strong ability of probability distribution learning, PregGAN can also be used for the prognosis prediction of other diseases.[7]

Osayba Al-Azzam, Ibrahem Shatnawi used nine machine learning classification algorithms for supervised and semi-supervised learning 1) Logistic regression; 2) Gaussian Naive Bayes; 3) Linear Support vector machine; 4) RBF Support vector machine; 5) Decision Tree; 6) Random Forest; 7) Xgboost; 8) Gradient Boosting; 9) KNN. The Wisconsin Diagnosis Cancer dataset was used to train and test these models. To ensure the robustness of the model, they have applied K-fold cross-validation and optimized hyperparameters. They have evaluated and compared the models using accuracy, precision, recall, F1-score, and ROC curves to compare and evaluate the performance and accuracy of the key supervised and semi-supervised machine learning algorithms for breast cancer prediction. The SSL has high accuracy (90%–98%) with justhalf of the training data. The KNN model for the SL and logistic regression for the SSL achieved the highest accuracy of 98%. Using a small sample of labeled and low computational power, the SSL is fully capable of replacing SL algorithms in diagnosing tumor type.[8]

Computer-assisted pathology analysis is an emerging field in health informatics and extremely important for effective treatment. Herein, Shallu Sharma, Sumit Kumar demonstrated the ability of the pre-trained Xception model for magnification-dependent breast cancer histopathological image classification in contrast to handcrafted approaches. The Xception model and SVM classifier with the ‘radial basis function’ kernel has achieved the best and consistent performance with the accuracy of 96.25%, 96.25%, 95.74%, and 94.11% for 40X, 100X, 200X and 400X level of magnification, respectively. A comparison with existing state-of-the-art techniques has been conducted based on accuracy, recall, precision, F1 score, area under ROC and precision–recall curve evaluation metrics.[9]

Breast cancer (BC) is the most found disease among women all over the world.The early diagnosis of breast cancer can potentially reduce the mortality rate and increasethe chances of a successful treatment. The paper which is proposed by V.Nanda Gopal, Fadi Al-Turjman, R.Kumar, L. Anand, M. Rajesh, focuses on proposing a methodology to conduct early diagnosis of breast cancer using the Internet of Things and Machine Learning. The main objective of this paper is to explore the machine learning techniquesin predicting breast cancer with IoT devices. The proposed classifier resulted in 98%, 97%, 96% and 98% of precision, recall, F_Measure and accuracy, respectively. The minimum error rate for the classifier has also been determined and found to be

34.21%, 45.82%8, 64.47% of Mean Absolute Error (MAR), Root Mean Square Error (RMSE) and Relative Absolute Error (RAE), respectively. It was evident through the obtained results that the MLP classifier yields a higher accuracy with a minimum error rate when compared to LR and RF. [10]

Feature selection helps select an optimal subset of features from a large feature space to achieve better classification performance. The performance of KNN classifier can beimproved significantly using an appropriate subset of features from a large feature space.Recent development in General Purpose Graphics Processing Units (GPGPU) has provided us with low cost yet high-performance computing support for wide range of applications. The paper purposed by Shashank Shekhar,Nazrul Hoque, Dhruba K. Bhattacharyya presented a parallel KNN classifier powered by a mutual information based feature selection called PKNN-MIFS for effective classification of real life data. It selects an optimal subset of features from the original feature set by exploiting the mutual information concept for the estimation of feature-class and feature-feature relevance. It selects non-redundant features by giving higher priority on feature-classrelevance. The performance of the proposed PKNN-MIFS has been evaluated over several datasets and has been found to be superior to its closed counterpart.[11]

The study proposed by Abdul Majid, Safdar Ali, Mubashar Iqbal, Nabeela Kausar presents a novel prediction approach for human breast and colon cancers using different feature spaces. The proposed scheme consists of two stages: the preprocessor and the predictor. In the preprocessor stage, the mega-trend diffusion (MTD) technique is employed to increase the samples of the minority class, thereby balancing the dataset. In the predictor stage, machine-learning approaches of K-nearest neighbor (KNN) and support vector machines (SVM) are used to develop hybrid MTD-SVM and MTD-KNN prediction models. MTD-SVM model has provided the best values of accuracy, G-mean and Matthew's correlation coefficient of 96.71%, 96.70% and 71.98% for cancer/non-cancer dataset, breast/non-breast cancer dataset and colon/non-colon cancer dataset, respectively. They found that hybrid MTD-SVM is the best with respect to prediction performance and computational cost. MTD-KNN model has achieved moderately better prediction as compared to hybrid MTD-NB (Naïve Bayes) but at the expense of higher computing cost. MTD-KNN model is faster than MTD-RF (random forest) but its prediction is not better than MTD-RF. To the best of our knowledge, the reported results are the best results, so far, for these datasets. The proposed scheme indicates that the developed models can be used as a tool for the prediction of cancer. This scheme may be useful for study of any sequential information such as protein sequence or any nucleic acid sequence.[12]

Predictive models for the occurrence of cancer symptoms by using machine learning (ML) algorithms could be used to aid clinical decision-making in order to enhance the quality of cancer care. This study aimed to develop and validate a selection of classification models that used ML algorithms to predict the occurrence of breast cancer- related lymphedema (BCRL) among Chinese women. This was a retrospective cohort study of consecutive cases that had been diagnosed with breast cancer, stages I-IV. Forty-Evariables were grouped into five feature sets. Five classification models with

ML algorithms were developed, and the models' performance and the variables’ relative importance were assessed accordingly. Of 370 eligible female participants, 91 had BCRL (24.6%). The mean age of this study sample was 49.89 (SD = 7.45). All participants had had breast cancer surgery, and more than half of them had had a modified radical mastectomy (n = 206, 55.5%). The mean follow-up time after breast cancer surgery was 28.73 months (SD = 11.71). Most of the tumors were either stage I (n = 49, 31.2%) or stage II (n = 252, 68.1%). More than half of the sample had had postoperative chemotherapy (n = 227, 61.4%). Overall, the logistic regression model achieved the best performance in terms of accuracy (91.6%), precision (82.1%), and recall (91.4%) for BCRL. Although this study included 48 predicting variables, we found that the five models required only 22 variables to achieve predictive performance. The most important variable was the number of positive lymph nodes, followed in descending order by the BCRL occurring on the same side as the surgery, a history of sentinel lymph node biopsy,a dietary preference for meat and fried food, and an exercise frequency of less than three times per week. These factors were the most influential predictors for enhancing the ML models’ performance. This study found that in the ML training dataset, the multilayer perceptron model and the logistic regression model were the best discrimination models for predicting the outcome of BCRL, and the k-nearest neighbors and support vector machine models demonstrated good calibration performance in the ML validation dataset.Future research will need to use large-sample datasets to establish a more robust ML model for predicting BCRL deeply and reliably.[13]

The KNN classification algorithm is one of the most used algorithms in the AI field. This paper proposes two improved algorithms, namely KNNTS, and KNNTS-PK+.The two improved algorithms are based on KNNPK+ algorithm, which uses PK-Means++ algorithm to select the center of the spherical region and sets the radius of the region to form a sphere to divide the data set in the space. The KNNPK+ algorithm improves classification accuracy on the premise of stabilizing the classification efficiency of KNN classification algorithm. In order to improve the classification efficiency of KNN algorithm on the premise that the accuracy of KNN classification algorithm remains unchanged, KNNTS algorithm is proposed. It uses tabu search algorithm to select the radius of spherical region and uses spherical region division method with equal radius todivide the data set in space. Based on the first two improved algorithms, KNNTS- PK+ algorithm combines them to divide the data sets in space. Experiments are carried out on the new data set and the classification results are obtained. Results revealed show that the two improved algorithms can effectively improve the classification accuracy andefficiency after the data samples are cut reasonably.[14]

Breast cancer is the second prevalent type of cancer among women. Breast Ultrasound (BUS) imaging is one of the most frequently used diagnostic tools to detect and classify abnormalities in the breast. To improve the diagnostic accuracy, the Computer Aided Diagnosis (CAD) system is helpful for breast cancer detection and classification. Normally, a CAD system consists of four stages: pre-processing, segmentation, feature extraction, and classification. In this paper, the pre-processing step includes speckle noiseremoval using Speckle Reducing Anisotropic Diffusion (SRAD). The goal of segmentation is to locate the Region of Interest (ROI) and Active contour-based segmentation is used in this work. The texture features are extracted and fed to a classifierto categorize the images as Normal, Benign and Malignant. In this work three classifiers namely K-Nearest Neighbors (KNN) algorithm, Decision tree algorithm and Random Forest classifier are used, and the performance is compared based on the accuracy of classification.[15]

2.4 PROPOSED SYSTEM

In the proposed system we plan on using existing data of breast cancer patients whichhas been collected for several years and run different machine learning algorithms on them. These algorithms will analyze the data from the datasets to predict whether the patient has breast cancer or not and it will also tell us if the canceris malignant or benign.

It is done by taking the patient's data and mapping it with the dataset and SSSL checking whether there are any patterns found with the data. If a patient has breast cancer, then instead of taking more tests to check whether the cancer is malignant or benign, ML can be used to predict the case based on the huge amount of data on breast cancer. This proposed system helps the patients as it reduces the amount of money they needto spend just for the diagnosis.

Also, if the tumor is benign, then it is not cancerous, and the patient doesn't needto go through any of the other tests. This saves a lot of time as well.

Advantages:

- Reduces costs for medical tests.
- Does not take a huge amount of time.
- Intelligent way of using available data.

2.5 MODULE DESCRIPTION

- **DATASET**

Numerical Dataset

The Wisconsin Diagnostic Breast Cancer (WDBC) dataset which can be found in University of California, Irvin's Machine Learning Dataset Repository will be used for this project. All ML algorithms will be performed on this dataset. The features which are in the dataset were computed from a digitized image of a fine needle aspirate (FNA) of a breast mass. These features describe different characteristics of the cell nuclei found in the image. There are 569 data points in the dataset: 357 for Malignant and 212 for Benign.

