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Breast Tumor Classification using Machine Learning

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Abstract

One of the most contagious illnesses and the second-leading cause of cancer-related death in women is breast cancer. Early detection of tumor is critical for providing healthcare providers with useful clinical information that can help them make a more accurate diagnosis. To accurately diagnose breast cancer, a computer-aided detection (CAD) system that employs machine learning is required. The paper proposes a web-based tumor prediction system that analyzes different machine learning algorithms for breast tumor classification to determine the best-performing model. Different evaluation criteria namely accuracy, ROC AUC, etc are mostly employed for evaluating models but they make the selection of the best model strenuous. A multi-criteria decision-making (MCDM) approach has been employed for selecting the best performing model. Further, a web-based portal has been developed to provide the user interface for this functionality.

Keywords: Machine Learning, Tumor, Classification, Accuracy, MCDM

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1. Introduction

Cancer has been and continues to be a monster of intrigue, which medical science has been until now, unsuccessful in taming. Early detection, followed by aggressive chemotherapy and radiation treatment, has been the mainstay of management for several decades now. Tumors which are amenable to surgery, i.e., the ones which are not present near or are yet to infiltrate life-sustaining structures, are resected from the body making sure that the margins are clear, i.e.- there is no residual mutant tissue which might wreak havoc in the future. The uncontrolled growth of normal human cells owing to the rogue genetic machinery acquired by them is still a matter of great interest in the scientific fraternity. The continuous clamor to come up with new pathological mechanisms and novel treatment strategies augurs well for medicine at large. If we consider the prevalence and frequency of different types of cancer among genders, then it is worth noticing that breast cancer which is the focal domain of discussion in this paper, is the most common non-skin cancer in women and is trumped only by lung cancer as far as cause of cancer deaths worldwide is concerned.

There are a multitude of risk factors and several genetic mutations which play a pivotal role in the development of breast cancer. Risk factors which are of particular concern and which are key determinants in the origin of carcinoma include among others, first-degree relatives with breast cancer, African and Asian race/ethnicity, age, early menarche (11 years or younger), age at first live birth (women who have their first live birth before 20 have a lower risk), benign breast disease, Estrogen exposure as a part of Hormone Replacement therapy, breast density, radiation exposure, obesity, diet, exercise etc.

These factors along with the probability of mutational changes, form the background determinants with substantial predictive value as far as development of breast malignancy is concerned.

The other significant part of the pathological process is the genes, which exhibit mutation when there is commencement of malignant changes in the breast. The most common “single-gene” mutations when it comes to hereditary susceptibility to breast cancer are as follows: BRCA1 (17q21), BRCA2 (13q, 12-13), TP53 (17p13.1) and CHEK2 (22q12.1). These genetic mutations either in isolation or in combination with one another heavily influence the pathological process. A third important distinction is the molecular mechanism through which these tumors occur.

There are three important pathways that when set in motion, give rise to different types of carcinomas of the breast: ER (positive) HER2 (Negative), ER-Negative HER 2 (positive) and ER (Negative) HER2-Negative.

The quest for the definitive treatment of cure hinges significantly on the cytological behavior of the suspected breast mass and the degree of anaplasia exhibited by the cells constituting the incriminating entity, i.e., whether the mass is benign or malignant. A benign mass is one which is more or less confined to its area of origin and has minimal potential to metastasize, i.e., spread to distant areas of the body through lymphatic or hemaotogenous routes. The treatment protocol for such an innocuous growth is aimed at fully eradicating and eliminating it from the body through surgical resection keeping in mind an adequate margin of safety so that any pre-malignant behavior can also be mitigated then and there. In contrast, a malignant breast mass is quite the opposite both in behavior and response to therapy, when compared to its benign counterpart. Malignant breast tumors show a high degree of dysplasia and ananplasia and also pose a high nucleo-cytoplasmic ratio as far as cytology is concerned. Additionally, the probability of them metastasizing and forming secondary tumours at different remote sites in the body is also quite substantial. To ameliorate the situation in such cases, careful planning of management strategies is required. After confirmation of malignancy has been obtained, a combination of chemotherapy, radiotherapy and, in most cases, surgery is carried out. The surgical resection in such cases, more often than not, involves the complete removal of either the affected breast only or both breasts, i.e., a modified radical mastectomy, which may be unilateral or bilateral. The sites to which the tumor has metastasized are localized through either a CT or PET scan, after which appropriate dosages of chemotherapy and radiotherapy are administered either in isolation or in combination. Therefore, the role of AI and machine learning in formulating such a distinction and subsequent gradation of both types of tumors based on their infiltration and spread is being explored at a very significant scale. Also, the ability to detect secondary's automatically is what these systems will be trained to do. This will involve creating a database of a prototype of each kind of tumor and training the machine learning algorithm to apply it to the test sample to create a corroborative match and potentially provide possible treatment mechanisms as well.

Histopathologically and behaviorally there are several different types of breast cancers that have been classified, but the major broad stratification is based on whether the carcinoma is of the infiltrating type or is confined in situ. The focus of research in this paper is ductal carcinoma in situ (DCIS), which has been defined as a malignant clonal proliferation of epithelial cells that is limited to ducts and lobules. Early and accurate detection of such a tumor through AI-trained models employing deep machine learning algorithms proved to be a game changer as far as reducing morbidity and mortality were concerned.

For this study, the Wisconsin Breast Cancer Data Set [12] has been selected for training machine learning models. Overall performance evaluation of a model cannot be accomplished by utilizing few performance metrics, so this paper proposes an MCDM-based models (alternatives) ranking method that handles all the selected criteria's (performance metrics) and ranks the alternatives correspondingly. The technique for order preference by similarity to the ideal solution (TOPSIS) is employed in the study for ranking purposes, with the Analytic Hierarchy Process (AHP) selected in MCDM to derive evaluation criterion weights.

The paper is divided into sections that are structured logically. The earlier literature on this topic is discussed in Section II, along with the pertinent shortcomings that led to the advancements in this work. Section III dives into the project's strategy in greater depth, with an emphasis on the numerous machine learning algorithms used. The observations, as well as an in-depth investigation of the resolution of the most appropriate system and the subsequent results, are presented in Section IV. The discussion of the suggested technique is included in Section V. Section VI of the paper finishes with a futuristic conclusion.

