

# Exploring the Best Machine Learning Models for Breast Cancer Prediction in Wisconsin

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**Abstract**—This research focuses on predicting Wisconsin Breast Cancer Disease using machine learning algorithm, employs a dataset offered by UCI repository (WBCD) dataset. The under-gone substantial preparation, includes managing missing values, normalization, outlier elimination, increase data quality. The Synthetic Minority Oversampling Technique (SMOTE) is used to alleviate class imbalance and to enable strong model training. Machine learning models, include SVM, kNN, Neural Networks, and Naive Bayes, were built and verified using Key performance metrics and K-Fold cv. included as recall, accuracy, F1-score, precision and AUC-ROC were employed to analyze the models. Among these, the Neural Network model emerged the most effective, obtaining a prediction accuracy 98.13%, precision 98.21%, recall 98.00%, F1Score of 97.96%, AUC-ROC score 0.9992. Study underscores promise of ML boosting the diagnosis and treatment of WBCD illnesses, giving scalable and accurate ways for early detection and prevention.

**Keywords**—Wisconsin breast cancer disease prediction; ML; SVM; KNN; AUC-ROC; Naive Bayes

## I. INTRODUCTION

Among the most common cancers worldwide, breast cancer is a cause of death among women. Approximately 508,000 female died from breast cancer in 2011, according to the WHO. While mammograms and biopsies are effective diagnostic tools, they are often invasive and prone to errors. Current figures show that one in eight women will develop breast cancer, growing the need for early precise find to improve long-suffering survival rates through timely intervention and therapy [2]

Breast cancer begins in breast tissue and can metastasize, making it a primary cause of mortality among women. In 2018, the disease caused 9.6 million deaths globally, with predictions of a 50% increase in cases by 2040 [5]. Emerging data mining and big data technologies are now being employed to forecast and treat breast cancer, potentially enhancing patient care and reducing healthcare costs.

Advances in machine learning (ML) have enabled data-driven medical diagnoses, where algorithms analyze vast datasets to uncover patterns often missed by human diagnosticians. This paper compares multiple ML models for breast cancer of event anticipation using WBCD dataset, SVM, KNN, D-T, R-F, and L-R.

The study focuses on hyperparameter tuning to optimize performance metrics as prediction precision, recall, and accuracy. Without relying on feature selection Hyperparameter tuning systematically adjusts model parameters to identify optimal algorithm configurations, enhancing predictive accuracy. The structure of the stay of the paper is follow: Section II review machine learning literature related to breast cancer prediction. Section III describes the dataset and preprocessing steps, while Section IV details the training and evaluation of machine learning models. Section V present results and discussion models performance. Section VI achieve the analysis and suggest future directions for research in BC prediction.

This project aims to harness ML algorithms such as SVM, DT, and Neural Networks for predicting breast cancer using the WBCD dataset. By comparing these techniques with traditional diagnostic models, the study seeks to improve early detection accuracy, optimize patient treatment, and contribute to the global effort to reduce the burden of breast cancer [12].

## II. RELATED WORK

In Emilija Strelcenia et al. [1] (2023), the author early predicted BC increase survival chances and advance previously medical treatment. Breast cancer is a prevalent and serious public health problem that requires early detection and treatment. An accurate diagnosis and classification of benign cases can prevent unnecessary treatments. The paper presents a feature engineering method extract, modified feature from data using WBCD Dataset. Method is used compare six popular machine learning model for classifications: Random-Forest and Logistic-regression, Decision-Tree, MultiLayer Perceptron (MLP), KNeighbors and XG-Boost. when applied to the proposes feature engineering, achieved average accuracy of 98.64%.

The study, Aboudr MAA et al. [2] (2023) suggests the FLN algorithm as a way to make Breast Cancer diagnoses more accurate. (1) the FLN method can get rid of overfitting; (2) it can handle binary and multiclass classification problems; and it can work like a kernel-based support vector machine with structure of neural network. They used WBCD, which is breast cancer database. The experiment showed that the suggested FLN method worked very well, with an average of 98.37% accuracy, 95.44% precision, 99.40% memory, 97.644% F-measure, 97.654% G-mean, 96.444% MCC, and 97.854% specificity using the WBCD. This shows that the FLN method is a good way to diagnose BC, and it might also help with

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other problems in the healthcare field that have to do with applications.