The dataset contains these features:

- Radius
- Texture
- Perimeter
- Area
- Smoothness

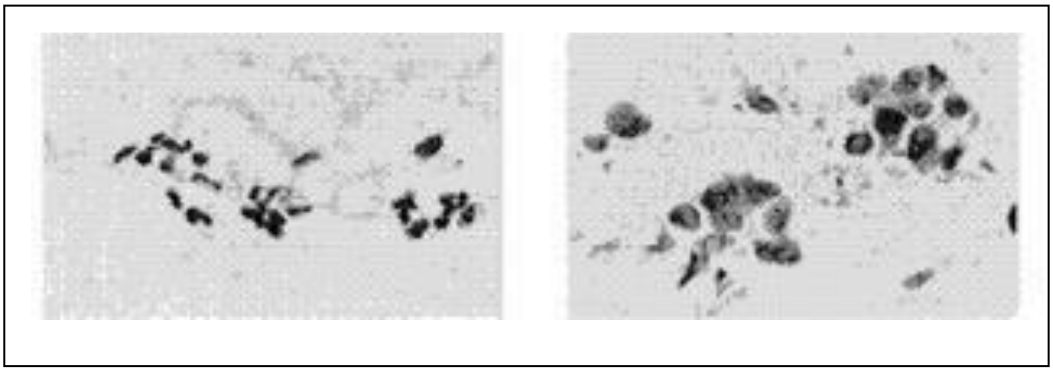


Fig 2.3 Digitized images of FNA (a) Benign (b) Malignant

- Compactness
- Concavity
- Concave points
- Symmetry
- Fractal dimension

Each of these features have information on mean, standard error, and “worst” or largest. (Mean of the three largest values) computed. Hence, the dataset has a total of 30 features.

Features description

Radius	Mean of distances from center to points on the perimeter.

Texture	Standard deviation of gray-scale values
Perimeter	The total distance between the snake points constitutes the nuclear perimeter.
Area	Number of pixels on the interior of the snake and adding one-half of the pixel in the perimeter.
Smoothness	Local variable in radius length, qualified by measuring the difference between the length of a radial line and the mean length of lines surrounding it.
Compactness	Perimeter ^ 2 / area
Concavity	Severity of concave portions of the contour
Concave points	Number of concave portions of the contour
Symmetry	The length difference between lines perpendicular to the major axis to the cell boundary in both directions.
Fractal dimension	Coastline approximation. A higher value corresponds to a less regular contour and thus to a higher probability of malignancy.

Table 2.1 Description of features used in the dataset.

Image dataset

Breast histopathology image dataset is taken from Kaggle. The dataset consists of both malignant and benign images. IDC is the most common type of all breast cancers. The original dataset consisted of 162 whole mount slide images of breast cancer specimens which were scanned at 40x.

We have taken 615 images of benign and 587 images of malignant.

All images were labelled as 1(IDC positive) or 0 (IDC negative).

The following figure presents examples of positive and negative tissues.

Examples of IDC (+) and IDC(-).

(a) (b)

(a) IDC (+) tissue and (b) IDC(-) tissue.

ARTIFICIAL NEURAL NETWORKS

Artificial neural networks are a very important tool used in machine learning. This technique, as the name suggests, is inspired by the brain and its activities. They were designed in a way to replicate the way humans learn. Neural networks normally consist of input as well as output layers, and sometimes a hidden layerconsisting of units that change the input into something that the output layer canuse. These tools help in finding different patterns which are too hard for a human to find himself. A programmer programs the machine to recognize it.

ML ALGORITHM

K-NEAREST NEIGHBOUR

This algorithm is one of the simplest Machine learning techniques. It is a lazy learning algorithm used for regression and classification. It classifies the objects using their “k” nearest neighbors. k-NN only considers the neighbors around theobject, not the underlying data distribution. If k = 1, it basically assigns the unknown to the class of the nearest neighbor. If k > 1, the classification is decided by majority vote based on the k nearest neighbor prediction result. Both for classification and regression, a useful technique can be used to assign weight to the contributions of the neighbors, so that the nearer neighbors contribute more to the average than the more distant ones. For example, a common weighting scheme consists in giving each neighbor a weight of 1/*d*, where *d* is the distance to the neighbor.

When KNN is used for classification, the output can be calculated as the class with the highest frequency from the K-most similar instances. Each instance inessence votes for their class and the class with the most votes is taken as the prediction. If you are using K and you have an even number of classes, it is a good idea to choose a K value with an odd number to avoid a tie. And on the inverse, usean even number for K when you have an odd number of classes. Ties can be broken consistently by expanding K by 1 and looking at the class ofthe next most similar instance in the training dataset.

Here are some things to keep in mind:

- As we decrease the value of K to 1, our predictions become less stable.
- Inversely, as we increase the value of K, our predictions become more stable due to majority voting / averaging, and thus, more likely to make more accurate predictions (up to a certain point). Eventually, we begin to witness an increasing number of errors. It is at these points we know we have pushed the value of K toofar.
- In cases where we are taking a majority vote (e.g., picking the mode in a classification problem) among labels, we usually make K an odd number tohave a tiebreaker.

Advantages:

- The algorithm is simple and easy to implement.
- There's no need to build a model, tune several parameters, or make additional assumptions.
- The algorithm is versatile. It can be used for classification, regression, and search.

Disadvantage

- The algorithm gets significantly slower as the number of examples and/or predictors/independent variables increase.

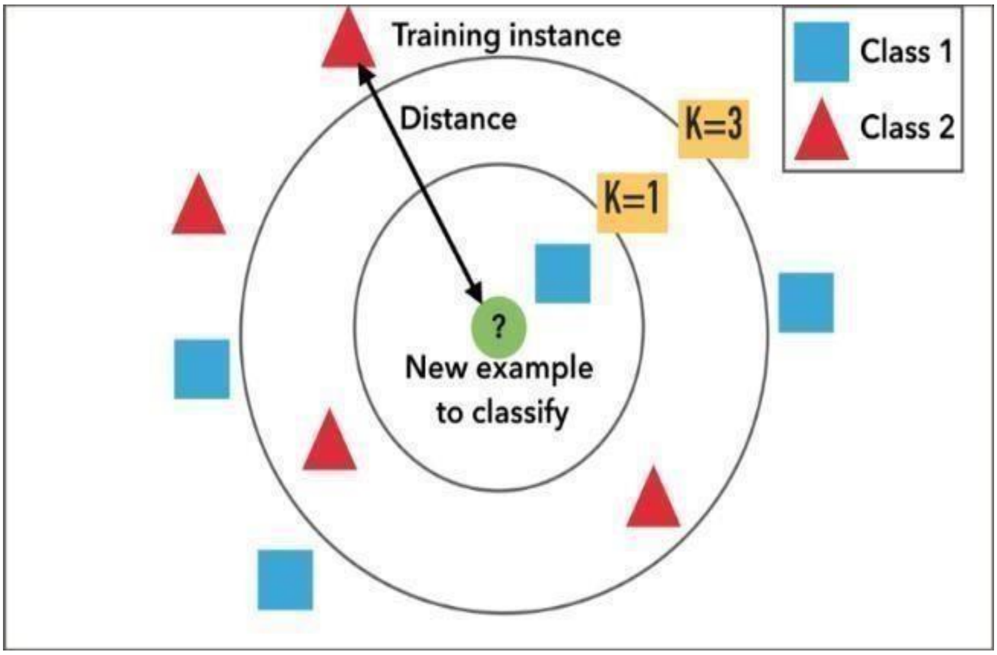


Fig 2.4 K-NN

SUPPORT VECTOR MACHINE (SVM)

SVM is a set of related supervised learning methods used in medical diagnosis for classification and regression. SVM simultaneously minimizes the empirical classification error and maximizes the geometric margin. So SVM is called Maximum Margin Classifiers. SVM is a general algorithm based on guaranteed risk bounds of statistical learning theory i.e., the so-called structural risk minimization principle. SVMs can efficiently perform non-linear classification using what is called the kernel trick, implicitly mapping their inputs into high-dimensional feature spaces. The kernel trick allows constructing the classifier without explicitly knowing the feature space. An SVM model is a representation of the examples as points in space, mapped so that the examples of the separate categories are divided by a clear gap that is as wide as possible. For example, given a set of points belonging to either one of the two classes, an SVM finds a hyperplane having the largest possible fraction of points of the same class on the same plane. This separating hyperplane is called the optimal separating hyperplane (OSH) that maximizes thedistance between the two parallel hyperplanes and can minimize the risk of misclassifying examples of the test dataset.

Advantages

- It is a decision-maker with a smaller dataset as it is memory efficient (stores supportvector values).
- It requires less time forprocessing.

Drawbacks

- Overfitting occurs if no of variables > no of samples.

- Instead of direct probability, it uses expensive cross-validation for probability checking.

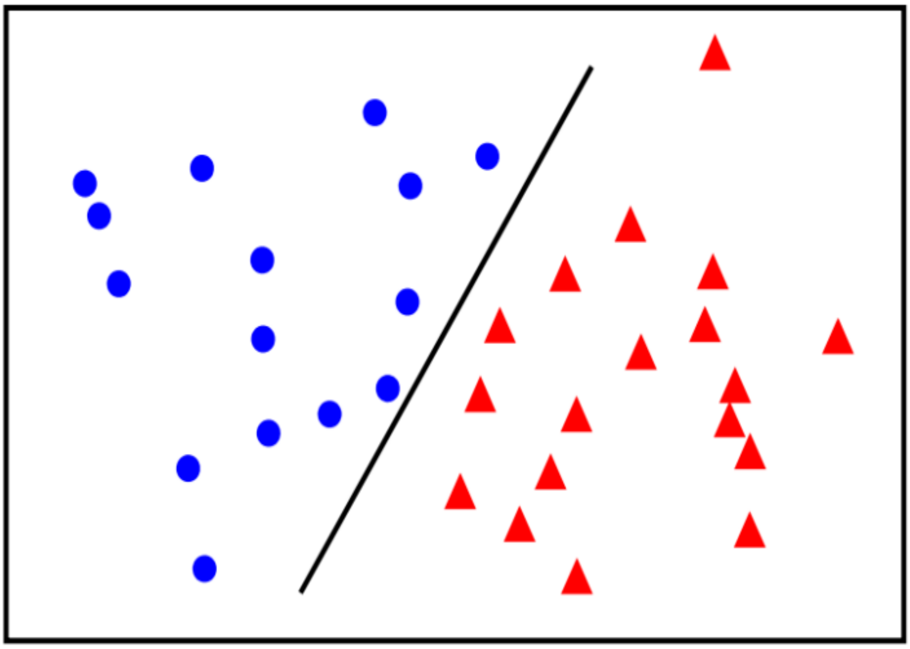


Fig.2.5 SVM

NAIVE BAYES ALGORITHM

Naïve Bayes algorithm is a supervised learning algorithm, which is based on Bayes theorem and used for solving classification problems. It is mainly used in text classification that includes a high-dimensional training dataset. Naïve Bayes Classifier is one of the simplest and most effective Classification algorithms which helps in building fast machine learning models that can make quick predictions. It is a probabilistic classifier, which means it predicts based on the probability of an object. Some popular examples of Naïve Bayes Algorithm are spam filtration, Sentimental analysis, and classifying articles.

