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A Methodological Research On Prediction of Breast Cancer Based On Machine Learning Algorithm

Author: JAYA MEHRA, Department of Computer Science & Engg. , UIT RGPV BHOPAL (M.P.),India,

Dr. MANISH KUMAR AHIRWAR Associate Professor, Department of Computer Science & Engg. , UIT RGPV BHOPAL (M.P.),India

Dr. RAJEEV PANDEY , Associate Professor, Department of Computer Science & Engg. , UIT RGPV BHOPAL (M.P.),India ,

Abstract: **In this study, a breast cancer (BC) detection system using computer-aided design (CAD) is presented. Using the BC Wisconsin data-set from the UCI repository, which uses attribute clump thickness as an evaluation class, random forest, logistic regression, decision trees, SVM , KNN , and conventional neural networks (CNNs) classifiers are used in BC detection. These machine learning (ML) based algorithms are trained to predict BCs (malignant or benign). Every experiment is carried out on the JUPYTER platform in a simulation environment. The research objective is divided into three categories. The accuracy and F-measure of these machine learning algorithms are used to assess their efficacy; random forest fared better than the other classifiers, achieving 93% accuracy and 96% F-measure.**

Keyword : Breast Cancer , Machine Learning , Cancer Detection , UCI , CAD System.

1. INTRODUCTION

Both men and women may have BC [1], a condition that develops in the breasts and causes certain cells, particularly those of the milk-producing ducts, to grow abnormally. Its symptoms include odd thickening and lumps, changes to the size, shape, and appearance of the breast skin, the appearance of an inverted nipple, and more. The most common cancer, according to the Global Cancer Statistics 2020, released in February 2021 [1], is breast cancer, accounting for 11.7% of all cases.

Additionally, the 2021 annual cancer report, available on the website of the Jordanian Ministry of Public Health, states that breast cancer is the most common cancer among Jordanians, with 1279 cases, or 21.3% of all cases. Breast cancer (BC) is a prevalent malignancy in women that is regarded as one of the most deadly tumors worldwide. BC is categorized into two groups based on the morphology of the cells: (i) invasive ductal carcinoma and (ii) ductal carcinoma in situ. The former is the most deadly type of BC since it can spread to all breast tissues and kill most BC patients [2].

One of the prevalent malignancies that endangers the lives of a lot of women worldwide is BC [3]. It is the third leading cause of mortality in Jordan, behind colorectal and lung cancers, and one of the most prevalent malignancies that kills many women in the country. Moreover, it significantly improves health prospects in many other Arab, European, and American nations. There aren't many BC articles in Jordan [4], with just 85 papers published in PubMed between 1985 and 2019. Statistical techniques including grouping, clustering, and estimating are used in this study to determine the aptitude of cancer patients. In our study, we proposed this cancer prediction technique based on the information-mining approach. The amount of breast cancer cases in humans in the near future is displayed by this computer.

This device is verified to be finished using prior clinical expertise. This model's objectives are to safeguard clients and keep costs down for the user. Thus the diagnosis and prevention of physical injuries will be aided by a prediction model. This research aids in early cancer treatment detection by estimating an individual's risk of contracting the disease.

When breast cancer develops, it may spread.When cells start to proliferate uncontrollably, cancer is born. Typically, breast cancer cells develop into a tumor that is felt as a lump or frequently seen on an x-ray. When cancer cells enter the blood or lymphatic system and travel to different areas of the body, breast cancer may spread. Breast cancer is caused by alterations and mutations in DNA.

In order to optimize successful treatment choices and prospects, radiologists and physicians are eager to use such excellent clinical applications in detecting BCs to early detection and diagnosis of BCs. The use of machine learning

(ML) algorithms to automatically identify breast cancers (BCs) on mammograms is encouraged in this work since ML is a field of study that has the potential to handle challenging problems and enhance performance diagnosis in a variety of classification jobs. Among these machine learning algorithms are , Random Forest, Decision Tree, KNN , SVN, Logistic Regression, and Deep Learning.

The remainder of this essay is structured as follows: The latest work in this area is described in part II, the implemented machine learning methods are shown in section III, the findings and associated discussions are offered in section IV, and the conclusion and future directions are presented in section V.

