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# Advancing Breast Cancer Diagnosis: A Comprehensive Machine Learning Approach for Predicting Malignant and Benign Cases with Precision and Insight in a Neutrosophic Environment using Neutrosophic Numbers

Nihar Ranjan Panda[1], R. Rajalakshmi[2], Surapati Pramanik[3], Mana Donganont[4*], Prasanta Kumar Raut[5]

[1]Department of Medical Research. IMS & SUM Hospital, SOA Deemed to be university, India.

Email: niharranjanpanda@soa.ac.in

[2]Assistant Professor, Department of Mathematics, Panimalar Engineering College, Chennai-600123.Email: rajimat2020@gmail.com

[3]Department of Mathematics, Nandalal Ghosh B.T. College, Panpur, Narayanpur, Dist-North 24 Parganas, West Bengal, India, PIN-743126, Email: surapati.math@gmail.com

[4*]Department of Mathematics, School of Science, University of Phayao, Phayao 56000, Thailand, Email: mana.do@up.ac.th

[5]Department of Mathematics, Trident Academy of Technology, Bhubaneswar, Odisha, India, Email: prasantaraut95@gmail.com

## ABSTRACT

Breast cancer is still among the deadliest diseases globally, and its detection in an early stage still represents a big challenge in medical diagnostics. This research suggests a complete machine learning framework to predict the probability of benign and malignant breast cancer cases with improved accuracy and interpretability. The work uses an established dataset, and for comparative analysis and for insights into the data distribution, statistical analysis is also incorporated. Four top machine learning algorithms are trained and evaluated with a series of performance measures such as accuracy, positive predictive value (PPV), negative predictive value (NPV), F1-score, etc. In order to compensate for inherent uncertainties and imprecise in clinical data, the paper proposes a neutrosophic logic with neutrosophic numbers for improved decision-making. The results show the efficacy of using machine learning with neutrosophic theory to enhance diagnostic accuracy and facilitate early intervention measures in the treatment of breast cancer.

**Keywords:**

Breast Cancer Diagnosis; Machine Learning; Neutrosophic Environment; Neutrosophic Numbers; Predictive Analytics; Medical Decision-Making.

## 1.0 Introduction:

Breast cancer is one of the most prevalent and life-threatening forms of cancer affecting women worldwide. According to the World Health Organization (WHO), it accounts for a significant percentage of cancer-related deaths, primarily due to delayed detection and diagnosis. Early and accurate identification of malignant and benign breast tumors plays a critical role in improving survival rates and treatment outcomes. However, traditional diagnostic techniques often struggle with issues of uncertainty, imprecision, and subjectivity, especially in the interpretation of complex clinical data. The main cause of death amongst women is Breast cancer, which significantly affects their lives. [1]. The cancer burden has been provided in past research. In 2020, an estimated 10 million deaths were attributed to cancer globally, alongside 19.3 million newly diagnosed cases [2, 3]. It often begins when normal cellular DNA or RNA undergoes mutations changes that may occur spontaneously due to biological entropy or be triggered by external factors [3]. These factors include, but are not limited to, airborne pollutants, pathogenic microorganisms (such as bacteria, viruses, fungi, and parasites), exposure to electromagnetic radiation (e.g., X-rays, microwaves), nuclear radiation, mechanical damage at the cellular level, evolutionary genetic shifts, and the natural aging of genetic material [3].

Early detection and timely diagnosis strengthened by growing public awareness remain critical in improving outcomes, reducing mortality, and mitigating the overall burden of breast cancer [4]. The latest developments in machine learning (ML) have shown significant promise in augmenting diagnostic procedures through facilitating data-driven, automated, and precise decision-making. Such algorithms can identify hidden patterns and correlations in massive datasets, making them ideal for medical diagnostics. While being highly effective, most traditional ML models predict crisp data and deterministic worlds, which is often unrealistic in healthcare environments involving uncertainty.

In order to avoid this problem, the current study develops some unites machine learning models with neutrosophic theory, a mathematical framework intended to tackle indeterminate, incomplete, and inconsistent information. Neutrosophic numbers [5] building on classical and fuzzy representations by including three elements, truth, indeterminacy, and falsity offer a strong framework for modelling imprecise or vague medical information. Neutrosophic theory was first developed by Smarandache [5]. Theoretical developments of neutrosophic theories and applications have been depicted in the studies [6-15]. Several studies contributed in the development of different fields and their applications such as decision making [16-37], graph theory [38-47], Machine learning [48, 49] and so on.