Hossin, M. M., et al. [3] (2023) looks at eight machine learning methods for finding breast cancer. These are LR,RF,KNN,DT,AB,SVM,GB, and GNB. The Wisconsin Diagnostic Dataset is used to test these models and make sure they work. Sensitivity, specificity, Accuracy, area under curve (AUC) were used to measure how well model worked. Logistic Regression: Out of all the methods, it works 99.12% of the time. Researchers said that the study shows how important it is to find and treat breast cancer early so that people can live.

Arpit Bhardwaj et al. [4] (2022) compares four algorithms that are used for the WBCD dataset. These are MLP, KNN, GP, and RF, which are all classification algorithms. which was made by taking samples of the breast with a fine needle. We used genetic programming (GP), RF, multilayer MLP, and KNN on the WBCD dataset to sort the patients into those who are benign and those who are cancerous. RF has a classification rate of 96.24%, which is better than all the other classifiers. Based on the data of the suggested method, probable breast cancer is labelled.

Rasool, Abdur, et al. [5] (2022) is mostly about the WDBC approach. The author used a four-layer data exploratory method (DET) to make the model work better. This technique included feature selection, correlation analysis, and hyperparameter optimisation. The polynomial SVM model was the most accurate 99.3%. It was followed by the LR model 98.6%, the KNN model 97.35%, and the EC model 97.61%. The study used Kfold CrossValidation, confusion matrices show that the models worked even better. These results are in line with other study that has shown that SVM models are better at diagnosing breast cancer.

This is Kadhim, R. R. et al. [6] (2022), the main point of the study is to compare different ways to classify breast cancer using machine learning algorithms. With a score of 96.77, extreme randomise trees had the best F1-score out of the eleven models tested using the Wisconsin dataset. Specificity, sensitivity, precision, accuracy, and F1 score were used to rate how well each model worked. The goal of this study is to help find breast cancer early by finding the best Machine Learning models for classification.

In Sara Ibrahim et al. [7] [2021], the WBCD was used to test the author's suggested approach in this paper. For reducing the number of dimensions, analysis of correlation. Well-known machine learning models were tested to see how well they worked, and the seven best ones were picked for the next step. Tuning the hyperparameters was done to make the algorithms work better. Two different vote methods mixed with the classification algorithms that worked the best. Hard voting picks class that pick the most votes, while soft voting picks the class that has the best chance of winning. With accuracy 98.24%, a high precision 99.29%, and recall value 95.89%, the suggested method did better than the best work that had been done before.

In S.A. Abdulkareem, et al. [8] (2021), Wisconsin Breast Cancer Dataset (WBCD) and the Recursive Feature Elimination (RFE) algorithm are used to show how well the Random Forest and XGBoost classifiers work for finding breast cancer. The high level of accuracy reached by XGBoost 99.02% shows

that ensemble models are useful for medical tasks. When it comes to classification tasks, ensemble methods often work better than single classifiers. This is often seen in finding breast cancer, and machine learning classifiers like SVM and Random Forest have been used a lot.

In Naji Mohammed Amine et al. [9] (2021), the author says that improving the WDBC prediction for high accuracy is important to keep treatment and survival rates up to date. Once they had the results, they used five machine learning algorithms on the Breast Cancer Wisconsin Diagnostic dataset: SVM, RF, LR, DT (C4.5), and KNN. Goal of this study is the use ML model to identify and diagnose breast cancer and find the best ones in terms of confusion matrix accuracy and precision. Support vector Machine did better than all the other.