The Naïve Bayes algorithm is comprised of two words Naïve and Bayes, which can be described as:

- **Naïve:** It is called Naïve because it assumes that the occurrence of a certain feature is independent of the occurrence of other features. Such as if the fruit is identified on the bases of color, shape, and taste, then red, spherical, and sweet fruit is recognized as an apple. Hence each feature individually contributes to identifying that it is an apple without depending on each other.

- **Bayes:** It is called Bayes because it depends on the principle of Bayes' Theorem.

Bayes' Theorem:

Bayes' theorem is also known as Bayes' Rule or Bayes' law, which is used to determine the probability of a hypothesis with prior knowledge. It depends on the conditional probability.

The formula for Bayes' theorem is given as:

$$\mathrm{P(A|B)}= \frac{P(B|A)P(A)}{P(B)}$$

Here,

- P(A|B) is Posterior probability: Probability of hypothesis A on the observed event B.

- P(B|A) is Likelihood probability: Probability of the evidence given that the probabilityof a hypothesis is true.

- P(A) is Prior Probability: Probability of hypothesis before observing the evidence.
- P(B) is Marginal Probability: Probability of Evidence.

Advantages

- Naïve Bayes is one of the fast and easy ML algorithms to predict a class of datasets.
- It can be used for Binary as well as Multi-class Classifications.
- It performs well in multi-class predictions as compared to the other Algorithms.
- It is the most popular choice for text classification problems.

Disadvantages

- Naive Bayes assumes that all features are independent or unrelated, so it cannot learn the relationship between features.

LOGISTIC REGRESSION

Logistic regression is one of the most popular Machine Learning algorithms, which comes under the Supervised Learning technique. It is used for predicting the categorical dependent variable using a given set of independent variables. It predicts the output of a categorical dependent variable. Therefore, the outcome must be of a categorical or discrete value. It can be either Yes or No, 0 or 1, true or False, etc. but instead of giving the exact value as 0 and 1, it gives the probabilistic values which lie between 0 and 1. Logistic Regression is much like Linear Regression except that how they are used. Linear Regression is used for solving Regression problems, whereas Logistic regression is used for solving the classification problems. Logistic Regression is a significant machine learning algorithm because it can provide probabilities and classify new data using continuous and discrete datasets. Logistic Regression can be used to classify the observations using different types of data and can easily determine themost effective variables used for the classification. Logistic regression uses the concept of predictive modeling as regression; therefore, it is called logistic regression, but is used to classifysamples; Therefore, it falls under the classification algorithm.

Advantages

- Performs well on low-dimensional data.
- Very efficient when the dataset has features that are linearlyseparable.
- Outputs well-calibrated probabilities along with classification results.

Disadvantages

- Assumes linearity between dependent and independentvariables.
- Fails to capture complex relationships.

2.6 SOFTWARE DESCRIPTION

PYTHON

Python is a translated, question situated, abnormal state programming dialect with dynamic semantics. Its abnormal state worked in information structures, joined with dynamic composing and dynamic authoritative, make it exceptionally appealing for Rapid Application Development, and for use as a scripting or paste dialect to interface existing parts together. Python's straightforward, simple to learn sentence structure accentuates intelligibility and subsequently decreases the expense of program upkeep. Python underpins modules and bundles, which energizes program seclusion and code reuse. The Python mediator and the broad standard library are accessible in source or parallel frame without charge for every single significant stage and can be openly disseminated.

SCIKIT-LEARN

Scikit-learn is a free software machine learning library for the Python programming language. It features various classification, regression and clustering algorithm including support vector machines, random forests, gradient boosting, *k*-means and DBSCAN, and is designed to interoperate with the Python numerical and scientific libraries NumPy and SciPy. The scikit-learn project started as scikits. learn, a Google Summer of Code project by David Cournapeau. Its name stems from the notion that it is a "SciKit" (SciPy Toolkit), a separately developed and distributed third-party extension to SciPy. The original codebase was later rewritten by other developers. Of the various scikits, scikit-learn as well as scikit-image were described as "well- maintained and popular" in November 2012. As of 2018, scikit-learn is under active development.

CHAPTER 3

REQUIREMENT ANALYSIS

3.1 METHODOLOGY FOLLOWED

The steps followed to do this project are:

1 Dataset collection: Numerical data set for evaluating the performance of various machine learning algorithms WBCD repository provided the numerical dataset. Features are composed of fine needle aspirate (FNA) of a breast mass. There are 30 features that were extracted to describe characteristics of cell nuclei present in the scanned images. The data set consists of 569 patients ,212 have an outcome of malignancy and 357 are Benign. The classes in the data set are separated into 2 or 4 groups, with 2 corresponding to the benign case and 4 corresponding to the malignant case.

Breast histopathology image dataset is taken from Kaggle. The dataset consists of both malignant and benign images. IDC is the most common type of all breast cancers. The original dataset consisted of 162 whole mount slide images of breast cancer specimens which were scanned at 40x. 615 images of benign and 587 images of malignant are taken.

2. Data cleaning: The term "data pre-processing" refers to the process of converting unstructured data to structured data, as well as resizing and removing undesirable data from a data set. The data set's missing traits are replaced by the mean value. The data is then randomly selected from the data set to ensure that the data is circulated properly.

3. Training and Testing: Training phase extracts the features from the data set, and the testing phase will deliver new data to be examined to see how well our algorithm works and behaves when it comes to prediction.

4. Proposed Method for Numerical Data set: In Numerical data set we are using 4 different algorithms and identifying which algorithm is suitable for the data set and gives the most accurate output. Algorithms used are SVM, KNN, Logistic regression and Naïve bayes.

5. **Proposed Method for Image Data set:** We are utilizing the CNN algorithm for analysis and prediction in this proposed model. Dataset is divided into three sets:

train set shape: (1028, 2)
test set shape: (61, 2)
validation set shape: (115, 2)

Then, data augmentation is done for increasing training set by creating modified copies of a dataset using existing data. Training (batch size=32), validation (batch size=16) and testing (batch size=16). Binary is chosen as class mode as we have two classes Benign and malignant. We have used Transfer learning (reuse of a previously learned model on a new problem).

CNN Model has layers namely input, Global average pooling and output, which are checked with a dropout regularization of 20% to cancel overfitting. Sigmoid activation function is used. The model has been trained with 100 epochs.

3.2 FUNCTIONAL REQUIREMENTS

The functional requirement defines the system or the components of the system. A function is basically inputs, behaviors, and outputs. Stuff that can be called functional requirements are calculations, technical details, data manipulation and processing. It tells us what a system is supposed to do.

Here, the system must perform the following tasks:

- Understand all the features as well as the data provided in the dataset.
- Map the data in the dataset with the given input data. Find patterns, if any,with both the dataset as well as input data.
- Check whether the input data of a patient will result in the diagnosis ofbreast cancer or not.
- If breast cancer is diagnosed, provide information on the type of breastcancer, i.e., benign, or malignant.
- Provide the percentage accuracy of the proposed prediction.

3.3 NON- FUNCTIONAL REQUIREMENTS

A non-functional requirement is a requirement that gives the criteria that can be used to judge how well a system can function. It comes under system/requirements engineering. It gives a judgement on the overall unlike functional requirements which define specific behavior or functions. Functional requirements are implemented by using the system design whereas system architecture is what is used for implementingthe non-functional requirements.

Non-functional requirements are also called constraints. Some of the quality attributes are as follows:

3.3.1 ACCESSIBILITY:

Accessibility is a term that is used to describe if a product or software is accessible to the public and how easily it can be accessed. It is easy to access as the dataset is open source and can be found on the University of California, Irvin’s ML dataset repository. Unlike breast cancer diagnosis tests in hospitals which cost a lot, anyone can access this dataset for free.

3.3.2 MAINTAINABILITY:

Maintainability tells us how easily a software or tool or system can be modified to:

(a) Correct defects. (b) Meet new requirements.

Different programming languages can be used to make the predictive model based on the programmer’s wishes. The datasets can also be modified, and new data can be added as and when the data is updated by doctors. Different ML algorithms can also be used to check which algorithm will give the best result.

As python programming language that can adapt to new changes easily, it is easy to maintain this type of system.

3.3.3 SCALABILITY:

The system can work normally under situations such as low bandwidth and huge datasets. The R studio as well as Excel can take care of these data and can perform the algorithms with ease.

3.3.4 PORTABILITY:

Portability is a feature which tells us about the ease at which we can reuse an existingpiece of code when we move from one location or environment to some other.

This system uses python and R programming languages, and they can be executed under different operation conditions provided it meets its minimum configurations. Only system files and dependent assemblies would have to be configured in such a case.

3.4 HARDWARE REQUIREMENTS

- Processor: Any Processor above 500 MHz
- RAM: 512Mb
- Hard Disk: 10 GB
- Input device: Standard Keyboard and Mouse
- Output device: VGA and High-Resolution Monitor

3.5 SOFTWARE REQUIREMENTS

- Operating System: Linux, Windows (8,7,10,11) [Anyone]
- Application Required: PyCharm
- Technology: Python language
- Library Used: NumPy, Pandas, SkLearn
- Framework: Flask

3.6 Feasibility Study

Feasibility Study is a study to evaluate feasibility of proposed project or system. As the name suggests, feasibility study is the feasibility analysis, or it is a measure of the software product in terms of how much beneficial product development will be for the organization from a practical point of view. Feasibility study is carried out based on many purposes to analyze whether software product will be right in terms of development, implantation, contribution of project to the organization etc.

3.6.1 Technical feasibility

This project scheme was developed to reduce the amount of work for the physicians and other doctors so that they don’t have to conduct many tests on the patients. It also helps minimize the amount of time and money spent by the patients undergoing these tests. As everything is digitalized and based on data analysis, it takes less amount of time to get results. Based on the results, further action can be taken. It also helps researchers in the medical as well as IT sector to understand how different algorithms can predict different outcomes.