2. Review of Literature

Several studies have been carried out in the field of breast tumor detection and classification, each with a different subarea of interest and showing different ways to combat the spread of the disease.

Tumor classification via Ensemble learning Method, i.e. - making the algorithm analyze the efficacy of existing models by calculating their F3 score (which indicates the rate of false negatives produced by any model algorithm) is the basis of the work carried out by [1]. Using a vote mechanism, the three top classifiers—a multilayer perceptron network, support vector machine learning with stochastic gradient descent optimization, and basic logistic regression learning—are employed in an ensemble setting to classify data. They also assessed how well the hard and soft voting mechanisms worked. They have also given due attention to probability-based voting methods to bring about an improvement in performance. The research by Mengwan et al. [2] focuses on the classification methodology formulation by using the combined characters of morphology and texture of the various ultrasound images. It employs local binary patterns (LBPs), histograms of oriented gradients (HOGs), gray-level co-occurence matrices (GLCM), Support Vector machines (SVMs) and naive Bayes (NB) to churn out a classification.

In the research work by Majid et al. [3], the fulcrum of the process rests on the application of Convolutional Neural Networks (CNNs) which have been trained using machine learning. These models have been designed to produce advanced classification and in-depth sub classification of the tumors based on histopathological evidence. The suggested method tries to categorize breast tumors into subclasses other than benign or malignant, such as fibroadenoma,

lobular carcinoma, etc. When compared to state-of-the-art models, experimental findings on histopathology images using the BreakHis dataset demonstrate that the DenseNet CNN model obtained great processing performances with 95.4% accuracy in the multi-class breast cancer classification test. The paper [4] by Maleika Heenaye et al. has its priorities defined, i.e.,- to come up with the most efficient and sensitive detection algorithm so that the incidence of false positive and false negative diagnoses can be curtailed significantly thus saving both time and resources in the process. This it does by making use of ResNet50 and then further going on to sub classify the lesions into various types. The performance of the suggested deep learning model in classifying these four forms of breast cancer abnormalities, including masses, calcifications, carcinomas, and asymmetry mammography, was 88%. In the work [5] done by David A et al, we get to witness an integration of the various machine learning techniques with feature selection/extraction methods so that their performances can be compared and the selection of the most suitable method can be effected. The authors have tried to make computer-aided detection (CAD) systems as their scaffold on which their research will rest. By employing linear discriminant analysis (LDA) to reduce the high dimensionality of features and applying the new reduced feature dataset to SVM, this article offered a hybrid technique for the diagnosis of breast cancer. The proposed method had a 98.82% accuracy rate.

Epimack et al [6] have attempted to address the issue of optimization of frameworks for breast carcinoma classification and subsequently come up with a novel framework which incorporates all desirable features that are expected from an efficient classification algorithm. Consequently, it is intended by the authors that such a framework would enable suitable modifications in treatment. A classification-based model based on ensemble learning has been developed in [7]. One of the three CNNs was directly trained using the photos from the dataset. The decomposed images produced by the 1D Empirical Wavelet Transform applied to rows and columns and transformation to make two dimensional data are used to train one of the other two CNNs. In a similar way, the third CNN model is likewise trained using VMD. In order to train the models at the molecular level, the deconstructed forms of the original dataset are taken into consideration. The results of the first stage of classification are known as the meta data, which is utilized to train the MLP classifier in the second stage. The goal of the paper [8] is to develop an ensemble model for decision support utilizing Bayesian networks and the radial basis function. The well-investigated open access data set "Wisconsin Breast Cancer Data set (WBCD)" was extensively used in this study. Training and testing portions of the data set are separated. The new strategy beat the existing methodologies, according to experimental findings, and recorded a remarkable accuracy of 97% when classifying data related to breast cancer. In the study [9], they suggested a stacking ensemble deep learning model based on a 1D-CNN to conduct a multi-class classification on the five most prevalent malignancies in women using RNASeq data. The R software's GDCquery function was used to download the RNASeq gene expression data from the Pan-Cancer Atlas using the TCGA biolinks package. In the study [10], different ML algorithms were investigated on 20 exome datasets from 5 different cancer types. A derivative dataset was created using natural language processing and probabilistic distribution after data cleaning was done on 4181 cancer variants with 88 characteristics. To minimize the large dimensionality of the data, an exploratory dataset analysis utilizing principal component analysis was then carried out on 1 and 2D axes. In order to categorize breast cancer as malignant or benign, 20 ML classifiers are explored and used in the study [11] using Wisconsin's Breast Cancer dataset. Nine of the twenty algorithms are written in Python and executed in Colab notebooks, while the remaining algorithms are run through the Waikato Environment for Knowledge Analysis (WEKA) programme. The algorithm with the highest accuracy, 98%, was discovered to be stochastic gradient descent.

To get the best results, many classification methods were used in the paper [13]. Brain MRI images are seen as being more significant than CT imaging. Along with the dataset from the Cancer Archives, this dataset includes roughly 300 MRI pictures that have been split into aberrant and normal classes to produce results for binary classification. In the study [14], SELF, a stacked-based ensemble learning framework, is presented for computer-aided diagnosis tools to classify breast cancer at an early stage using histological pictures of tumour cells. In this study, the author uses the Wisconsin Breast Cancer Database (WBCD) with 569 occurrences and the BreakHis dataset with 7909 histopathological pictures for the performance evaluation of our suggested framework. In a study [15], textural features from MRI scans of breast tumors and their surrounding tissue were classified using machine learning, together with genetic subtypes, to predict the pathological complete response (PCR) following neoadjuvant chemotherapy. Attempts were made in this work [16] to investigate the issue of miss-classification in the diagnosis of breast cancer in women, and to create models based on machine learning and predictive analytics. Their main goal was to aid in minimizing mistakes made when determining whether a breast tumour was malignant or not. For the classification of breast cancer, the paper [17] suggested an Ensemble Bagging Weighted Voting Classification (EBWvc). Initially, bagging is used for the obtained data to address overfit in machine learning. The ensemble bagging classification offers machine learning an efficient foundation for faster computation and better results. For the classification of breast cancer, weighted voting is used. The research [18] aims to create a DL-based algorithm that can identify metastatic regions that are present in small image patches that are acquired from larger digitally-based pathology images of lymph nodes. For classifying our photos, they used a hybrid CNN-based classification technique. For transfer learning and full training, two well-known deep and

pre-trained CNN models (Resnet50, VGG16) and two fully-trained CNNs (Mobile-net, Google net) were used.