In Sahar A. El Rahman et al. [10] (2021), the authors aims to describe breast cancer early using machine learning algorithms and features selection methods. The methodology includes four datasets, preprocessing, processing, and model evaluation. Different classifiers such as decision tree, RF, LR, Naïve-Bayes, Knearest-neighbor, and support vector machine are compared using four different breast cancer datasets. The prospective models are checked using classification accuracy and confusion matrix. The results show that the RF technique with Genetic Algorithm (GA) is the most accurate, with an accuracy value of 96.82% on the WBC dataset. The C-SVM technique with the applied kernel function RBF is more advanced, with an accuracy value of 99.04% on the WDBC dataset. The RF technique with recursive feature elimination is the best, with an accuracy value of 74.13% on the WPBC dataset. The proposed models are useful compared to extant models.

In Neha Panwar et al. [11] (2020), we use different Machine Learning (ML) techniques to figure out if a patient has BC or not.SVM,k-NN,NB,DT, and LR will be used to sort the WBCD dataset in this work. Before classification, there is a preprocessing step where five different classifiers are used with the five fold cross-validation method. Performance factors like sensitivity, accuracy,and specificity are used to measure how well classification works. Confusion metrics are also used to measure performance. It was found that SVM worked best, with a precision of 99.12% after the normalisation process in.

In Adel S. Assiri et al. [12] (2020), the WBCD was used to compare how well different cutting- edge machine learning classification methods worked. Based on their F3 score, the three best models were then chosen. The F3 score is used to stress how important false positives are in classifying breast cancer. Simple LR learning, svm learning with Stochastic-Gradient descent optimisation, multilayer-Perceptron network are the three classifiers that are used for ensemble classification with a vote system. With a success rate of 99.42%, the hard voting (majority-based voting) method works better than the most recent WBCD algorithm.

### III. PRELIMINARY SECTION

Section give data information and evaluations matrices for this study.

### A. Data Description

the WBC dataset derived from the UCI repository ML datasets [17]. This collection includes 569 instances, categorized as either benign or malignant, with 357 instances (62.74 per cent) identified as benign and 212 instances (37.25 per cent) as malignant. The dataset is segmented into two categories, B for benign and M for malignant. Breast cancer stands as the most frequently diagnosed condition in healthcare, and its incidence is on the rise annually. Beyond the sample code numbers and class labels, the dataset features 32 characteristics related to breast cancer, such as the mean radius, texture, area, smoothness, compactness, and concavity [18, 19]. Cases labeled as benign are considered less harmful to the body, whereas those labeled as malignant are deemed harmful due to their cancerous nature in our research. The dataset contains 16 instances with missing values for features, which are typically filled using the mean method. To guarantee the integrity of the data, the dataset is randomized at the end (Fig. 1).

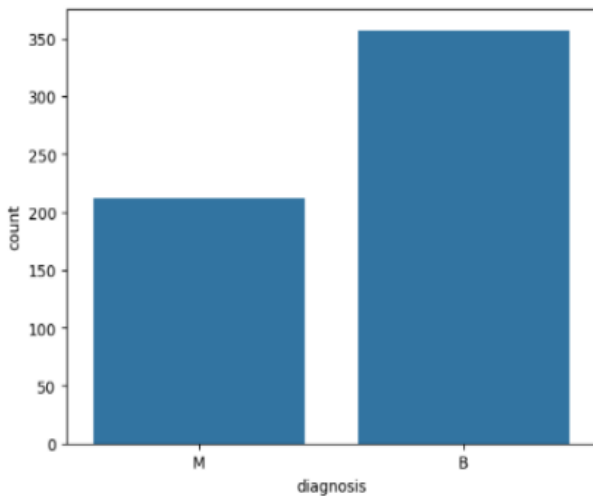


Fig. 1. Wisconsin breast cancer diagnostic datasets.

### B. Data Preprocessing

Ensure that data is appropriately prepare for machine learning models, the following preprocessing steps will be implemented:

### C. Handling Missing Data

Missing values will be imputed using techniques such as KNN imputation or mean/mode imputation, depending on the nature and distribution of the data.

### D. Categorical Data Encoding

Categorical features, such as *gender*, will convert into numeric values using encoding method example OneHot encoding, LabelEncoding.