3.6.2 Operational Feasibility

This prediction can help doctors prescribe different medical examinations for patients based on the cancer type. This helps save a lot of time as well as money for the patient. These tools can help discover and identify patterns and relationships between cancer data, from huge datasets, while they are able to effectively predict future outcomes of a cancer type. Patients must spend a lot of money on different tests and treatments to check whether they have breast cancer or not. These tests can take a long time and the results can be delayed. Also, after confirmation that the patient has cancer, more tests need to be done to check whether the cancer is benign or malignant.

3.6.3 Behavioral Feasibility

This scheme normally requires a huge amount of data about different patient histories and the cancer details. This data has been collected by many doctors for a long period of time and willbe used to do the analysis. This reduces the computational time required to gather all the data necessary.

CHAPTER 4

DESIGN

4.1 DESIGN GOALS

Under our model, the goal of our project is to create a design to achieve the following:

4.1.1 ACCURACY

Only accurate outcomes can help make this model a good one. It can be reliable only when all the outcomes are correct and can be trusted. As this data is required for healthcare purposes, it is important that no errors occur.

4.1.2 EFFICIENCY

The model should be efficient as there is no requirement of manual data entry work or any work by doctors. It takes less time to predict outcomes after all the ML algorithms have been used on the data.

4.2 SYSTEM ARCHITECTURE

4.2.1 Numerical dataset

This project has UI, and the architecture is basically the dataset and the features of the dataset. It is trying to understand the dataset and try making the system as simpleand easy as possible.

The dataset is first split into a training and testing set. The training set is first exposed to the machine learning algorithms so that the system understands what data gives what type of outcome.

After the system is trained, the testing data is used to test whether the system can correctly predict the class of the data. It checks the percentage accuracy of the model.

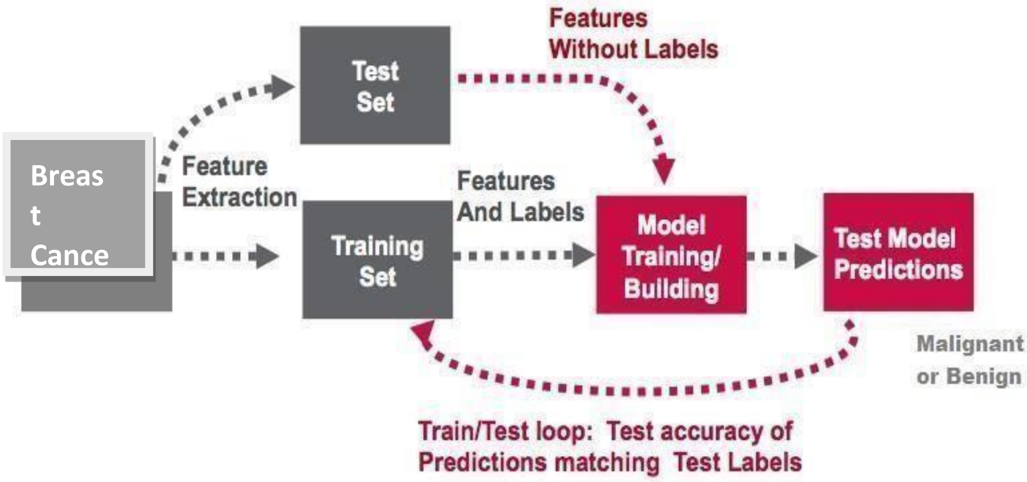


Fig 4.1 System Architecture

4.2.2 Image dataset

Dataset is divided into three sets:

train set shape: (1028, 2)
test set shape: (61, 2)
validation set shape: (115, 2)

Then, data augmentation is done for increasing training set by creating modified copies of a dataset using existing data.

training (batch size=32), validation (batch size=16) and testing (batch size=16). Binary is chosen as class mode as we have two classes Benign and malignant.

We have used Transfer learning (reuse of a previously learned model on a new problem).

CNN Model has layers namely input, Global average pooling and output, which are checked with a dropout regularization of 20% to cancel overfitting. Sigmoid activation function is used. This model has been trained with 100 epochs.

4.3 DATA FLOW DIAGRAM

The data flow diagram shows the way in which the data from the dataset moves.

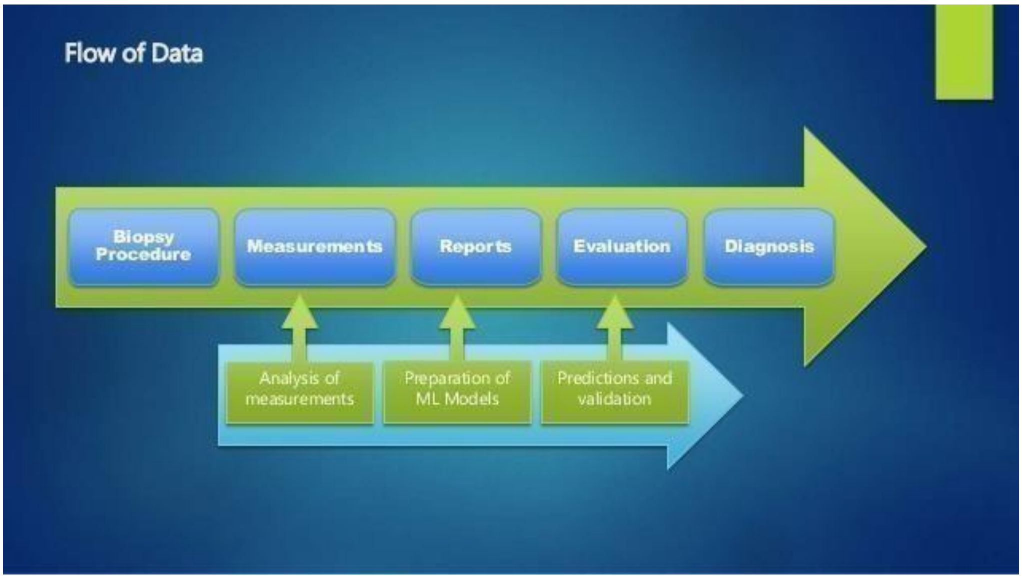

Flow of Data

Fig 4.2 Data Flow Diagram

4.4 EXPECTED OUTCOME

Numerical dataset

The outcome of this model is to correctly check and predict whether a patient has breast cancer or not. If yes, the model should also be able to tell if the patient has malignant or benign type of cancer.

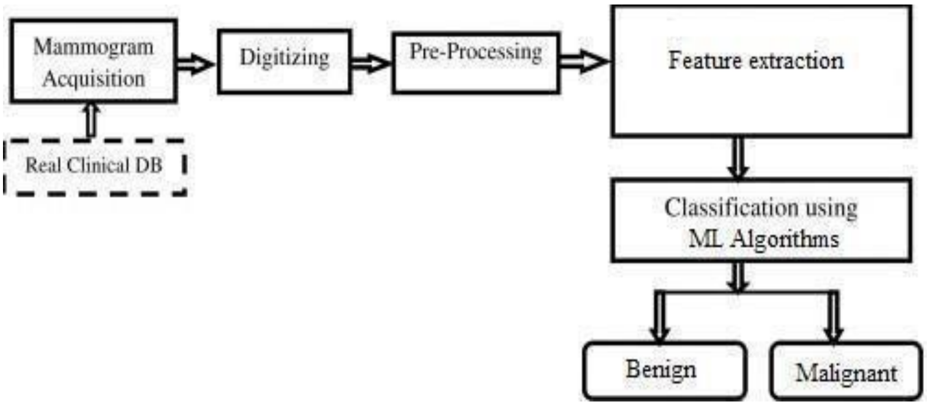
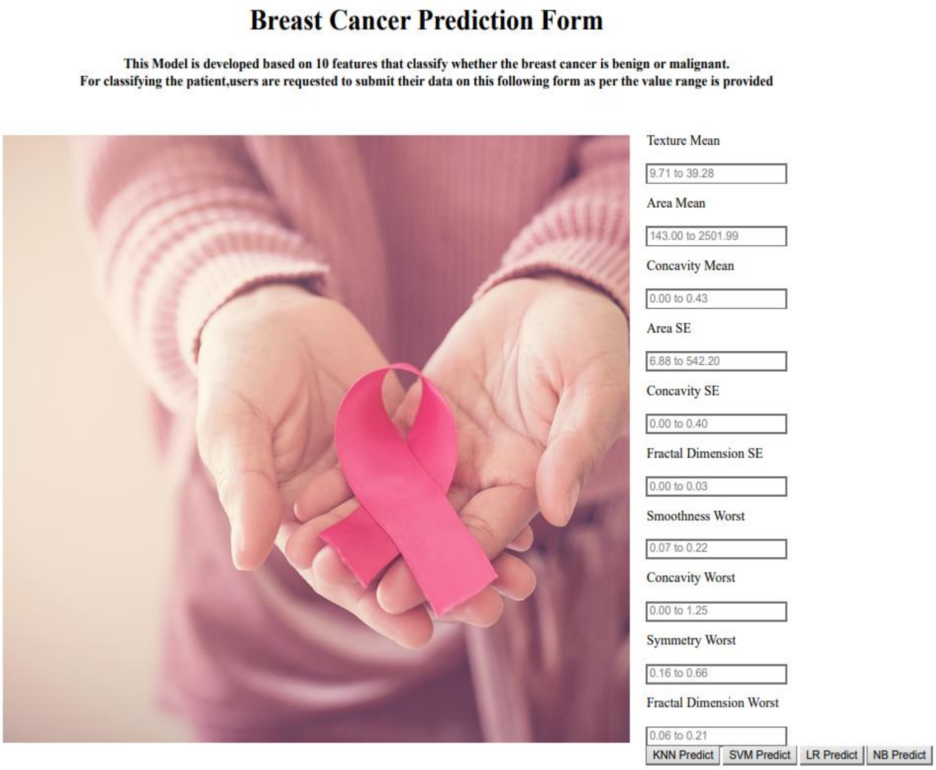


Fig 4.3 Expected Outcome

Input Form



Breast Cancer Prediction Form

This Model is developed based on 10 features that classify whether the breast cancer is benign or malignant.
For classifying the patient,users are requested to submit their data on this following form as per the value range is provided