Breast cancer disease has stunned the nation in recent times and continues to attack the health of individuals and communities worldwide. Extra trees, Adaboost, KNN, Random forest, and SVM are five computer vision methods used in this article to recognise or validate tumor in breast tumor dataset. The current paper builds on previous work by demonstrating a novel complete solution based on a web-based tumor prediction system. Furthermore, the article compares and contrasts various machine learning algorithms using an MCDM based approach before recommending the most efficient model for breast tumor type classification. The contributions of this study are fourfold:

- The study considers an independent breast tumor dataset to check the effectiveness of the proposed model.
- Multiple machine learning models are trained and tested with different hyperparameter to find the best.
- The study proposes an MCDM method to rank different models (alternatives).
- Designing a web platform for the user interface to the health server on which the selected trained model is running.

3. Methodology

The present paper proposes a web based breast tumor classification system. Tumor type detection is done based on trained machine learning algorithm. Different machine learning algorithms were trained and tested to find and rate the best performing one using proposed MCDM approach. In the proposed system user (Lab technician/Researcher) is provided with a web based facility to upload the tumor CSV file to the server for prediction. Overall proposed MCDM approach and workflow for using web based application is shown in Figure 1 a), b) below.

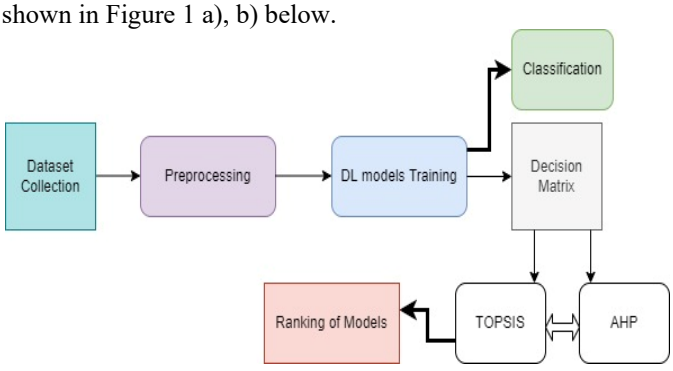


Figure 1 a. Proposed approach

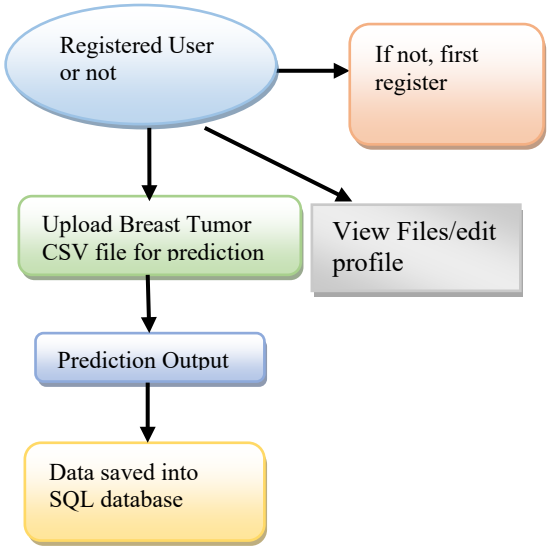


Figure 1 b. System Overview

3.1 Dataset Collection and Preprocessing

Open source "Wisconsin Breast Cancer Data Set (WBCD)" [12] dataset has been used for the task, Different machine learning (ML) models such as Extremely Randomized Trees (Extra-Trees), Adaptive Boosting, Extreme Gradient Boosting (XGBoost), Support Vector Machine (SVM), Random forest classifiers were trained using feature viz. The dataset does not contain any null values.

Data from the microscopic investigation of breast lumps was included in this dataset. To compute features, fine-needle aspirates were scanned digitally. One of the greatest ways to determine whether malignant tumors are present is via fine-needle aspiration.

There were 569 cases in this dataset. 32 characteristics were taken from photos of atomic nuclei for each case. These consist of the fractal dimension, symmetry, smoothness, area, compactness, concave points, radius, and perimeter of the nucleus. The mean, standard error, and worst or largest mean of the aforementioned attributes were used to calculate the remaining features. The dataset is then preprocessed before training. The dataset consist of 2 classes viz. benign or malignant. This is a binary classification as there are 2 classes so benign classes were encoded with 0 and malignant with 1. If two or more features are strongly correlated, it means that they contain similar information, and using both of them in the model might not be necessary. The intuition is that highly correlated features might introduce multicollinearity in the model, which can lead to unstable estimates and incorrect predictions. Therefore, removing one of the correlated features may be a good idea. This way we can keep the most relevant and independent features in the model. The correlation matrix of features produced using heatmap is shown in Figure 2. The features that are highly correlated with others like "radius_mean" is highly correlated to some features like "radius worst", "perimeter_worst", and "area_worst" are removed. The perimeter_mean and the radius_mean have a 100%

correlation, the perimeter_mean and area_mean has 99% correlation.

After removing the highly correlated columns and the unwanted features such as "Id" column, the data is left with 23 columns. Since evaluating model with one criterion such as accuracy or precision is not a good idea especially for the imbalanced dataset. Different evaluation criteria namely accuracy, precision, recall, macro average F1 score and ROC AUC has been used with MCDM method to rank and select different models. The equation of first four is shown below.

The number of right predictions divided by the total number of predictions is how a classification model's accuracy is summarized. The ratio of actual positives to the sum of true positives and false positives is known as precision. The recall is determined by dividing the overall number of Positive samples by the number of Positive samples accurately categorized as Positive. A receiver operating characteristic curve (ROC curve) is a graph that shows how well a classification model performs across all categorization levels. The Area under the Curve (AUC) is a summation of the ROC curve that measures a classifier's capacity to discern between classes. The greater the AUC, the stronger the model's ability to differentiate among positive and negative outcomes.