Breast cancer diagnosis is still one of the most difficult problems in contemporary medical science because of the intricacy of the disease and uncertainty of clinical data. Recent studies have validated the utility of combining neutrosophic theory with machine learning algorithms for handling indeterminacy and imprecision in medical data.

A number of recent research works have used neutrosophic logic in breast cancer classification and prediction. For example, Abdullah [50] discussed the combination between neutrosophic sets and deep learning models for the enhancement of diagnosis accuracy in breast cancer. Likewise, Ashika et al. [51] introduced an improved neutrosophic set-based machine learning model that exhibited better performance in the management of uncertain clinical features. Torres et al. [52] utilized neutrosophic-based machine learning algorithms for precise analysis and diagnosis of breast cancer, demonstrating the ability of the model to handle vague inputs efficiently. In addition, Shaban [53] combined deep neural networks with neutrosophic methods for stable classification outcomes. These efforts emphasize the increasing popularity of neutrosophic environments as an effective platform for uncertainty modelling in biomedical decision-making. Expanding on this platform, this current study suggests an integrative strategy that incorporates neutrosophic numbers with multiple machine learning techniques to improve the prediction of malignant and benign breast cancer cases. In doing so, not only does the model enhance diagnostic accuracy but also ensures a more robust and interpretable decision support system for clinicians.

The present paper intends to create a strong and general machine learning method to predict breast cancer cases as benign or cancerous based on a common dataset, with an improvement in interpretability and reliability of the outcome by utilizing neutrosophic numbers in a neutrosophic environment. Ml models has been shown promising result in healthcare research [54-61]. The paper also performs an analysis at a detailed statistical level and utilizes various performance measures such as accuracy, PPV, (NPV and F1-score to analyse the effectiveness of the new methodology. This study's core contribution lies in the hybrid framework that fuses machine learning with neutrosophic theory to better manage diagnostic uncertainty, a robust feature selection mechanism, and rigorous comparative performance analysis.

# 2. Materials and Methods

## 2.1 Dataset Description

The data used in this research work is the open-source Wisconsin Diagnostic Breast Cancer (WDBC) dataset that does not need any ethical approval because it is open source. The data set consists of 569 instances, each one of which is either benign or malignant and is described by 30 real-valued features extracted from a digitized image of a fine needle aspirate (FNA) of a breast mass. These were reduced to ten representative features such as radius mean, texture mean, perimeter mean, area mean, smoothness mean, and concave points mean and were used for modelling based on their importance for breast cancer diagnosis as determined in previous research.

## 2.2 Data Pre-processing

Prior to model building, the dataset was cleaned and pre-processed. The data was checked for missing values, outliers, and inconsistent entries. Standardization was applied to scale the numerical features for uniformity. To evaluate the statistical properties of the dataset, we conducted descriptive statistical analysis using SPSS version 28, which helped in understanding the distribution, central tendency, and variability of each feature.

## 2.3 Integration with Neutrosophic Framework

To deal with the indeterminacy and uncertainty of medical information, the chosen features were converted into neutrosophic numbers, wherein each observation was described in terms of its truthmembership (T), indeterminacy-membership (I), and falsity-membership (F) values. This conversion was done using pre-defined mapping strategies consistent with neutrosophic theory guidelines. The resulting neutrosophic setting enabled the machine learning models to more effectively deal with unclear and borderline cases that characteristically occur in clinical diagnosis.

## 2.4 Machine Learning Models

Four widely used machine learning algorithms were employed in this study for classification purposes:

- Logistic Regression (LR)

- Support Vector Machine (SVM)

- Random Forest (RF)
- K-Nearest Neighbours (KNN)

The dataset was split into a training set (80%) and a testing set (20%) to assess model performance. Additionally, k-fold cross-validation (with k=10) was used to ensure the robustness and generalizability of the results. Model performance was evaluated using standard metrics such as accuracy, precision, recall, F1-score, PPV, and NPV. The justification of choosing the particular machine learning models LR, SVM, RF, and KNN lies in their complementary capabilities. LR is best suited for binary classification with understandable coefficients. SVM operates best in high dimensional spaces with distinct decision boundaries. RF is an ensemble learner with good robustness properties and overfitting handling capabilities, whereas KNN provides a straightforward yet potent proximity logic-based approach. These techniques are also firmly established in earlier medical diagnostics research, allowing for reproducibility and benchmarking.