Texture Mean

9.71 to 39.28

Area Mean

143.00 to 2501.99

Concavity Mean

0.00 to 0.43

Area SE

6.88 to 542.20

Concavity SE

0.00 to 0.40

Fractal Dimension SE

0.00 to 0.03

Smoothness Worst

0.07 to 0.22

Concavity Worst

0.00 to 1.25

Symmetry Worst

0.16 to 0.66

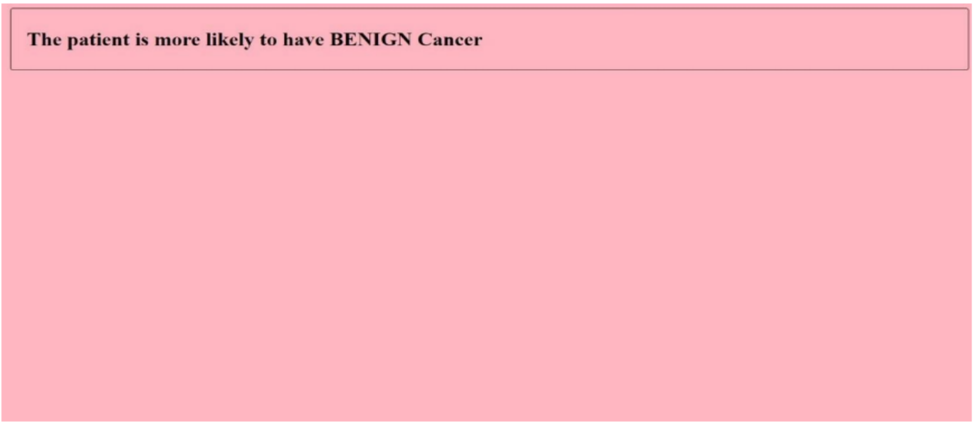
Fractal Dimension Worst

0.06 to 0.21

Fig 4.4 Prediction Form

In the prediction we fill all 10 features including in the form and after that will choose one ML algorithm among KNN, SVM, LR and NB for prediction and see the result after applying.

Output



The patient is more likely to have BENIGN Cancer

Fig 4.5 Output

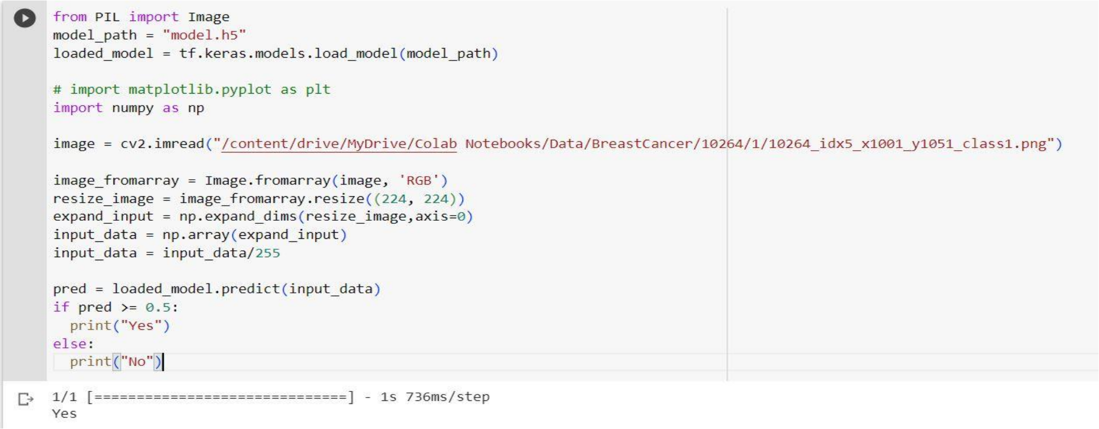
In the output we see which type of cancer predicts Benign or Malignant after applying the selected ML algorithm.

Image dataset

Breast cancer histopathology image classification using CNN on Google Colab

Taking a single image for prediction.

Taking an image of the Breast cancer histopathology image and loading it into the image variable.



```
from PIL import Image
model_path = "model.h5"
loaded_model = tf.keras.models.load_model(model_path)

# import matplotlib.pyplot as plt
import numpy as np

image = cv2.imread("/content/drive/MyDrive/Colab Notebooks/Data/BreastCancer/10264/1/10264_idx5_x1001_y1051_class1.png")

image_fromarray = Image.fromarray(image, 'RGB')
resize_image = image_fromarray.resize((224, 224))
expand_input = np.expand_dims(resize_image,axis=0)
input_data = np.array(expand_input)
input_data = input_data/255

pred = loaded_model.predict(input_data)
if pred >= 0.5:
  print("Yes")
else:
  print("No")
```

```
1/1 [==============================] - 1s 736ms/step
Yes
```

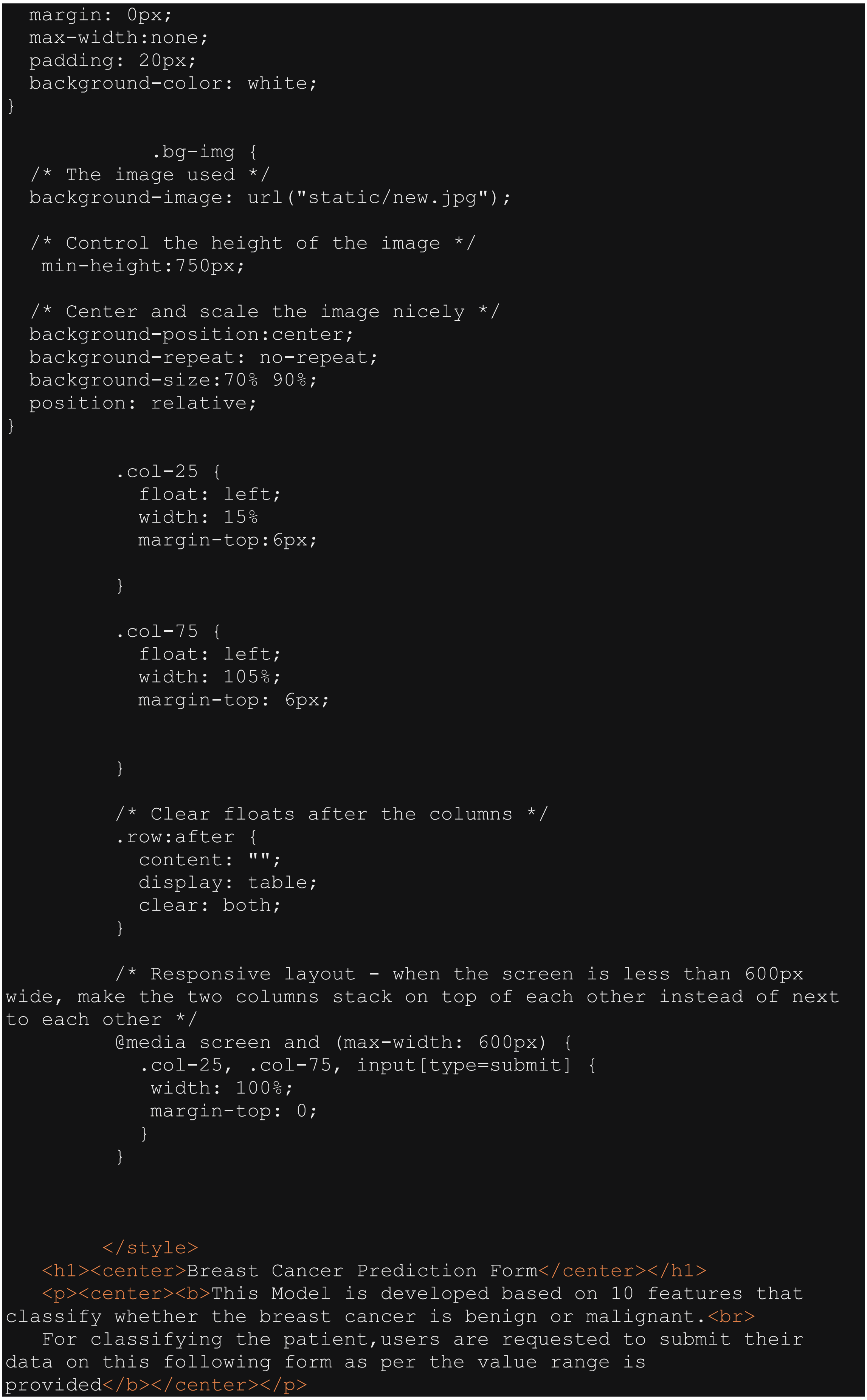
Fig 4.6 CNN output

We are getting **Yes** as output that indicates patient is having cancer.