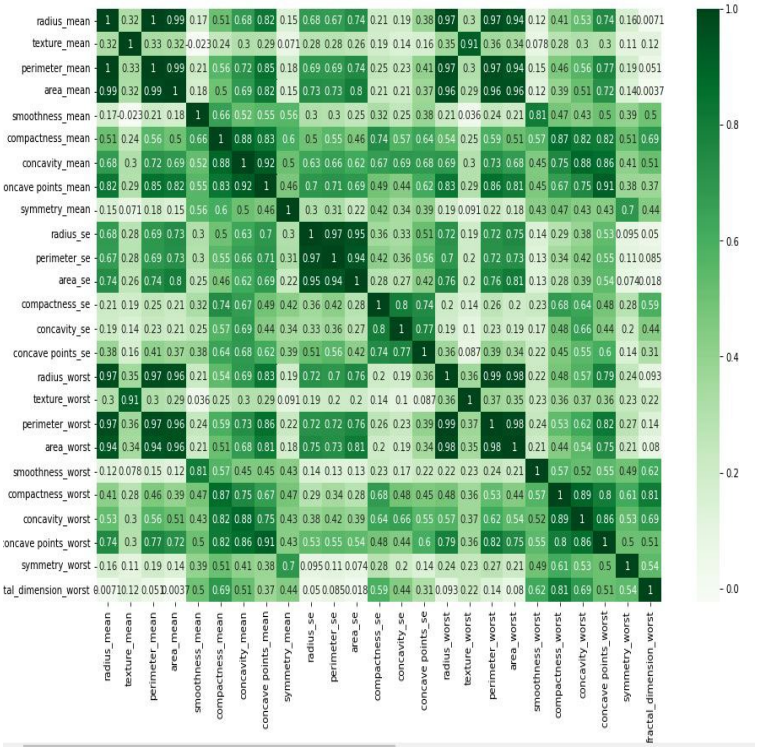


Figure 2. correlation matrix of features

$$\text{Accuracy} = \frac{TP+TN}{TP+FN+FP+TN} * 100 \quad (1)$$

$$\text{Precision} = \frac{TP}{TP+FP} \quad (2)$$

$$\text{Sensitivity} = \frac{TP}{TP+FN} \quad (3)$$

$$\text{F1 Score} = \frac{2*sensitivity*precision}{sensitivity+precision} \quad (4)$$

Figure 3 shows the data distribution of the features against the density distribution. It shows the univariate distribution of features.

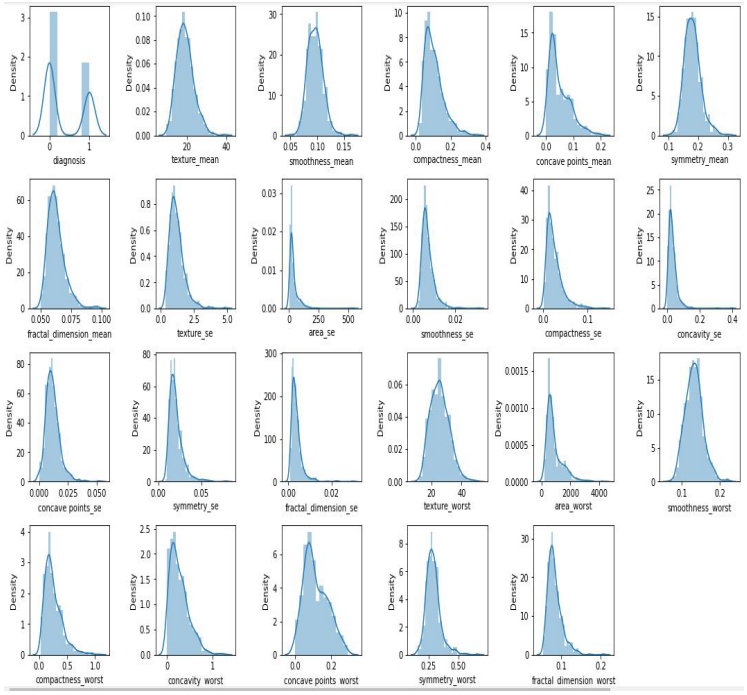


Figure 3. Data Distribution of features

3.2 Machine Learning Models

The study aims at classifying tumor into two classes (binary classification) viz. benign and malignant, for this machine learning (ML) algorithms were employed. ML models such as Extra trees, Adaboost, KNN, Random forest and SVM were trained and tested. Extremely randomized trees (Extra-Trees) employs averaging to increase predictive accuracy and control over-fitting by fitting a number of randomized decision trees on various sub-samples of the dataset. Extra tree classifier with criterion gini, bootstrap false and rest parameter as default was chosen for training.

AdaBoost, also referred as Adaptive Boosting, is a Computational Model used in the Ensemble Method. The most common method employed along with AdaBoost is decision trees with one level, or decision trees having only one split. Decision Stump is another name for these trees. Adaboost algorithm with random state zero and estimator 100 was chosen for the task.

A supervised machine learning (ML) technique known as K-nearest neighbours (KNN) can be applied to classification and regression predicting issues. The K Nearest Neighbor method, as its name suggests, uses K Nearest Neighbors to forecast the class or continuous value for a new data point. It is predicated on the notion that the most "similar" observations in a data set are those that are closest to a certain data point. The chosen number of closest neighbours is K. By calculating the distance between the test data and all of the training points, KNN tries to predict the proper class for the test data. Support vector machines (SVMs) are a class of supervised learning methods for classification, regression, and detec``tion of outliers. The following are some of the benefits of support vector machines: In high-dimensional spaces, it works well.
Random Forest is a classifier that combines a numerous decision trees on diverse subsets of a dataset and averages the results to increase the dataset's predicted accuracy. After testing with different hyperparameter, Random forest with 100 tree and entropy criterion was selected for training the model

3.3 Web based Deployment

The present study provides a web page for user (Lab technician/Researcher) interface for predicting breast tumor type. The web page asks the user to register there and then allow uploading breast tumor CSV file for ML testing on server and editing of one's profile and then data will be saved on SQL database. The servers for breast tumor check viz. health server is designed on the WAMP platform. This server for health service or care provides facilities of information storage, user data management and most important of breast tumor detection; it is constructed on the Windows-Apache-MySQL-PHP (WAMP) platform. The acronyms WAMP (Windows, Apache, MySQL, and PHP) stand for Windows, Apache, MySQL, and PHP. It's a software stack that ensures Apache, MySQL, and PHP are installed on your operating system when you run WAMP (Windows in the case of WAMP). Despite the fact that they can be installed separately, they are frequently packed together, and for good reason. WampServer is a website development platform for Windows. With Apache2, PHP, and a MySQL database, one can build web apps. WAMP Server allows us to construct dynamic web applications using MySQL, PHP, and Apache. WAMP Server installs everything you need to develop Web applications quickly and easily. MySQL services include database management, switch online/offline access to provide everyone access or only localhost access, and server management. Additionally, PhpMyAdmin makes it simple to handle ones PHP files. The server consists of two parts: database and website. The database stores information, whereas the website performs operations such as managing user information, accessing data files, predicting tumor type and so on as shown in Figure 4 and Figure 5a) b). The website is built using the PHP programming language. Database is designed using MySQL and consist of number of tables for storing patient information. Thus it provides an all inclusive web based system with efficient memory utilization and breast tumor prediction system.