### E. Data Splitting

Dataset will be divide two subset: 80% for train & 20% for test. This split will facilitate model evaluation and prevent overfitting.

### F. Performance Evaluation Metrics

Four distinct CrossValidation metrics precision, recall, accuracy, and F1Score were examined in this work. The values of the confusion matrix allow one to ascertain these measures. The confusion matrix consists of the following elements:

- TP: The model predicts “yes” and the actual data is also “yes”.
- TN: The model predicts “no” and the actual data is also “no”.
- FP: The model predicts “yes” but the actual data is “no”.
- FN: The model predicts “no” but the actual data is “yes”.

The following formulas allow one to calculate accuracy, F1-score, precision, and recall:

### G. Formula

$$\text{accuracy} = \frac{TP + TN}{TP + TN + FP + FN}$$

Accuracy measures the overall correctness of the model and the ratio of correctly prediction (both truely-positive and truely-negative) to total number of prediction.

### H. Formula

$$\text{Precision} = \frac{TP}{TP + FP}$$

Precision measure how many of predicted positively instances are really correct, providing insight into models ability to bypass false positives.

### I. Formula

$$\text{Recall} = \frac{TP}{TP + FN}$$

Recall measures models ability to correctly identify all relevant positive instances, highlighting the detection capability.

### J. Formula

$$\text{F1-Score} = \frac{2 \times \text{Precision} \times \text{Recall}}{\text{Precision} + \text{Recall}}$$

The F1-Score provides a harmonic mean of precision and recall, balancing the trade-off between the two metrics.

### K. Formula

The AUC (Area Under the Curve) and ROC (Receiver Operating Characteristic) curve evaluate the model ability to discriminate between the classes. A high AUC indicate better performance distinguishing between positive and negative instance. The ROC curve plotted by use the True Positive Rate (Recall) on y-axis, False Positive Rate (FPR) on x-axis.

$$\text{True Positive Rate (Recall)} = \frac{TP}{TP + FN}$$

$$\text{False Positive Rate (FPR)} = \frac{FP}{FP + TN}$$

Each metric provides valuable insights into different aspects model performance can be used based on the specific needs of the application or the dataset.

### L. Methodology

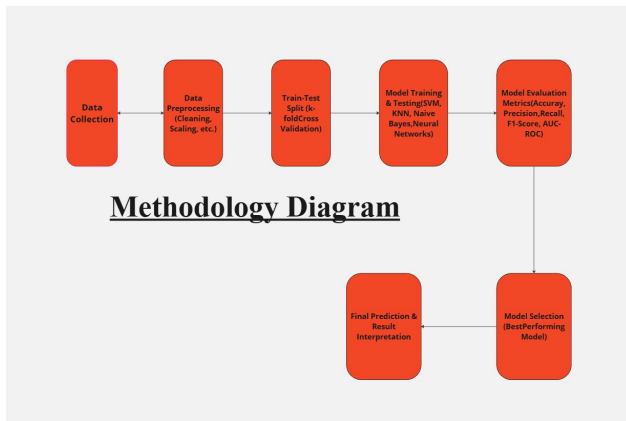


Fig. 2. Process flow diagram.

Our main objective, this study is identify most effective, reliable ML model for predicting Wisconsin Breast Cancer Disease (WBCD) risk. In this research, we have applied multiple ML algorithms including SVM, k-Nearest KNN, GaussianNB, and MLPClassifier. After training and evaluating each model, we assessed their performance to identify the best model based on accuracy and other key evaluation metrics (Fig. 2).

Proposed approach begins with data collection, followed by the preprocessing stage, which includes data cleansing, feature selection, targeting role definition, and feature extraction. Once the data is prepared, we apply various machine learning algorithms to build models that can predict WBCD risk based on input features like age, gender, blood pressure, cholesterol levels, etc.

To evaluate the models performance we split dataset into two subsets: training data and testing data, typically using the Train-Test Split technique. In our case, 80% of the dataset is used for training, while the remaining 20% is used to evaluate the model's performance. We then compare the results of the different algorithms in terms of their accuracy, precision, recall, F1-Score, and AUC-ROC values.