II. RELATED WORK

In [5], BCs are predicted using ensemble learning techniques like AdaBoost and Random Forest. The findings show that random forest achieves 97% accuracy. Support vector machines (SVMs) were able to predict BCs on the Wisconsin BC dataset with 96.25% accuracy in [6]. Metric evaluations are employed in [7] to create a discriminator between benign and malignant tumors. An enhanced Mamdani fuzzy inference is used in [8]

Predict benign or malignant tumors and can perform better when handling complicated malignancies. A unique hybrid classifier based on majority voting is applied in [9] in an attempt to improve the accuracy of BC prediction; nevertheless, the accuracy of their suggested technique was only 79%. A comparison of many machine learning strategies for BC detection is done in [10] and it is shown that these algorithms an accuracy 93.60.Several machine learning techniques are tested in [11] utilizing the Wisconsin BC dataset in order to recognize BCs.

It is shown that random forest and SVM yielded 96.5% accuracy. A comparison between their suggested hybrid method and the one used in [12] to categorize BCs uses a mix of DL and random forest. When studies using different classifiers, such SVM, are done, the accuracy of the ensemble-based methods improves by 4.3%, with the greatest gain reaching 9.8%.

The mortality component of BCs in India is examined in [13] in relation to a number of risk factors, including water consumption, lifestyle choices, and demographic traits. An ensemble algorithm is then utilized to forecast BCs for Malwa women in India, with a 98.21% accuracy rate.An ensemble algorithm that uses a variety of classification techniques to distinguish between benign and malignant tumors was presented in [14]; its stacked ensemble classifier produced an accuracy of 97.20%.

A comparative study of many machine learning (ML)-based methods for predicting BCs, including deep learning, was conducted in [15]. The study found that deep learning achieves the best accuracy (96.99%), as reported in [16].Neural networks have attained accuracy levels of 96.2% in [17], 97.66% for convolutional neural networks (CNNs) in [18], 99.73% for deep learning algorithms in [19], and 99.73% for BC prediction.

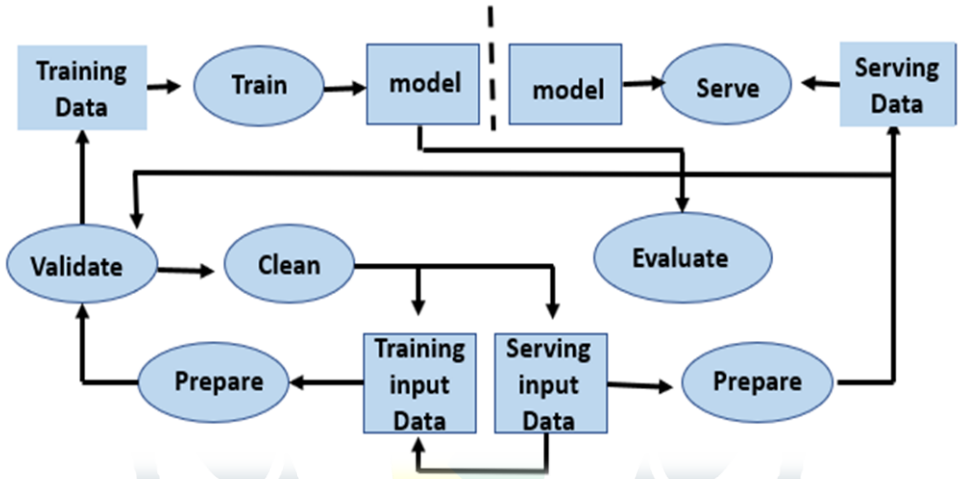
An accuracy ranging from 84% to 92%. In conclusion, CNN had the best prediction accuracy. Data pre-processing, as we all know, is a data mining technique used to filter data into a format that is useful. as real-world datasets are nearly always accessible in several formats. Since it isn't available in the way we need it, it has to be filtered in a comprehensible manner. Pre-processing data is a tried-and-true way to fix problems like these. Data preprocessing uses the standardized procedure to transform the dataset into a format that is readable and useable.

TABLE 1. A LITERATURE REVIEW OF THE BREAST CANCER PREDICTION USING MACHINE LEARNING

AUTHOR	YEAR	DIFFERENT TECHNIQUE USED IN BREAST CANCER PREDICTION
Gershon – cohen et al.[21]	1961	The authors suggested a standard examination in the Albert Einstein Medical Center's Radiology Department to identify malignancy.
Stevens et al .[22]	1966	The authors suggested using a modified Egan approach in conjunction with a mammography survey to identify breast cancer.
Barrett et al .[23]	1977	The authors suggested diagnosing breast cancer with microwave radiometry.
Martin et al .[24]	1979	The problems with the mammography strategy, which include subpar radiography technique, a lack of radiographic models of malignant development, and obvious supervision by the radiologist, as well as the disregard for subtle radiological indicators.
Li et al .[25]	2001	In order to diagnose cancer, the scientists suggested a two-dimensional, anatomically accurate FDTD model of the diseased breast obtained from MRI data.