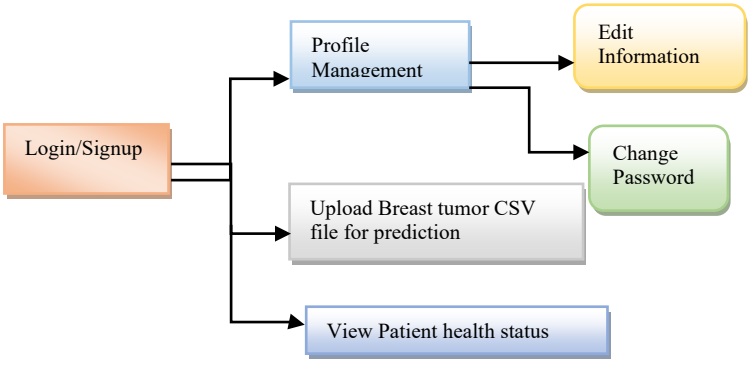
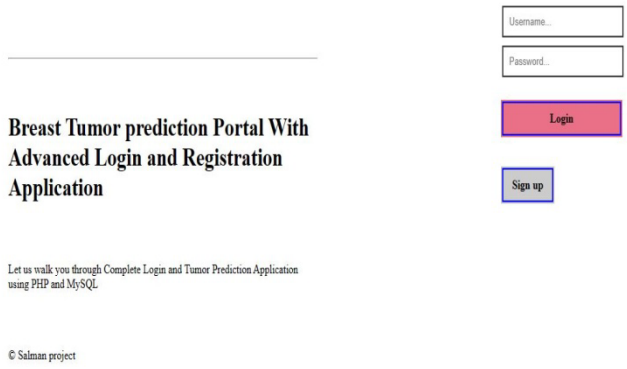
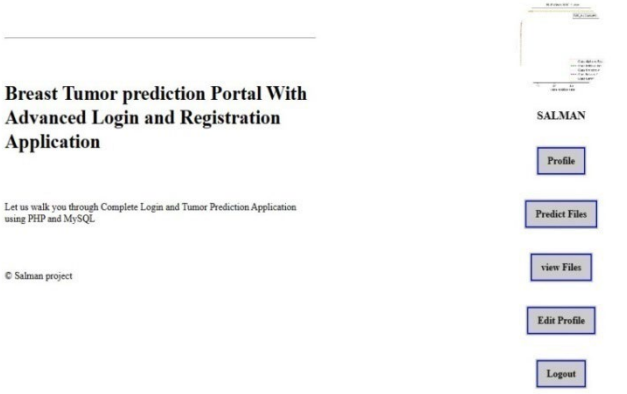


Figure 4. Website Design



a)



b)

Figure.5a) b) User interface for Breast Tumor Prediction

3.4 MCDM

When many criterion (or objectives) must be evaluated together in order to list or choose between options, MCDM is used. It can resolve issues with various criteria and make relevant and high-quality decisions, especially when choosing the best option. In this study, the TOPSIS method was integrated with the analytical hierarchy process (AHP). The study applies the hierarchy structure of AHP for assigning weights, and the TOPSIS method utilizes these weights with a decision matrix to allocate ranks. Different evaluation criteria or performance matrix's such as accuracy, macro average F1 score, Precision, Recall and ROC AUC score has been employed for alternatives (models) Extra trees, Adaboost, XGBoost, Random Forest and SVM. The steps for AHP and TOPSIS with the decision matrix m*n are presented below where each element L_{ij} represents the value of the j^{th} criterion for the i^{th} alternative. Decision matrix as defined by:

	A1	A2.....	Aq
R1	L_{11}	L_{12} ….	L_{1q}
R2	L_{21}	L_{22} ….	L_{2q}
.			
Rp	L_{p1}	L_{p2} ….	L_{pq}

R1, R2... Rp are the ranking possibilities of models based on the assessment factors Aq.

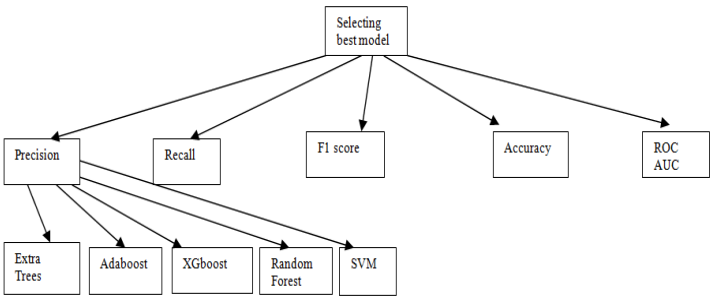


Figure 6. Hierarchical structure

Steps for AHP

Step 1) First step includes developing a hierarchical structure with the goal at the top, attributes/criteria at the second level and the models/alternatives at the third level as shown in Figure 6.

Each alternative has their own value of criteria associated with them, for example each model will have their own precision associated with them, and similarly each model will have their own value of Recall.

Step 2) Determine the relative importance of attribute/criteria with respect to goal (ranking the models). For this create a pair wise comparison matrix. This pairwise matrix gives the relative importance of various attribute with respect to the goal, for example how important is precision while selecting a model/attribute. This pairwise comparison matrix is created with the help of scale of relative importance (Saaty's scale (1980) of relative importance). This is the scale of relative importance in which one is for equal importance, 3 is given for moderate importance, five for strong importance, 7 for very strong, 9 for extremely important values. With 2, 4, 6 and 8 assigned for intermediate values.

The length of pair wise matrix is equivalent to the number of criteria used in decision making process. Here the study has a 5×5 matrix as this study has had five criteria.