Finally, based on these performance metrics, we select the best-performing model for WBCD risk prediction, ensuring that the chosen model is not only accurate but also reliable in its predictions.

## IV. MACHINE LEARNING ALGORITHMS

### A. Support Vector Machine (SVM)

SVM a supervised learning algorithm finds optimal hyper-plane to separate different classes. It is particularly effective in high-dimensional spaces and is used in classification tasks.

Mathematical Equation:

$$f(x) = w \cdot x + b$$

where:-

- $w$  - weight-vector,
- $x$  - feature-vector,
- $b$  - bias-term.

### B. KNearest Neighbor

KNN is simple, instance-based learning algorithm that use to classify data point based on the majority class of their  $k$  nearest-neighbors.

Mathematical Equation:

$$y = \frac{1}{k} \sum_{i=1}^k y_i$$

where:

- $y_i$  is the class of the nearest neighbors,
- $k$  is the number of neighbors.

### C. Naive Bayes (GaussianNB)

Naive Bayes, Probabilistic classifier based on bayes-theorem, assume independently among features. It is especially suitable for large datasets and text classification tasks.

Mathematical Equation:

$$P(C | X) = \frac{P(X | C) \cdot P(C)}{P(X)}$$

where:

- $P(C | X)$ , Posterior Probability of class  $C$  given features  $X$ ,
- $P(C)$ , Prior Probability of class  $C$ ,
- $P(X | C)$ , likelihood of observing  $X$  given class  $C$ .

D. Neural Networks (MLPClassifier)

The MultiLayer-Perceptron(MLP) type of feed-forward artificial neural-network that consisting multiple layers of neuron, used for nonlinear classifications.

Mathematical Equation:

$$y = \sigma(Wx + b)$$

where:-

- $W$  - weight matrix,
- $x$  - input vector,
- $b$  - bias,
- $\sigma$  - activation function (e.g. sigmoid or ReLU).

V. EXPERIMENTAL RESULTS AND DISCUSSIONS

A. Experimental Results

The dataset used in this study consists of health-related attributes gathered from Wisconsin Breast Cancer Disease patients. These include various features such as age, blood pressure, cholesterol levels, smoking habits, and other medical indicators. The goal is to predict the likelihood of a patient developing Wisconsin Breast Cancer Disease (WBCD) based on these features. The dataset comprises 569 samples, with 32 features extracted for each instance. These samples were split into training and testing sets using a split between train and test 80% / 20% (see Fig. 3 and 4).

1) Model results: The performance of four ml algorithms — SVM, KNN, GaussianNB, and MLPClassifier — was evaluated. The results show the following performance across the models:

a) Support Vector Machine (SVM):

- Accuracy: Ranges from 97.23% to 97.78% at k=39.
- Precision: Ranges from 0.9742 to 0.9791.
- Recall: Ranges from 0.9711 to 0.9785.
- F1-Score: Ranges from 0.9705 to 0.9769.
- AUC-ROC: Ranges from 0.9965 to 0.9980.

b) k-Nearest Neighbors (KNN):

- Accuracy: Ranges from 96.01% to 96.21% at k=39.
- Precision: Ranges from 0.9614 to 0.9663.
- Recall: Ranges from 0.9584 to 0.9624.
- F1-Score: Ranges from 0.9587 to 0.9621.
- AUC-ROC: Ranges from 0.9930 to 0.9960.

c) Naive Bayes (GaussianNB):

- Accuracy: Ranges from 93.93% to 94.16% at k=39.
- Precision: Ranges from 0.9459 to 0.9464.
- Recall: Ranges from 0.9367 to 0.9427.
- F1-Score: Ranges from 0.9352 to 0.9389.
- AUC-ROC: Ranges from 0.9865 to 0.9886.

d) Neural Networks (MLPClassifier):

- Accuracy: Ranges from 97.92% to 98.13% at k=37.
- Precision: Ranges from 0.9805 to 0.9821.
- Recall: Ranges from 0.9782 to 0.9814.
- F1-Score: Ranges from 0.9776 to 0.9799.
- AUC-ROC: Ranges from 0.9985 to 1.0000.