Zou et al .[26]	2003	The authors suggested using electrical impedance as a method of breast cancer detection.
Chi et al . [27]	2007	Artificial Neural Networks (ANNs) were suggested by the authors as a way to forecast the outcome of breast cancer.
Cheng et al .[28]	2010	The authors suggested using ultrasound imaging, which offers more enhanced diagnostic accuracy, as part of the Computer-Aided Diagnosis (CAD) system.

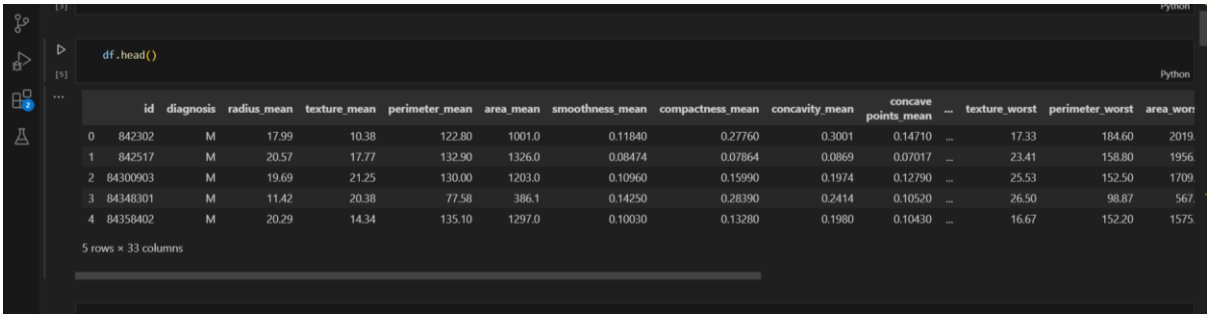
III. MACHINE LEARNING ALGORITHM



There are seven steps in Fig. (1) steps of Machine Learning, which are explained as follows:

Phase 1 - Pre-Processing Data

In the first stage, we gather the information we want to use for pre-processing and use regression and classification algorithms. One data mining approach is data pre-processing, which is converting unprocessed data into a comprehensible format. Real-world data is frequently unreliable, inconsistent, and likely full of mistakes. Pre-processing data is a tried-and-true way to fix problems like these. Preparing raw data for additional processing is known as data pre-processing. We have pre-processed the UCI dataset using the standardization procedure. This is a crucial phase since the quality and quantity of data you collect will directly impact the potential accuracy of your prediction model. In this instance, we gather samples of both benign and malignant breast cancer.This is a crucial phase since the quality and quantity of data you collect will directly impact the potential accuracy of your prediction model. In this instance, we gather samples of both benign and malignant breast cancer. We will use this as our training set.



```
df.head()
```

Python

	id	diagnosis	radius_mean	texture_mean	perimeter_mean	area_mean	smoothness_mean	compactness_mean	concavity_mean	concave points_mean	...	texture_worst	perimeter_worst	area_wor
0	842302	M	17.99	10.38	122.80	1001.0	0.11840	0.27760	0.3001	0.14710	...	17.33	184.60	2019.
1	842517	M	20.57	17.77	132.90	1326.0	0.08474	0.07864	0.0869	0.07017	...	23.41	158.80	1956.
2	84300903	M	19.69	21.25	130.00	1203.0	0.10960	0.15990	0.1974	0.12790	...	25.53	152.50	1709.
3	84348301	M	11.42	20.38	77.58	386.1	0.14250	0.28390	0.2414	0.10520	...	26.50	98.87	567.
4	84358402	M	20.29	14.34	135.10	1297.0	0.10030	0.13280	0.1980	0.10430	...	16.67	152.20	1575.

5 rows × 33 columns

Phase 2 - DATA PREPARATION

The process of loading our data into the appropriate location and getting it ready for use in our machine learning training is called data preparation. After compiling all of our data, we will randomly arrange it.