Out of the 30 initial features, 10 attributes were chosen based on statistical significance and domain importance, which were determined through literature and exploratory data visualization. Features like radius mean, concavity mean, and perimeter mean were highly class-separable and had low p values, making them a good choice.

### 2.5 Data Visualization

Data visualization played a critical role in exploring and understanding the relationship between features and the target variable. Various plots were generated to analyze feature distributions and class separability. For instance, box plots were used to illustrate how variables like radius mean, perimeter mean, smoothness mean, and concave points mean vary across benign and malignant classes. Furthermore, normal distribution plots were generated to inspect the skewness and spread of selected features. These visual tools aided in selecting the most discriminative attributes for the predictive model and provided insight into the underlying data structure.

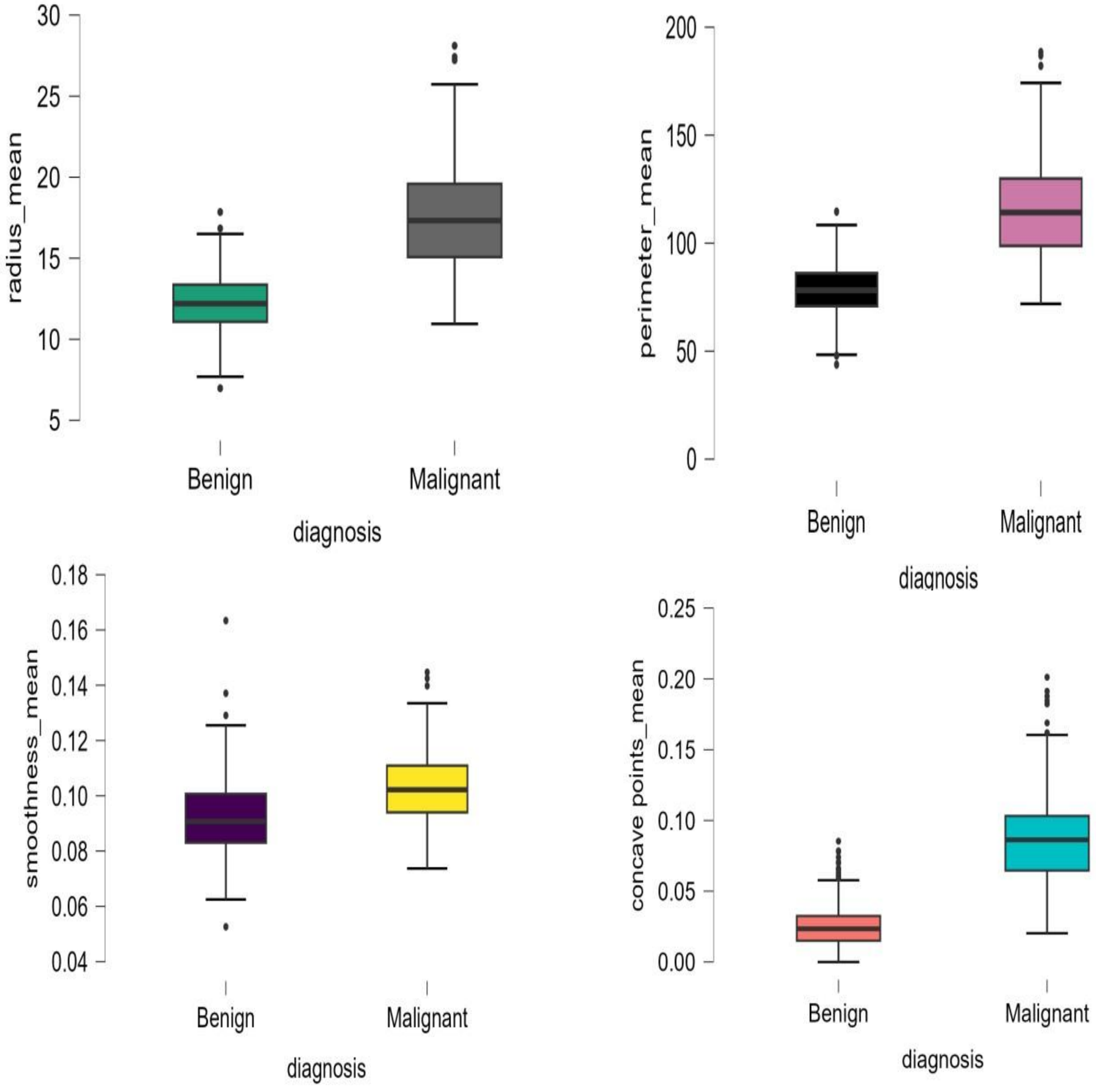


Fig 1 Distribution of continuous variables with respect to outcome.