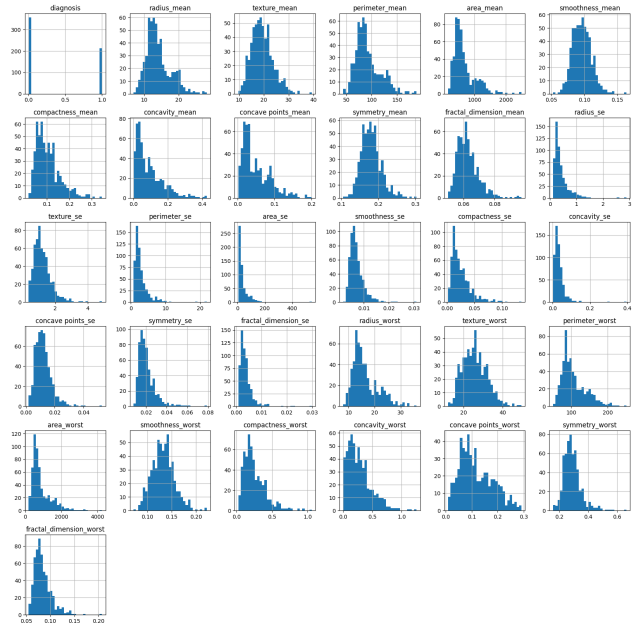


Fig. 3. Feature visualization result for WBCD.

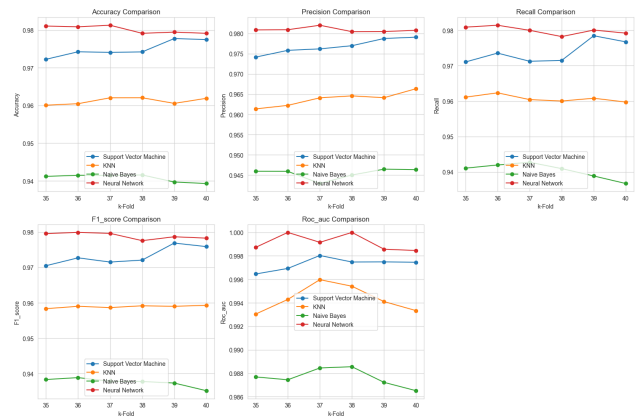


Fig. 4. Performance of model comparison WBCD.

B. Comparison of Results

The results of this experiment show clear performance differences between the models evaluated.

1) Best performing model: Neural networks (MLPClassifier):

- Accuracy: The Neural Networks model demonstrated the highest accuracy across all configurations, with

values consistently reaching above 97%, peaking at 98.13% at k=37.

- Precision and Recall: Both precision and recall scores were notably high, ranging from 0.9805 to 0.9821 for precision and 0.9782 to 0.9814 for recall. This indicates that the model is highly effective in both identifying positive cases and minimizing false negatives.
- F1-Score: The F1-Score was similarly high, ranging from 0.9776 to 0.9799, showing a strong balance between precision and recall.
- AUC-ROC: The model achieved AUC-ROC values between 0.9985 and 1.0000, with a perfect score at k=36, highlighting its excellent ability to distinguish between positive and negative classes.

#### 2) Second best model: Support Vector Machine (SVM):

- Accuracy: SVM model achieved accuracy between 97.23% and 97.78%, which was very close to that of Neural Networks.
- Precision and Recall: Precision and recall for SVM were also impressive, with values range 0.9742 to 0.9791 for precision and 0.9711 to 0.9785 for recall.
- F1-Score: The F1-Score ranged from 0.9705 to 0.9769, demonstrating good balance.
- AUC-ROC: The AUC-ROC score ranged from 0.9965 to 0.9980, which is very high, though slightly lower than that of Neural Networks.