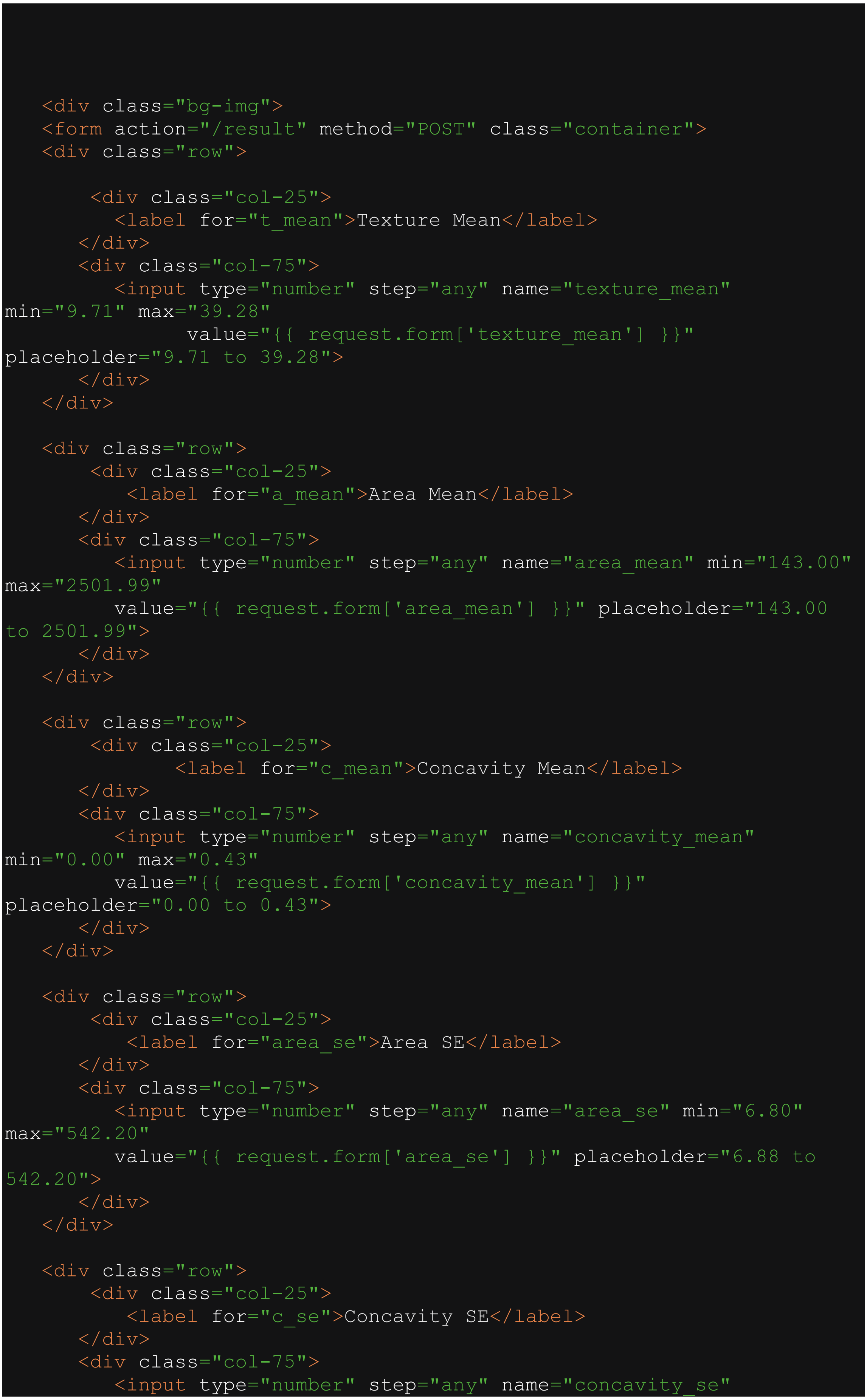
CHAPTER 5

CODING

```
PREDICTION_FORM.HTML


<!DOCTYPE html>
<html>
<body>
    <style>
         * {
           box-sizing: border-box;
         }

         input[type=text], select, textarea {
           width: 100%;
           padding: 12px;
           border: 1px solid #ccc;
           border-radius: 4px;
           resize: vertical;
         }

         label {
           padding: 12px 12px 12px 0;
           display: inline-block;
         }

         input[type=submit] {
           background-color: #04AA6D;
           color: white;
           padding: 12px 20px;
           border: none;
           border-radius: 4px;
           cursor: pointer;
           float: right;
         }

         input[type=submit]:hover {
           background-color: #45a049;
         }


         /* Add styles to the form container */
.container {
  position:absolute;
  right: 100px;
```



```
  margin: 0px;
  max-width:none;
  padding: 20px;
  background-color: white;
}

            .bg-img {
  /* The image used */
  background-image: url("static/new.jpg");

  /* Control the height of the image */
   min-height:750px;

  /* Center and scale the image nicely */
  background-position:center;
  background-repeat: no-repeat;
  background-size:70% 90%;
  position: relative;
}

         .col-25 {
           float: left;
           width: 15%
           margin-top:6px;

         }

         .col-75 {
           float: left;
           width: 105%;
           margin-top: 6px;


         }

         /* Clear floats after the columns */
         .row:after {
           content: "";
           display: table;
           clear: both;
         }

         /* Responsive layout - when the screen is less than 600px
wide, make the two columns stack on top of each other instead of next
to each other */
         @media screen and (max-width: 600px) {
           .col-25, .col-75, input[type=submit] {
            width: 100%;
            margin-top: 0;
           }
         }



        </style>
   <h1><center>Breast Cancer Prediction Form</center></h1>
   <p><center><b>This Model is developed based on 10 features that
classify whether the breast cancer is benign or malignant.<br>
   For classifying the patient,users are requested to submit their
data on this following form as per the value range is
provided</b></center></p>
```



```
   <div class="bg-img">
   <form action="/result" method="POST" class="container">
   <div class="row">

       <div class="col-25">
         <label for="t_mean">Texture Mean</label>
      </div>
      <div class="col-75">
         <input type="number" step="any" name="texture_mean"
min="9.71" max="39.28"
               value="{{ request.form['texture_mean'] }}"
placeholder="9.71 to 39.28">
      </div>
   </div>

   <div class="row">
       <div class="col-25">
          <label for="a_mean">Area Mean</label>
      </div>
      <div class="col-75">
         <input type="number" step="any" name="area_mean" min="143.00"
max="2501.99"
         value="{{ request.form['area_mean'] }}" placeholder="143.00
to 2501.99">
      </div>
   </div>

   <div class="row">
       <div class="col-25">
              <label for="c_mean">Concavity Mean</label>
      </div>
      <div class="col-75">
         <input type="number" step="any" name="concavity_mean"
min="0.00" max="0.43"
         value="{{ request.form['concavity_mean'] }}"
placeholder="0.00 to 0.43">
      </div>
   </div>

   <div class="row">
       <div class="col-25">
          <label for="area_se">Area SE</label>
      </div>
      <div class="col-75">
         <input type="number" step="any" name="area_se" min="6.80"
max="542.20"
         value="{{ request.form['area_se'] }}" placeholder="6.88 to
542.20">
      </div>
   </div>

   <div class="row">
       <div class="col-25">
          <label for="c_se">Concavity SE</label>
      </div>
      <div class="col-75">
         <input type="number" step="any" name="concavity_se"
```

```
min="0.00" max="0.40"
         value="{{ request.form['concavity_se'] }}" placeholder="0.00
to 0.40">
      </div>
   </div>

   <div class="row">
       <div class="col-25">
          <label for="fd_se">Fractal Dimension SE</label>
      </div>
      <div class="col-75">
         <input type="number" step="any" name="fractal_dimension_se"
min="0.00" max="0.03"
         value="{{ request.form['fractal_dimension_se'] }}"
placeholder="0.00 to 0.03">
      </div>
   </div>

   <div class="row">
       <div class="col-25">
          <label for="s_worst">Smoothness Worst</label>
      </div>
      <div class="col-75">
         <input type="number" step="any" name="smoothness_worst"
min="0.07" max="0.22"
         value="{{ request.form['smoothness_worst'] }}"
placeholder="0.07 to 0.22">
      </div>
   </div>

   <div class="row">
       <div class="col-25">
          <label for="c_worst">Concavity Worst</label>
      </div>
      <div class="col-75">
         <input type="number" step="any" name="concavity_worst"
min="0.00" max="1.25"
         value="{{ request.form['concavity_worst'] }}"
placeholder="0.00 to 1.25">
      </div>
   </div>

   <div class="row">
       <div class="col-25">
          <label for="s_worst">Symmetry Worst</label>
      </div>
      <div class="col-75">
         <input type="number" step="any" name="symmetry_worst"
min="0.16" max="0.66"
         value="{{ request.form['symmetry_worst'] }}"
placeholder="0.16 to 0.66">
      </div>
   </div>

   <div class="row">
       <div class="col-25">
          <label for="fdw">Fractal Dimension Worst</label>
      </div>
      <div class="col-75">
         <input type="number" step="any"
name="fractal_dimension_worst" min="0.06" max="0.21"
```

```
         value="{{ request.form['fractal_dimension_worst'] }}"
placeholder="0.06 to 0.21">
      </div>
   </div>

   <button type="submit">KNN Predict</button>

   <button type="submit">SVM Predict</button>
   <button type="submit">LR Predict</button>
   <button type="submit">NB Predict</button>



</form>
</div>
</body>
</html>


<!DOCTYPE html>
<html lang="en">
<head>
    <meta charset="UTF-8">
    <title>Result</title>
</head>
<body style="font-size:20";>

{{ prediction_text }}

</body>
</html>
```

APP.PY

```
import os
import numpy as np
from flask import Flask, request, jsonify, render_template
import pickle
from sklearn.preprocessing import StandardScaler
from sklearn.model_selection import train_test_split
import pandas as pd
from sklearn.metrics import accuracy_score
from sklearn.neighbors import KNeighborsClassifier

# create flask app
app = Flask(__name__)
df = pd.read_csv('BCPD.csv')
x = df[["texture_mean", "area_mean", "concavity_mean", "area_se",
"concavity_se",'fractal_dimension_se',
        "smoothness_worst", "concavity_worst",
"symmetry_worst","fractal_dimension_worst"]]
y = df[["diagnosis"]]
x_train, x_test, y_train, y_test = train_test_split(x, y,
test_size=0.33, random_state=42)


# load pickle model
model = pickle.load(open("model.pkl", "rb"))


@app.route("/")
```

```
def home():
    return render_template("prediction_form.html")



@app.route("/result", methods=["GET", "POST"])
def predict():
    l = []
    form_value = l
    if request.method == "POST":
        print(request.values)
    imd = request.form
    imd.to_dict(flat=False)
    print(imd)
    for k,v in imd.items():
        form_value.append(v)
    print(type(request.form))
    print(request.form)
    float_features = [float(x) for x in form_value]
    features = np.array([np.array(float_features)])
    sc=StandardScaler()
    Fit= sc.fit(x_train)
    features=Fit.transform(features)
    prediction = model.predict(features)
    if prediction[0] == 1:
        print("Malignant")
        return render_template("result.html", prediction_text="
MALIGNANT Cancer")
    else:
        print("Benign")
        return render_template("result.html", prediction_text=" BENIGN
Cancer")

    # Python program to define a function to compute accuracy score of
model's predicted class

    # Defining a function which takes true values of the sample and
values predicted by the model
'''
def accuracy():
    classifier = KNeighborsClassifier()

    y_pred = classifier.predict(x_test)
    av = accuracy_score(y_test, y_pred)
    return render_template('result.html', av=av)
'''


if __name__ == "__main__":
    app.run(debug=True,use_reloader=False,port=8080)
    ''''
    HOST = os.environ.get('SERVER_HOST', 'localhost')
    try:
        PORT = int(os.environ.get('SERVER_PORT', '5555'))
    except ValueError:
        PORT = 5555

    app.run(HOST, PORT)
    '''
```