The value in the pairwise matrix depends upon the decision maker or the person who want to select the model. To determine the value of first cell (1st row, 1st column), some question should be asked to the person who is selecting the model, such as how important precision with respect is to Recall.

Assuming precision is of a moderate importance than recall, then if recall is given X value precision will be given 3X value (Table 1, shown in bold), one can see here that for moderate importance a value of 3 is given. To proceed further one must divide the row element by the column element (Table 1).

Since precision is the row element and recall is a column element. The recall has become an x value and precision as 3x, so dividing 3X by X gives output 3. For 1st column 2nd row, recall is given X value and price 3X so it will give 1/3. Each Cell value will be computed like this depending on relative importance and the pairwise comparison matrix is shown in Table 1.

Table 1 Pairwise Matrix

	Precision (%)	Recall (%)	F1 score (%)	Accuracy (%)	ROC AUC
Precision (%)	1/1	**3/1=3**	1/5	1/7	1/4
Recall (%)	1/3=0.333	1	1/7	1/9	1/6
F1 score (%)	5	7	1	1/3	3
Accuracy (%)	7	9	3	1	5
ROC AUC	4	6	1/3	1/5	1
SUM (column)	17.33	26.00	4.68	1.79	9.42

Step 3) Create normalize pairwise metrics by dividing each cell value with the sum of the column elements as shown in Table 2.

Table 2 Normalize Pairwise Metrics

	Precision (%)	Recall (%)	F1 score (%)	Accuracy (%)	ROC AUC
Precision (%)	0.06	0.12	0.04	0.08	0.03
Recall (%)	0.02	0.04	0.03	0.06	0.02
F1 score (%)	0.29	0.27	0.21	0.19	3.00
Accuracy (%)	0.40	0.35	0.64	0.56	0.53
ROC AUC	0.23	0.23	0.07	0.11	0.11

Step 4) Next is calculation of Criteria weights. These are calculated by averaging all elements in a row of Table 2. Table 3 shows the calculated criteria's weights.

Table 3 Criteria weights

	Precision (%)	Recall (%)	F1 score (%)	Accuracy (%)	ROC AUC	Criteria Weights W_i
Precision (%)	0.06	0.12	0.04	0.08	0.03	0.064454
Recall (%)	0.02	0.04	0.03	0.06	0.02	0.033594
F1 score (%)	0.29	0.27	0.21	0.19	0.32	0.255223
Accuracy (%)	0.40	0.35	0.64	0.56	0.53	0.49611
ROC AUC	0.23	0.23	0.07	0.11	0.11	0.150139

Steps for TOPSIS

1. Input Decision Matrix =$[L]_{m\times n}$
2. Calculation of normalized decision matrix and weighted normalize matrix and is given by:

$$\bar{L}_{ij}=\frac{L_{ij}}{\sqrt{\sum_{k=1}^{m} L_{ij}^2}} \quad (5)$$

Weighted normalize matrix= $W_j * \bar{L}_{ij}$ where W_j is the weights of the criteria calculated using AHP as highlighted in step 4 of AHP process.

3. Next is the calculation of Ideal Best and Ideal worst value for the criteria. Since all the criteria are beneficial for the alternatives, hence ideal best will be maximum value and ideal worst will be minimum value.

V_j^+= correspond to ideal best value

V_j^- = corresponds to the ideal worst value

4. Calculate the distance from ideal best and ideal worst values for all entries in a row (Euclidean) by:

$$S_i^+ = \sqrt{\sum_{j=1}^{m}(V_{ij}-V_j^+)^2},\ S_i^- = \sqrt{\sum_{j=1}^{m}(V_{ij}-V_j^-)^2} \quad (6)$$

where S_i^+ is the Euclidean from ideal best and S_i^- Euclidean distance is from ideal worst.

5. Calculation of TOPSIS or performance score by:

$$P_i = \frac{S_i^-}{S_i^+ + S_i^-} \quad (7)$$

6. Finally based on performance score, rank is determined. Higher the score better is the rank. Table 4 shows the results of different steps of TOPSIS method.

4. Results and Analysis

- The dataset was divided into 80:20 ratios for train and test part.
- All the mentioned ML models were trained using processed breast tumor dataset.
- Accuracy and macro average F1-score got the highest weight based on AHP method (Table 3).
- Adaboost shows the best result in terms of most individual metrics as per Table 5.
- It achieves the mean accuracy of 96.92 % and macro F1 score of 96.67%.
- KNN and SVM shows the lowest performance with

Table 4 TOPSIS method Results

	Evaluation Criteria's								
alternatives	**accuracy**	**precision**	**recall**	**f1 score**	**ROC AUC**	S_i^+	S_i^-	P_i	**rank**
Etree	0.225091141	0.029892336	0.01513789	0.115963678	0.067981519	0.001397555	0.011196	0.889022	1
Adaboost	0.225091141	0.028080679	0.016114528	0.116083761	0.06897395	0.001811657	0.011369	0.862552	2
KNN	0.215940717	0.027174851	0.014649571	0.110824147	0.065429554	0.011553673	0.000651	0.053347	5
Random forest	0.223070616	0.028986507	0.01513789	0.114822894	0.067485304	0.003108492	0.008697	0.736683	3
SVM	0.220004991	0.029892336	0.013998479	0.112913582	0.065783994	0.007111143	0.005329	0.428345	4
V+	0.225091141	0.029892336	0.016114528	0.116083761	0.06897395				
V-	0.215940717	0.027174851	0.013998479	0.110824147	0.065429554				

mean accuracy of 92.98% (KNN) and 94.73 % (SVM) and macro average F1 score of 94.03% (SVM) and 92.29% (KNN).

- Extra Trees and Random Forest shows overall good performance as per Table 5. They achieve mean accuracy of 96.92% (Extra Trees) and 96.05% (Random Forest) and macro average F1 score of 95.62% (Random Forest) and 96.57% (Extra Trees)
- Figure 7 shows the confusion matrix of all trained models. The Confusion Matrix is a graphic depiction of true vs. predicted results. It is a table-like arrangement that gauges the effectiveness of the Machine Learning techniques.
- The ROC AUC curve for all the models is shown in Figure 8.
- Proposed MCDM approach based on TOPSIS and AHP ranks the alternatives (models). Table 4 shows the rank with Extra Tree being 1st, Adaboost 2nd and the rest as shown in Table 4. Table 5 which shows the results is the one which has been used as decision matrix. Accuracy got the highest criterion weight using AHP method followed by F1 score.
- Though Adaboost was having higher F1- Score than Extra Tree but it is placed 2nd in ranking because precision has been given less importance in comparison to recall in the Pairwise Matrix (Table 1).
- Table 6 below shows the comparison of different works with the proposed approach of this study. The proposed work excels in selecting best model based on different evaluation parameters and the web-based framework provides stable user interface for breast tumor prediction with secure SQL data storage.