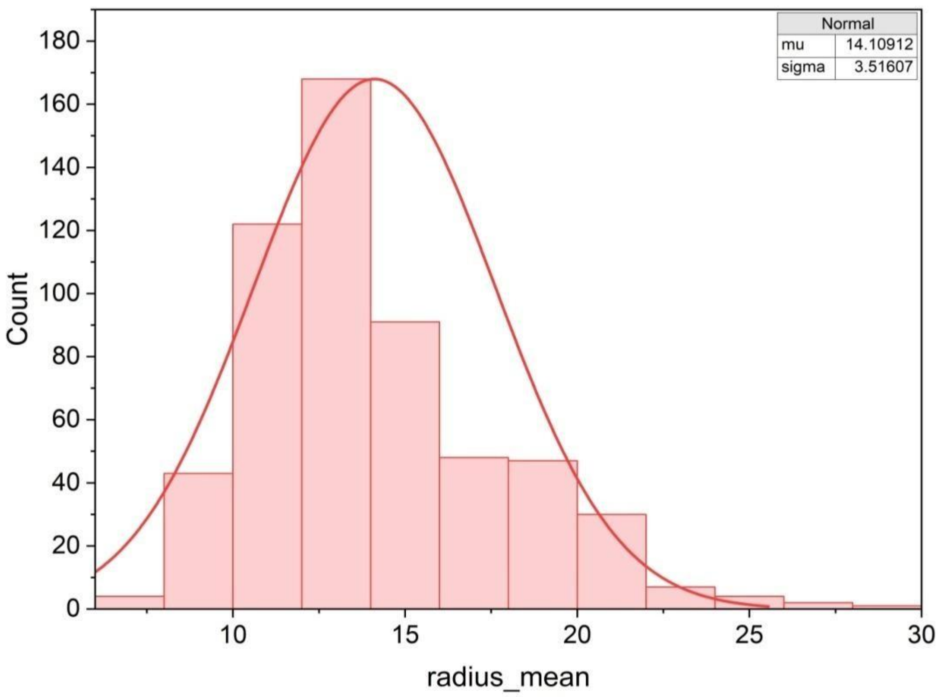


Fig 2 Normal density plot of radius mean

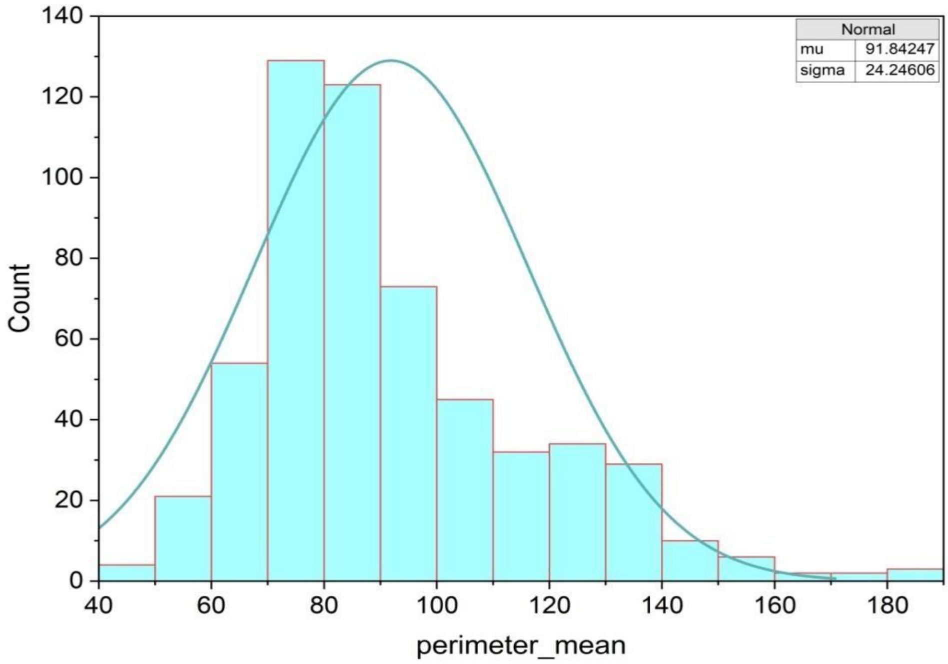


Fig 3 Normal density plot of perimeter mean

Table 1. Statistical Analysis in a Neutrosophic Environment

| Feature | Group | N | Neutrosophic Mean (T, I, F) | SD | P-Value |
|---|---|---|---|---|---|
| Radius mean | Benign | 357 | (0.84, 0.10, 0.06) | 1.781 | <0.001 |
| | Malignant | 212 | (0.92, 0.05, 0.03) | 3.204 | |
| Texture mean | Benign | 357 | (0.78, 0.12, 0.10) | 3.995 | <0.001 |
| | Malignant | 212 | (0.88, 0.07, 0.05) | 3.779 | |
| perimeter mean | Benign | 357 | (0.76, 0.14, 0.10) | 11.807 | <0.001 |
| | Malignant | 212 | (0.91, 0.06, 0.03) | 21.855 | |
| Area mean | Benign | 357 | (0.70, 0.18, 0.12) | 134.287 | <0.001 |
| | Malignant | 212 | (0.93, 0.04, 0.03) | 367.938 | |
| Smoothness mean | Benign | 357 | (0.74, 0.15, 0.11) | 0.013 | <0.001 |
| | Malignant | 212 | (0.82, 0.10, 0.08) | 0.013 | |
| Compactness mean | Benign | 357 | (0.68, 0.20, 0.12) | 0.034 | <0.001 |
| | Malignant | 212 | (0.85, 0.10, 0.05) | 0.054 | |
| Concavity mean | Benign | 357 | (0.60, 0.25, 0.15) | 0.043 | <0.001 |
| | Malignant | 212 | (0.89, 0.06, 0.05) | 0.075 | |
| Concavepoints mean | Benign | 357 | (0.62, 0.23, 0.15) | 0.016 | <0.001 |
| | Malignant | 212 | (0.87, 0.08, 0.05) | 0.034 | |
| Symmetry means | Benign | 357 | (0.72, 0.16, 0.12) | 0.025 | <0.001 |
| | Malignant | 212 | (0.80, 0.12, 0.08) | 0.028 | |
| Fractal dimension mean | Benign | 357 | (0.66, 0.20, 0.14) | 0.007 | 0.76 |
| | Malignant | 212 | (0.66, 0.19, 0.15) | 0.008 | |