KNN.PY

```
import pandas as pd
import numpy as np
import matplotlib.pyplot as plt
import seaborn as sns
import io
import os
import math
import pickle
from flask import render_template
from sklearn.model_selection import train_test_split
from sklearn.preprocessing import LabelEncoder, StandardScaler
from sklearn.neighbors import KNeighborsClassifier
from sklearn.metrics import accuracy_score

from sklearn.datasets import load_breast_cancer


df = pd.read_csv('BCPD.csv')
print(df.head())
#print("target name:", df[''])
# select dependent and independent variable
x = df[["texture_mean", "area_mean", "concavity_mean", "area_se",
"concavity_se",'fractal_dimension_se',
        "smoothness_worst", "concavity_worst",
"symmetry_worst","fractal_dimension_worst"]]
#x = df[[ "radius_mean",  'perimeter_mean', 'area_mean',
'symmetry_mean', 'compactness_mean', 'concave points_mean']]
y = df[["diagnosis"]]

# split the data into train and test

x_train, x_test, y_train, y_test = train_test_split(x, y,
test_size=0.33, random_state=42)

# feature scaling
sc = StandardScaler()
Fit = sc.fit(x_train)
x_train = Fit.transform(x_train)
x_test = Fit.transform(x_test)

# instantiate model
classifier = KNeighborsClassifier()






# fit the model90
classifier.fit(x_train, y_train)
# Make predictions on the testing data
y_pred = classifier.predict(x_test)

# Calculate the accuracy of the model
accuracy = accuracy_score(y_test, y_pred)
print('Accuracy:', accuracy)


# make pickle file of our model
```

```
pickle.dump(classifier, open("model.pkl", "wb"))


'''
y_pred = classifier.predict(x_test)
av = accuracy_score(y_test, y_pred)
print("accuracy is:",av)
'''
```

Support Vector Machine (SVM) Algorithm

```
from sklearn.datasets import load_breast_cancer
import pandas as pd
from sklearn.model_selection import train_test_split
from sklearn.svm import SVC
from sklearn.metrics import accuracy_score

# Load the breast cancer dataset
#data = load_breast_cancer()
data= pd.read_csv('BCPD.csv')
X = data[["texture_mean", "area_mean", "concavity_mean", "area_se",
"concavity_se",'fractal_dimension_se',
        "smoothness_worst", "concavity_worst",
"symmetry_worst","fractal_dimension_worst"]]
#X = data.data
Y = data[["diagnosis"]]
#y = data.target

# Split the dataset into training and testing sets
X_train, X_test, y_train, y_test = train_test_split(X, Y,
test_size=0.2, random_state=42)

# Create an SVM model with a linear kernel
model = SVC(kernel='linear')

# Train the model on the training data
model.fit(X_train, y_train)

# Make predictions on the testing data
y_pred = model.predict(X_test)

# Calculate the accuracy of the model
accuracy = accuracy_score(y_test, y_pred)
print('Accuracy:', accuracy)
```

Logistic Regression Algorithm

```
from sklearn.datasets import load_breast_cancer
import pandas as pd
from sklearn.model_selection import train_test_split
from sklearn.linear_model import LogisticRegression
from sklearn.metrics import accuracy_score

# Load the breast cancer dataset
#data = load_breast_cancer()
```

```
data= pd.read_csv('BCPD.csv')
X = data[["texture_mean", "area_mean", "concavity_mean", "area_se",
"concavity_se",'fractal_dimension_se',
        "smoothness_worst", "concavity_worst",
"symmetry_worst","fractal_dimension_worst"]]
#X = data.data
Y = data[["diagnosis"]]
#y = data.target

# Split the dataset into training and testing sets
X_train, X_test, y_train, y_test = train_test_split(X, Y,
test_size=0.2, random_state=42)

# Create a logistic regression model
model = LogisticRegression()

# Train the model on the training data
model.fit(X_train, y_train)

# Make predictions on the testing data
y_pred = model.predict(X_test)

# Calculate the accuracy of the model
accuracy = accuracy_score(y_test, y_pred)
print('Accuracy:', accuracy)
```

Naive Bayes Algorithm

```
from sklearn.metrics import accuracy_score

# Load the breast cancer dataset
#data = load_breast_cancer()
data= pd.read_csv('BCPD.csv')
X = data[["texture_mean", "area_mean", "concavity_mean", "area_se",
"concavity_se",'fractal_dimension_se',
        "smoothness_worst", "concavity_worst",
"symmetry_worst","fractal_dimension_worst"]]
#X = data.data
Y = data[["diagnosis"]]
#y = data.target


# Split the dataset into training and testing sets
X_train, X_test, y_train, y_test = train_test_split(X, Y,
test_size=0.2, random_state=42)

# Create a Naive Bayes model
model = GaussianNB()

# Train the model on the training data
model.fit(X_train, y_train)

# Make predictions on the testing data
y_pred = model.predict(X_test)

# Calculate the accuracy of the model
accuracy = accuracy_score(y_test, y_pred)
print('Accuracy:', accuracy)
```

RESULT.HTML

```
<!DOCTYPE html>
<html lang="en">
<head>
    <meta charset="UTF-8">
    <title>Result</title>
<style>
      body {
        margin: 8px 16px;
        background-color: LightPink;
        padding: 12px 24px;
        border: 1px solid black;
        border-radius: 4px;
      }
    </style>


</head>

<body style="font-size:20";  background-color="#212F3C"; color="
#FFFFF0";>


<h1>
    The patient is more likely to have {{ prediction_text }}</h1>

<!--
<h1>the accuracy is 94{{av}}</h1>

<p> classification report and accuracy score :{{av}} </p>

<p>print(av)</p></body>
-->
</body>
</html>
```

STEPS:

1. Remove the unnecessary columns or columns with nominal data.
2. Normalize the data as all data use different scales.
3. Split data into training and testing data (70-30).
4. Apply KNN, SVM, NAIVE BAYES and LOGISTIC REGREESION algorithms.
5. Compare the predicted values to actual values and calculate accuracy of model.
6. And see which algorithm’s performance is more accurate.

CHAPTER 6

RESULTS

The experimental work utilizes the classification techniques that generally contains two different steps. In the first step the training dataset which contains labelled classes is used to build classification model by selecting a suitable classification algorithm. In the second step which is prediction phase the accuracy of the built classification model is evaluated on the validation dataset.

The primary purpose of this study is to create and execute a novel computation for interpreting breast cancer data obtained from mammography and pathology results of patient scans that is obtained and UCI repositories' cloud. Python programming, a convolutional neural association model is utilised to accomplish this, and the results are confirmed. According to the findings, the suggested CNN outperforms estimations in recognizing and requesting breast cancer for image datasets. And SVM has proven to outperforms LR, NB and KNN in analysis and prediction of cancer with numerical dataset.

6.1 PERFORMANCE MATRICES AND CONFUSION MATRICES

Confusion matrix is a tabular representation for the number of correctly and incorrectly predicted outcomes of the evaluated model.

The attributes of stated matrix are-

- False Negative is termed as number of negatively anticipated outcomes that are positively verified.
- True Positive is termed as number of positively anticipated outcomes that are positively verified.
- False Positive is termed as number of positively anticipated outcomes that are negatively verified.
- True Negative is termed as number of negatively anticipated outcomes that are actually negative.

Accuracy: The accuracy of the classification model is the percentage of data records that are correctly classified through the classifier.

Accuracy = TN+TP /TN+TP +FP +FN

Sensitivity or Recall: Sensitivity is the proportion of True Positive records that are classified correctly. It is also termed as the true positive rate (TPR).

Sensitivity = TP /TP +FN

Precision: It is computed as the ratio of True Positive outcome vs. overall positive records.

Precision = TP /TP +FP

Specificity: It is computed the ratio of negative tuples that are recognized correctly.

Specificity = TN/ TN+FP

F-measure: It can be computed from below given formula.

F-measure = 2∗ Precision∗ Recall /Precision + Recall

FPR: A false positive ratio is the probability of neglecting the null hypothesis wrongly.

The FPR can be expressed as

FPR = 1- Specificity

6.2 RESULT

NUMERICAL DATASET

In this project, an experiment is carried out to compare the accuracy measures of selected four prominent classification models considering their performance qualitatively on Wisconsin Diagnostic Breast Cancer (WDBC) dataset at Kaggle. Support Vector Machine classifier is found to be best in overall performance. The four selected machine learning algorithms, are implemented on the same data as input for a number of times and the evaluated matrices are averaged in final results that are depicted in Table 2 from where it can be concluded that performance of aforesaid classifiers are closely competitive but support vector machine classifier is experimentally observed the best with accuracy of 97.8% and precision of 96.6% as compared to the other three classifiers namely Naïve Bayes, KNN and Logistic Regression with.

CLASSIFICATION MODEL	TP	TN	FP	FN
Logistic Regression	117	64	4	3
Naïve Bayes	114	61	7	6
K-nearest neighbour	117	61	4	6
Support Vector Machine	117	65	4	2