Table 5. Breast Tumor Classification Result

Model	Precision (%)	Recall (%)	F1 score (%)	Accuracy (%)	ROC AUC (%)
Extra-Trees	99	93	96.57	96.92	95.9
Adaboost	93	99	96.67	96.92	97.3
KNN	90	90	92.29	92.98	92.3
Random forest	96	93	95.62	96.05	95.2
SVM	99	86	94.03	94.73	92.8

5. Discussion

The suggested system leverages a web based infrastructure to gather Tumor CSV file [12] from users in order to detect potential cancer illnesses early, with the prediction result kept with the user personal info. On the WBCD testing dataset, the performances of five different classification algorithms are assessed. The current study provides a distinctive context for medical diagnosis. To make the decision, AI methods are utilized to analyze the gathered data. The technology is scalable and straightforward to use. It can give consumers with long-term and constant monitoring. A real-time tumor tracking system is proposed in the study. The system is made up of four key parts: data collection and uploading, data analysis server (which employs machine learning methods), user access, and database storage to swiftly identify probable tumors from supplied information in CSV file having same columns as in [12]. The novelty of this system is the provision of breast tumor prediction system in the form of webpage for the easy access of the users. Patients or users can check whether they have any form of tumor i.e., benign or malignant by themselves without any aid at just the click of the mouse. For the purpose of proof of concept, the system was deployed locally using WAMP. The motive of the system is to check the AI feature rather than the sustainability of the web interface. For production grade usage one must be deploying the system on any cloud platform using their software-as-a-service (SAAS) and Platform as a service (PAAS) service, thus shedding the responsibility of all security related concern to them.

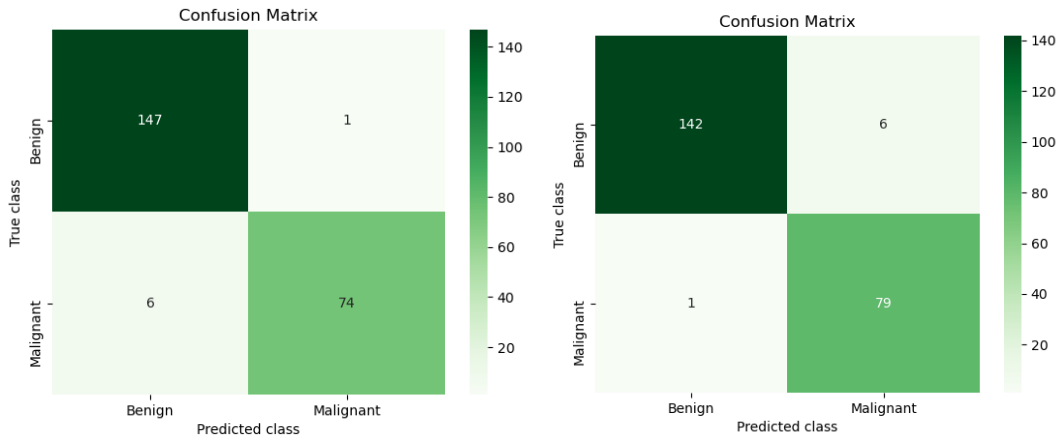
This platform will aid in the battle against breast tumor and early treatment of the same by assisting multidisciplinary researchers in continuing to build innovative medical procedures. The technique develops a web-based information storage system for collecting, storing, and analyzing tumor information from individuals at the national level with scalability to thousands of subscribers. The results of the current study can also serve as a suitable starting point for classifying breast tumors utilizing the picture dataset. The suggested method will raise the standard of breast cancer treatment programmes. This approach can help doctors make the best healthcare rational choice based on the tumor assessment while ensuring a secure distance from patients. This breast tumor categorization is low-cost, simple to use, and implement. MCDM method has been employed to rank the alternatives. Based on which Extra Tree receives first rank and Adaboost model also stood first in terms of all metrics as per Table 5, though all the models work well. The proposed system is designed keeping scalability in mind. More features in the form of CT scan classification facility or even skin disease classification can be incorporated in this. Medical practitioner along with patients or users can be given access to monitor the user profile by the admin who can control such access.

6. Conclusion

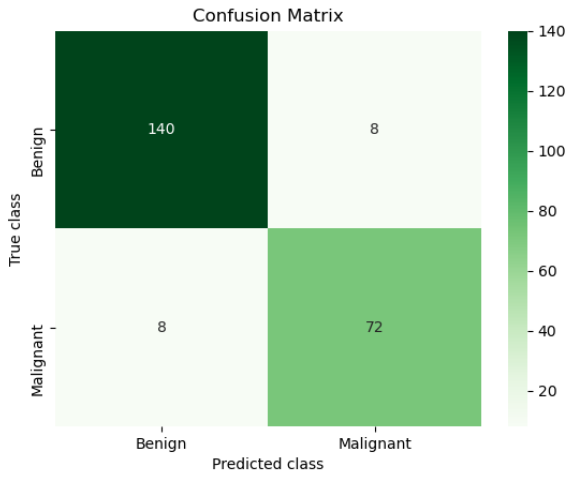
The present paper present analysis and selection of different machine learning algorithm for breast tumor type prediction. It proposes MCDM method for ranking different alternatives. With the data stored on a self-developed Web Portal with access to only authorized users, data privacy is ensured. The developed system has been tested using publicly available dataset of different patients showing their real time prediction output on local system with data storage and other operation of user information management and prediction algorithm being on remote health server. The proposed MCDM system would be viable in helping researchers in ranking models based on different alternatives. Adaboost outperforms all the models in terms of most individual evaluation metrics and was ranked first based on proposed MCDM approach. This developed web facility can be expanded to include more option of ML based prediction such as CT scan classification etc.