Phase 3 - FEATURES SELECTION

Feature selection, often referred to as variable selection or attribute selection, is the process of choosing a subset of pertinent characteristics to be used in the creation of a model in machine learning and statistics.
Selection of Features and Data Files Diagnostic Breast Cancer in Wisconsin:- Information taken from the Kaggle repository, and we have chosen around 8–9 parameters totaling out of the 31 available. The diagnosis of benign or malignant breast cancer is our aim criteria. For feature selection, we have employed the Wrapper Method. The study's key findings are as follows: Area se, Concave points worst, and Area worst Texture mean, Texture worst, Radius mean, Smoothness mean, and Symmetry mean.For feature selection, we have employed the Wrapper Method. The study's key findings are as follows: 1. The worst concave points 2. Worst area 3. Region se 4. Worst texture 5. Mean texture; 6. Worst smoothness 7. Mean smoothness 8. Mean radius 9. Symmetry means.

Information about the attribute: ID number 2) Diagnosis (B = benign, M = malignant) 3–32

Python

```
(569, 32)
```

```
## describe the data set
df.describe()
```

Python

	id	radius_mean	texture_mean	perimeter_mean	area_mean	smoothness_mean	compactness_mean	concavity_mean	concave points_mean	symmetry_mean	...	radius_worst	texture_wors
count	5.690000e+02	569.000000	569.000000	569.000000	569.000000	569.000000	569.000000	569.000000	569.000000	569.000000	...	569.000000	569.00000
mean	3.037183e+07	14.127292	19.289649	91.969033	654.889104	0.096360	0.104341	0.088799	0.048919	0.181162	...	16.269190	25.67722
std	1.250206e+08	3.524049	4.301036	24.298981	351.914129	0.014064	0.052813	0.079720	0.038803	0.027414	...	4.833242	6.14625
min	8.670000e+03	6.981000	9.710000	43.790000	143.500000	0.052630	0.019380	0.000000	0.000000	0.106000	...	7.930000	12.02000
25%	8.692180e+05	11.700000	16.170000	75.170000	420.300000	0.086370	0.064920	0.029560	0.020310	0.161900	...	13.010000	21.08000
50%	9.060240e+05	13.370000	18.840000	86.240000	551.100000	0.095870	0.092630	0.061540	0.033500	0.179200	...	14.970000	25.41000
75%	8.813129e+06	15.780000	21.800000	104.100000	782.700000	0.105300	0.130400	0.130700	0.074000	0.195700	...	18.790000	29.72000
max	9.113205e+08	28.110000	39.280000	188.500000	2501.000000	0.163400	0.345400	0.426800	0.201200	0.304000	...	36.040000	49.54000

8 rows × 31 columns

```
## count of maligant(M)and benign(B) cells
df['diagnosis'].value_counts()
```

Python

Phase 4 - Feature Projection
The process of transforming high-dimensional space data to a lower dimensional space (with few properties) is called feature projection. Depending on the kind of interactions between the features in the dataset, both linear and nonlinear reduction strategies can be applied.

Phase 5 - Feature Scaling
Your dataset will very certainly include characteristics with widely varied magnitudes, units, and ranges. That being said, the majority of machine learning algorithms compute the Euclidian distance between two data poiSnts. All characteristics must be brought to the same magnitude level. Scaling can be used to accomplish this.

Phase 6 - Model Selection
The process of training a system using well-labeled input and output data is known as supervised learning. Using training data, the model may learn and evaluate future data to forecast a result. They are arranged according to classification and regression methods. When the outcome is a real or continuous value, like "weight" or "salary," it is called a regression issue. A challenge with categorization arises when the outcome falls into a certain category, such as "spam" or "not spam."Unsupervised Learning: This type of learning involves feeding unlabeled or poorly categorized data to a computer and letting the program analyze it without human guidance. An unsupervised learning technique uses unlabeled or unclassified data to train the computer, allowing it to function without explicit instructions. The dependent variable, or outcome variable, in our dataset is Y, and it only has two sets of values: M (Malign) and B (Benign). Thus, it is subjected to the supervised learning classification method. Three distinct categories of machine learning classification methods have been selected.

Phase 7 – PREDICTION
Data is used in machine learning to provide answers to queries. Therefore, the stage when we get to provide some answers is called prediction, or inference. This is the culmination of our efforts, where machine learning truly adds value.