Table 6.1 Confusion matrices attributes

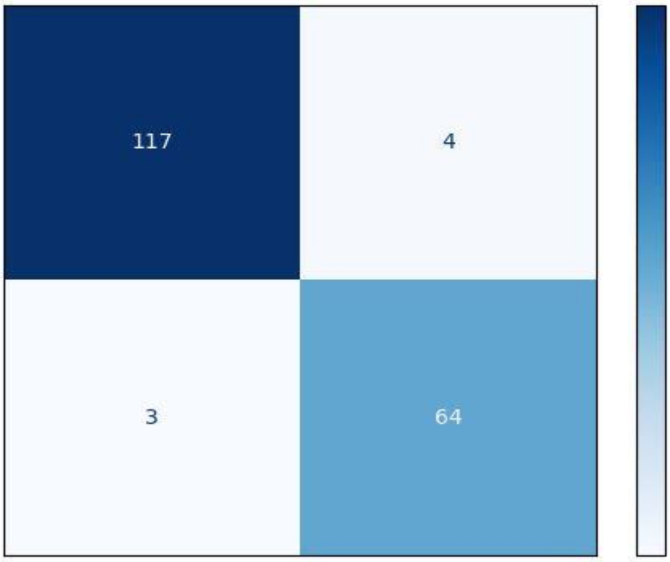


Fig 6.1 Confusion Matrix LR

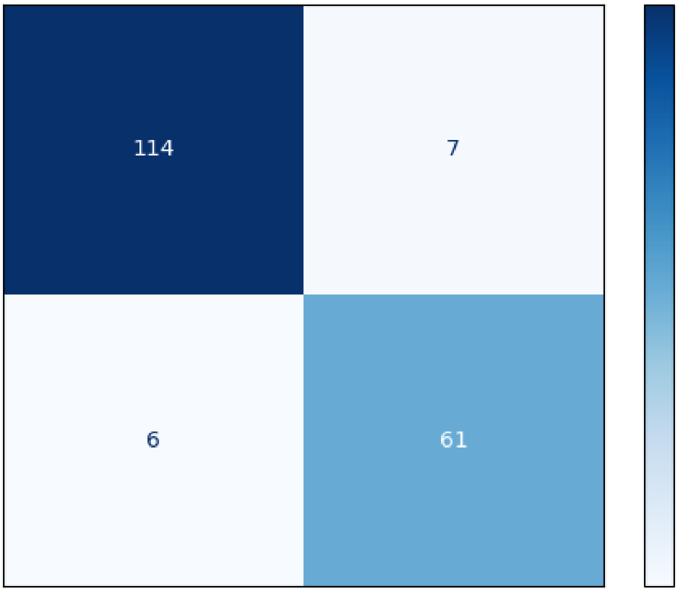


Fig 6.2 Confusion Matrix NB

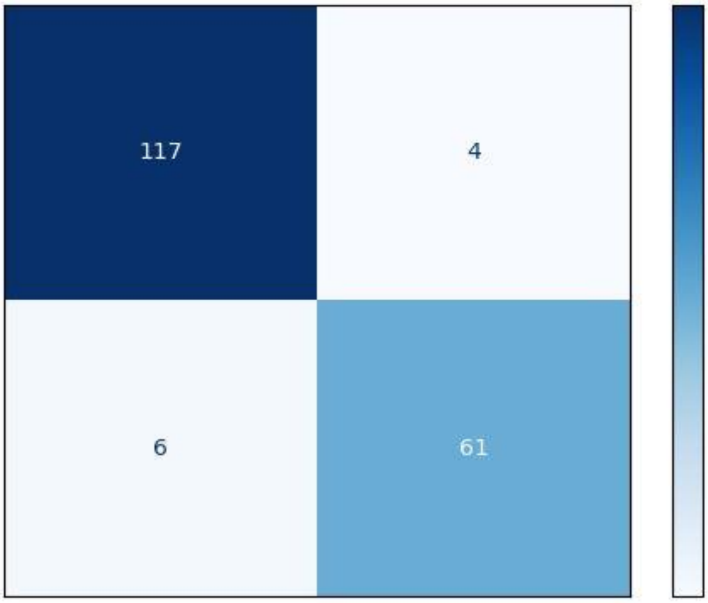


Fig 6.3 Confusion Matrix KNN

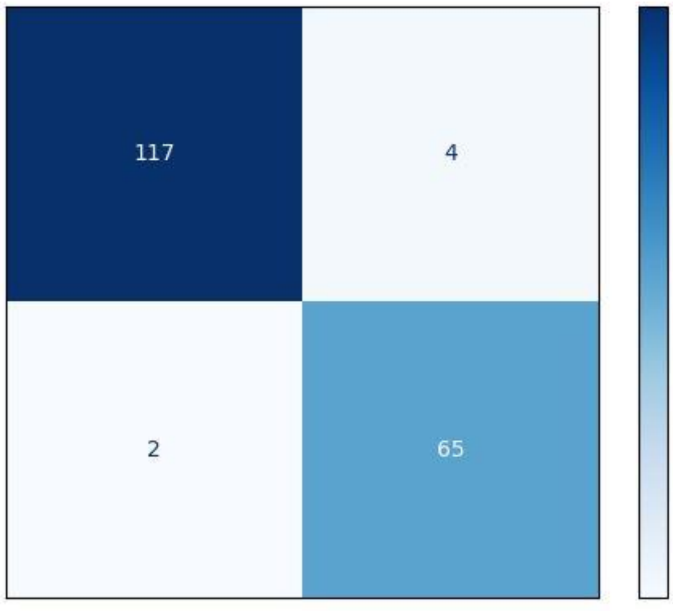


Fig 6.4 Confusion Matrix SVM

CLASSIFICATION MODEL	Accuracy	Precision	Recall	F-score
Logistic Regression	0.962	0.966	0.975	0.97
Naïve Bayes	0.93	0.92	0.95	0.934
K-nearest neighbour	0.946	0.966	0.95	0.957
Support Vector Machine	0.978	0.966	0.98	0.972

Table 6.2 Performance attributes comparison

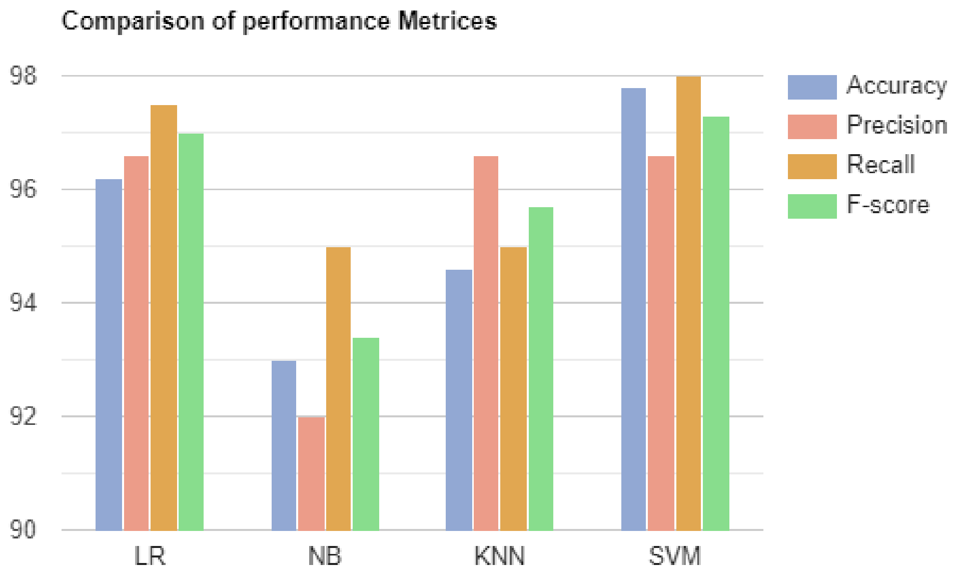


Fig 6.5 Comparison of performance

So, we have found that performance of aforesaid classifiers is closely competitive, but support vector machine classifier is experimentally observed the best with accuracy of 97.8% and precision of 96.6% as compared to the other three classifiers namely Naïve Bayes, KNN and Logistic Regression with.

IMAGE DATASET

The training loss is 21.17%, while the validation loss is 13.16%. The accuracy is 92.12%

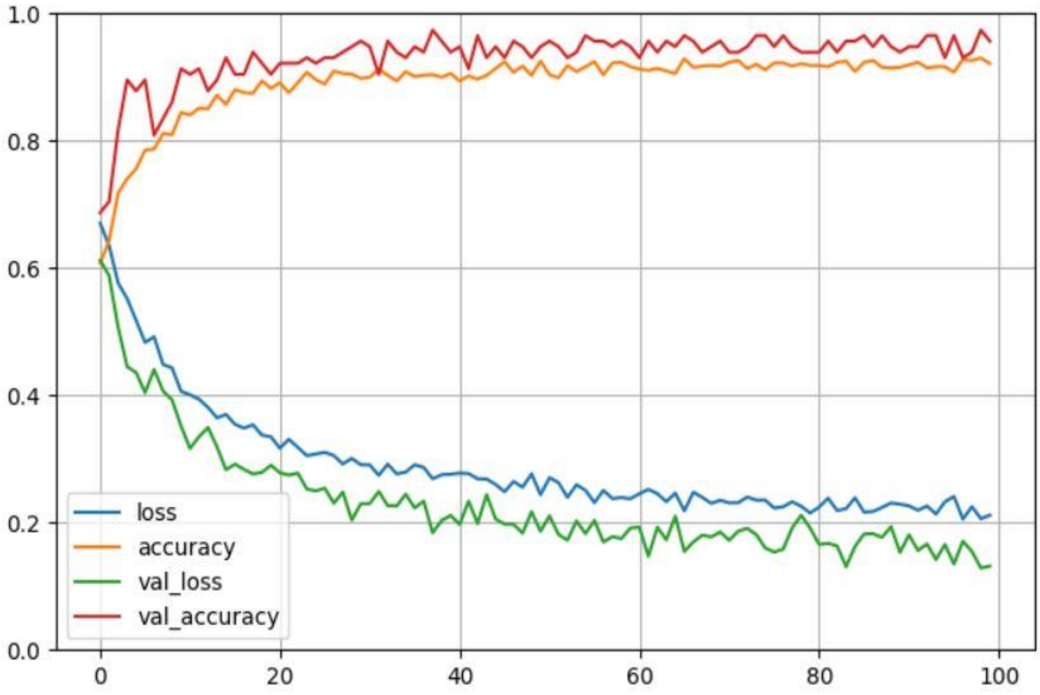


Fig. 6.6 The loss learning curve.

Detection of cancer is itself a challenging task. We have used CNN to analyze the IDC tissue regions. The proposed system using CNN model achieves 92.12% accuracy.

The main limitation of this study is that we are using secondary database like Kaggle and for future study, primary data should be used for getting more accuracy of the results for breast cancer detection.

CHAPTER 7

CONCLUSION

In this study we have worked to collect the suitable dataset needed to help in this predictive analysis. This dataset is then processed to remove all the junk data. The predictive analysis method is being used in many different fields and is slowly picking up pace. It is helping us by using smarter ways to solve or predict a problem’s outcome. Our scheme was developed to reduce the time and cost factors of the patients as well as to minimize the work of a doctor. We have tried to use a very simple and understandable model to do this job. Next, machine learning algorithms should be used on the training data and the testing data should be used to check if the outcomes are accurate enough. This work chose Support Vector Machine (SVM), Logistic Regression, KNN, Naïve Bayes algorithm for test. The performance analysis of all the algo comes as outcome and after comparing the performance and accuracy of the algorithms we will have which one is the most accurate and best to detect breast cancer.

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