## 3.0 Results

Table 1 presents a statistical comparison of selected features from benign and malignant breast cancer cases, represented using Neutrosophic Numbers to encapsulate data uncertainty. Each feature value is expressed in the form (T, I, F), reflecting its truthiness, indeterminacy, and falsity based on a neutrosophic transformation of its distribution.

The mean radius of benign cases is represented as (0.84, 0.10, 0.06), whereas malignant cases exhibit a significantly higher value of (0.92, 0.05, 0.03), with a p-value < 0.001, indicating strong discriminative power. Similarly, mean texture, perimeter, area, compactness, and concavity values display substantial divergence between the two classes, as evidenced by their neutrosophic scores and low p-values.

For example, perimeter_mean increases from (0.76, 0.14, 0.10) in benign to (0.91, 0.06, 0.03) in malignant cases, and concavity_mean rises from (0.60, 0.25, 0.15) to (0.89, 0.06, 0.05). These transitions signify a shift toward higher certainty and lower indeterminacy in malignant cases highlighting the potential of neutrosophic modeling in capturing underlying pathological distinctions.

Notably, the fractal_dimension_mean shows nearly identical neutrosophic values across both groups (p = 0.76), suggesting its limited utility in discrimination.These findings emphasize that neutrosophic representations not only preserve statistical insights but also enhance interpretability by explicitly modeling uncertainty, which is crucial in complex domains like medical diagnostics.