METHOD USED
LOGISTIC REGRESSION:

Machine learning was not yet established until DR Cox, a statistician, presented logistic regression in 1958. It is a supervised machine learning method used for predictions made using training data in classification tasks. Similar to linear regression, logistic regression also employs an equation, but its result is a categorical variable as opposed to a value in other regression models. It is possible to forecast binary outcomes based on the independent factors.

The general workflow is:

1. Get a dataset
2. Train a classifier
3. Make a prediction using such classifier

DECISION TREE:

In machine learning and data mining, decision trees are an effective tool for both regression and classification problems. This structure is similar to a flowchart, with each leaf node representing a class label or a continuous value, each branch representing the result of an attribute "test" (e.g., whether a feature is above or below a specific threshold), and each internal node representing a "test" on an attribute.

ALGORITHM:

1.Divide the dataset into training and testing sets after entering it.
2. Select an example from the testing sets and determine how far it is from the training set.
3’ Sort the distances by increasing order.
4.Of the three initial training examples (k=3), the instance's class is the most prevalent class.

RANDOM FOREST:

As its name suggests, random forests are made up of several separate decision trees that work together as a group. The class with the most votes becomes the prediction of our model, and each individual tree in the random forest produces a class prediction.
ALGORITHM
(1)Initially, it locates boundaries or lines that accurately categorize the training dataset.
(2) It then selects the line or boundary with the greatest distance from the nearest data points from among them.

RESULT AND DISCUSSION:

All of the tests on the classifiers presented in this study were carried out using libraries from the Anaconda machine learning environment. The work was executed on an i3 CPU running at 2.30GHz with 2 GB of RAM and 320 GB of external storage. In experimental research, training and testing are divided into 70–30% halves.A variety of machine learning methods for pre-processing data, classification, regression, clustering, and association rules are included in JUPYTER. JUPYTER's machine learning algorithms are used to solve a range of practical issues.The data analysis's findings are presented. We employ the 10-fold cross validation test, a method for assessing classifiers, to apply and assess them.prediction models that divided the initial set into a test set for model evaluation and a training sample for model training. We attempt to visually analyze the data and determine the distribution of values in terms of efficacy and efficiency after applying the pre-processing and preparation procedures.

We assess each classifier's efficacy based on how long it takes to create the model, how accurately it classifies instances, and how inaccurately it classifies instances.

TABLE 2.

Algorithms	Accuracy	Sensitivity/ Recall	Specificity	Precision	F1-Score	ROC
Logistic Regression	0.9624413145539906	TP / (TP + FN)	TN / (FP + TN)			
Decision Tree	1.0					
Random Forest	0.9929577464788732	TP/(TP + FN)	TN/(FP + TN)	(TP + TN) / (TP + FP + TN + FN)		

TP stands for true positive.
FN stands for false negative.
TN: Veritable negative
False Negative (FN)
This study also takes simulation error into account to properly quantify the performance of classifiers. In order to achieve this, we assess the performance of our classifier using the following metrics: x Root Mean Squared Error (RMSE), x Relative Absolute Error (RAE), x Root Relative Squared Error (RRSE), x Kappa statistic (KS), which is a chance-corrected measure of agreement between the classifications and the true classes.The findings of the data analysis are presented in this section. The 10-fold cross validation test, a method for assessing predictive models that divides the original set into a training sample to train the model and a test set to evaluate it, is what we utilize to apply and assess our classifiers. Following the use of preprocessing and preparation techniques, we attempt to visually analyze the data in order to determine the distribution of values with respect to efficacy and effectiveness.

EFFECTIVENESS:
This section assesses each classifier's efficacy in terms of accuracy, time to create the model, properly classified cases, and wrongly categorized instances. True positives and false positives are represented by the x and y coordinates, respectively, in the definition of the ROC space. The performance is summarized over all potential thresholds via the ROC curve. Classification models that fall below the diagonal of the ROC graph are regarded as inferior, and the diagonal itself might be seen as random guesswork. more accurate than a haphazard estimate.