Table 6. Work Comparison

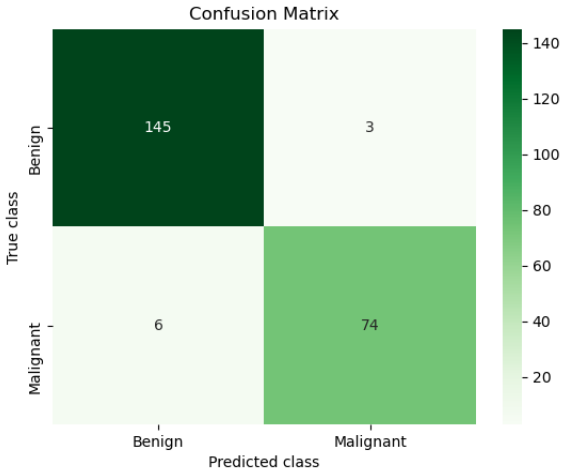
References	**Method Used**	**Dataset**	**Accuracy (%)**
Naga Deepti Ponnaganti et al[17]	Ensemble Bagging Weighted Voting Classification	Dataset based on Wisconsin Breast Cancer Dataset	95
Mengwan W et al [2]	ML models	Breast Ultrasound images	91.11
David A. Omondiagbe et al[5]	ML and DL models	Wisconsin Breast Cancer Dataset	98.82
Meerja Akhil Jabbar et al [8]	Ensemble Learning	Wisconsin Breast Cancer Data set	97
Taarun Srinivas et al[11]	ML models	Wisconsin Breast Cancer Dataset	98
Proposed Work	MCDM approach for ML models	Wisconsin Breast Cancer Dataset	97



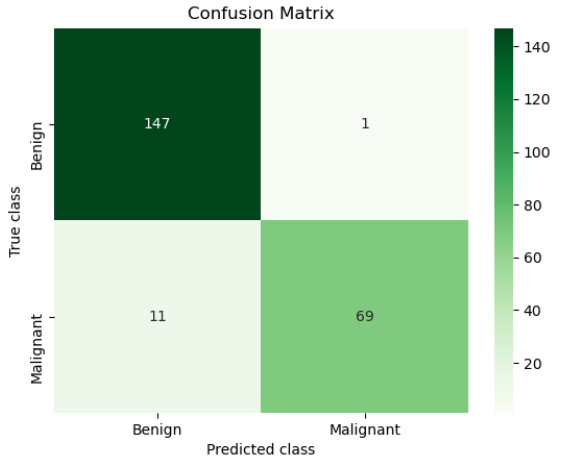
a) Extra-Trees b) Adaboost



c) KNN

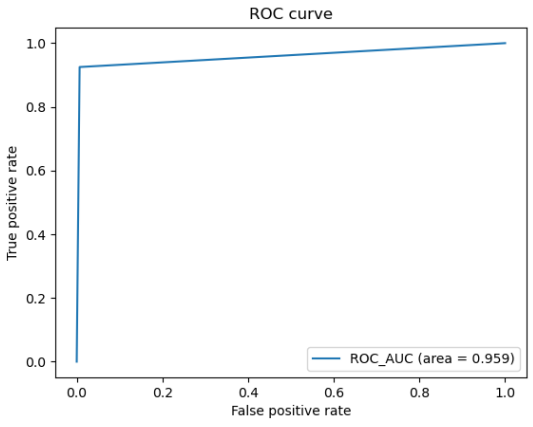


d) Random forest

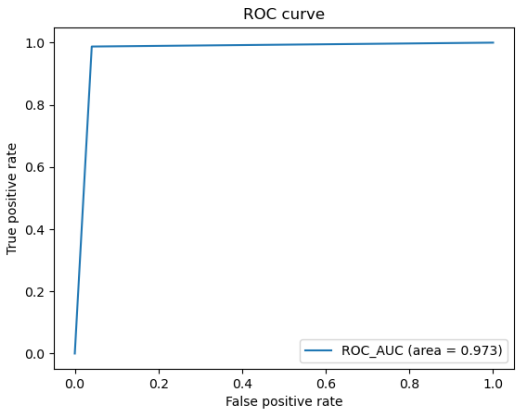


e) SVM

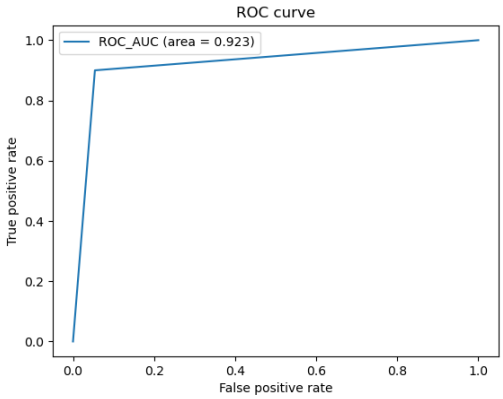
Figure 7. Confusion Matrix of all models



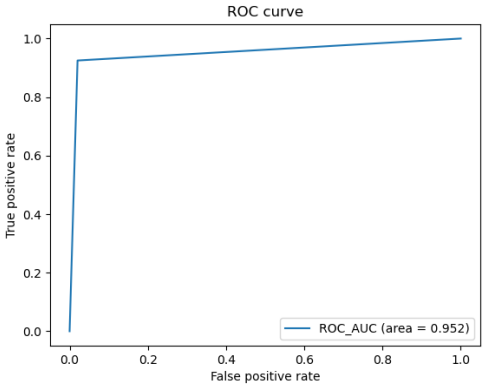
a) Extra-Trees



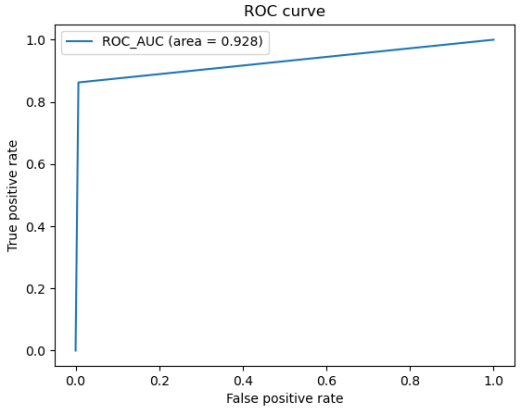
b) Adaboost



c) KNN



d) Random forest



e) SVM

Figure 8. ROC AUC curves

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