#### 3) Third best model: k-Nearest Neighbors (KNN):

- Accuracy: KNN demonstrated accuracy between 96.01% and 96.21%, which was lower than both SVM and Neural Networks.
- Precision and Recall: for KNN range from 0.9614 to 0.9663 for precision and 0.9584 to 0.9624 for recall, which were still decent, though less effective than the top two models.
- F1-Score: The F1-Score ranged from 0.9587 to 0.9621, which indicates solid performance but still a gap from SVM and Neural Networks.
- AUC-ROC: The AUC-ROC ranged from 0.9930 to 0.9960, which was good but not as high as SVM and Neural Networks.

#### 4) Least effective model: Naive Bayes (GaussianNB):

- Accuracy: Naive Bayes achieved the lowest accuracy, range from 93.93% to 94.16%.
- Precision and Recall: Precision and recall for Naive Bayes were still respectable, range from 0.9459 to 0.9464 for precision and 0.9367 to 0.9427 for recall, but these were lower than the other models.
- F1-Score: The F1-Score ranged from 0.9352 to 0.9389, which again was the lowest among the models.
- AUC-ROC: Naive Bayes had AUC-ROC scores between 0.9865 and 0.9886, which were decent but not as high as the other models.

## VI. CONCLUSION

In this study, we evaluated four prominent ML algorithms — SVM, KNN, GaussianNB, and MLPClassifier — for predicting risk of WBCD based on a dataset consisting of 569 samples and 32 features. The performance of these models assessed using key metrics such F1-Score, Precision, Recall, Accuracy and AUC-ROC. Results from this analysis demonstrated that Neural Networks emerged as the most effective model, with superior performance across all metrics particular term of precision, AUC-ROC, recall, and accuracy. Specifically, Neural Networks achieved an accuracy range of 97.92% to 98.13%, and AUC-ROC values between 0.9985 to 1.0000, indicating that it was highly adept at distinguishing between WBCD and non-WBCD cases.

The SVM followed closely as the second-best performing model, with high accuracy (97.23% to 97.78%) and AUC-ROC scores (0.9965 to 0.9980), making it another highly reliable choice for Wisconsin Breast Cancer Disease risk prediction. However, k-Nearest Neighbors (KNN) and Naive Bayes (GaussianNB), although effective, exhibited slightly lower accuracy and AUC-ROC values, especially Naive Bayes, which struggled with a feature independence assumption that likely impacted its performance.

Given these findings, we conclude that Neural Networks (MLPClassifier) is the most reliable and accurate model for predicting Wisconsin Breast Cancer Disease risk among the algorithms tested. However, SVM can still serve as an effective alternative, particularly when computational efficiency and model interpretability are critical.

## VII. FUTURE SCOPE

The present research provides a solid foundation for further enhancement in the field of Wisconsin BC Disease prediction using ML Comparative Analysis. Several directions for future work can be identified:

- Data Expansion and Feature Engineering: Incorporating additional feature such lifestyle factors, genetic data, or advanced imaging techniques help improve model accuracy. More diverse datasets, including different demographics and geographical populations, will ensure the generalizability of the model.
- Model Optimization: Hyperparameter tuning for the models used, including the number of layers and neurons in neural networks or kernel choice in SVM, could potentially enhance performance. Additionally, exploring ensemble techniques like Random Forest or Boosting could help raise prediction accuracy by combining backbone of multiple models.
- Real-time Applications & Deployment: For clinical use, models need to be deployed in real-time systems, where they can continuously learn and adapt to new data. Explainable AI (XAI) techniques will be crucial for gaining the trust of healthcare professionals by providing transparency in decision-making.
- Ethical Considerations: Applications of AI in healthcares grown, it is vital ensure that models are fair and the unbiased, particularly in diverse populations.

Ethical guidelines for AI deployment, along with ensuring patient data privacy, will be paramount in future research.

This research development more accurately, efficient, and trustworthy ML models for predicting WBCD, which can greatly benefit healthcare systems worldwide.

#### ACKNOWLEDGMENT

This is supported by School of IT, Washington University of Science and Technology, VA, USA

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