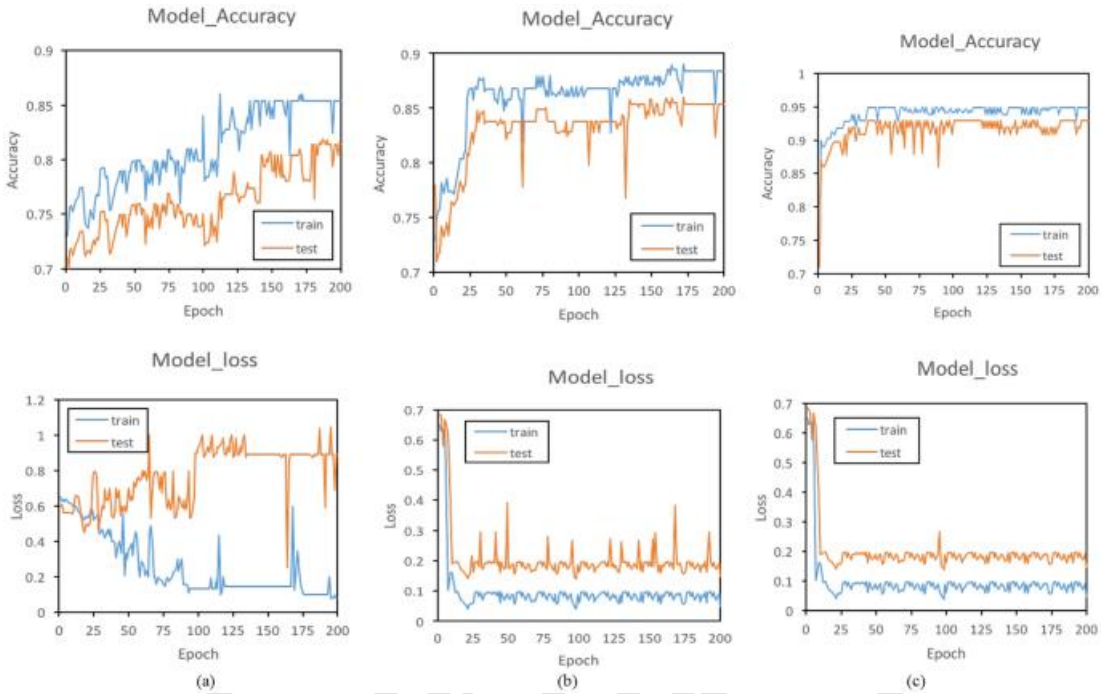
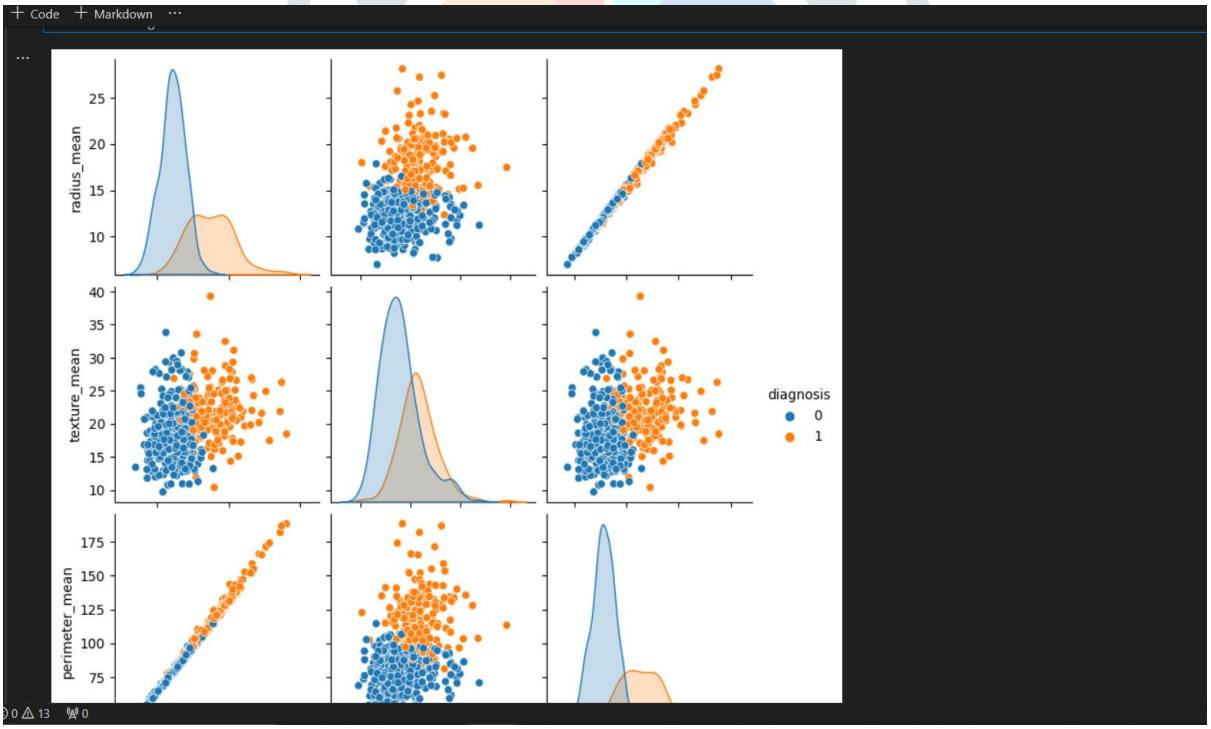


Fig. 2 Comparative graph of different classifier

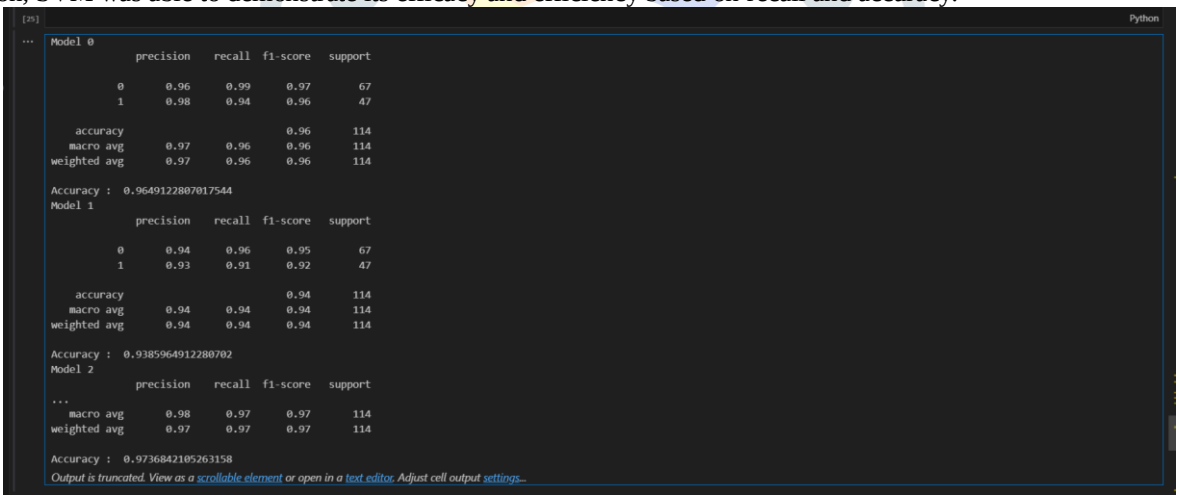
Comparing the smoothness mean and compactness mean, with orange denoting benign and blue denoting malignant



CONCLUSION AND FUTURE WORK

It is evident that k-NN builds its model in under 0.01 seconds, while SVM takes approximately 0.07 seconds. This may be explained by the fact that, in contrast to other classifiers that construct the models, k-NN is a lazy learner and does not accomplish anything during training. Conversely, the accuracy of SVM (97.13%) is higher than that of C4.5, Naïve Bayes, and k-NN, which range in accuracy from 95.12% to 95.28%. Additionally, it is evident that, in comparison to the other classifiers, SVM has the highest value of properly classified instances and the lowest value of wrongly classified instances. Now that the projected model has been created, we can examine the outcomes of our algorithmic efficiency evaluation. While k-NN accurately predicts 97% of instances that belong to the malignant class, SVM and C4.5 obtained the greatest value (97%) of TP for the benign class. SVM classifiers have a reduced false positive rate (0.03 for benign class and 0.02 for malignant class). k-NN, C4.5, and NB are the next algorithms to be used. These findings help us to understand why SVM has performed better than other classifiers.

In conclusion, SVM was able to demonstrate its efficacy and efficiency based on recall and accuracy.



FUTURE WORK

The findings of the investigation show that multidimensional data integration along with various feature selection, classification, and dimensionality reduction strategies might offer beneficial tools for inference in this field. In order to improve classification technique performance and expand its predictive capacity, additional study in this area is necessary. Our goal is to get high accuracy by learning how to parametrize our categorization approaches. We are investigating a variety of datasets and the potential applications of machine learning techniques in the characterization of breast cancer. Our goal is to minimize mistake rates while maintaining optimal accuracy.

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