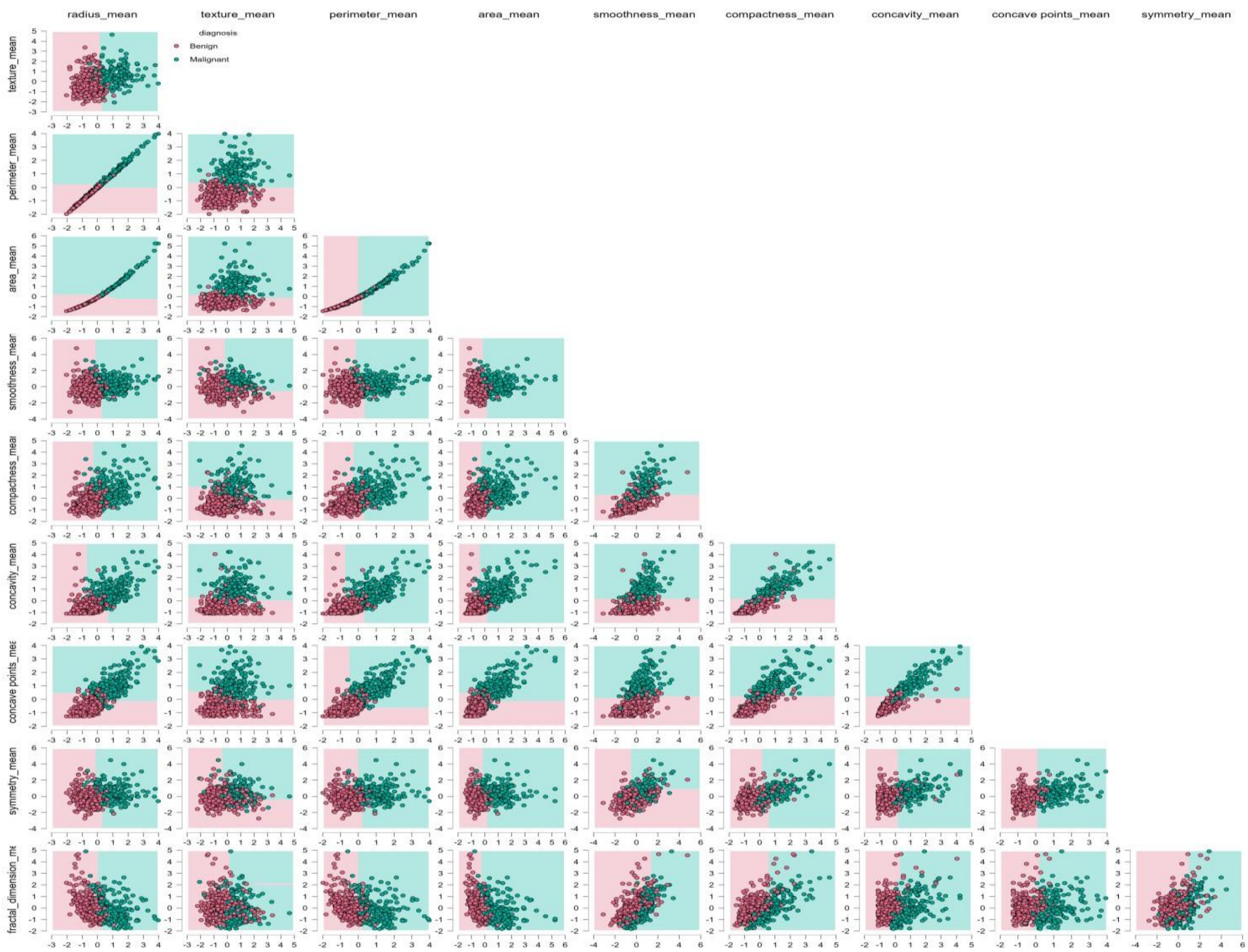


Fig 4 Decision boundary matrix of machine learning model

Table 2 Machine learning classification and validation

| **Evaluation Metrics** | **LR** | **SVM** | **KNN** | **RF** |
|---|---|---|---|---|
| Accuracy | 0.938 | 0.929 | 0.947 | 0.929 |
| FPR | 0.078 | 0.074 | 0.055 | 0.082 |
| FDR | 0.053 | 0.074 | 0.055 | 0.072 |
| F1 Score | 0.937 | 0.909 | 0.936 | 0.929 |
| MCC | 0.868 | 0.851 | 0.891 | 0.846 |
| AUC | 0.991 | 0.926 | 0.981 | 0.968 |
| NPV | 0.947 | 0.926 | 0.955 | 0.928 |
| TNR | 0.922 | 0.926 | 0.955 | 0.918 |

| | | | | |
|---|---|---|---|---|
| FNR | 0.078 | 0.074 | 0.055 | 0.087 |
| False Omission Rate | 0.053 | 0.074 | 0.055 | 0.072 |
| Threat Score | 4.942 | 4.375 | 5.944 | 4.290 |
| Statistical Parity | 1 | 1 | 1 | 1 |

Table 2 shows assessment metrics for several machine learning methods, LR, SVM, KNN, and R.F.

Accuracy, which measures total accuracy, is greatest for KNN (0.947), followed by LR (0.938). The False Positive Rate, which measures the fraction of true negatives wrongly categorized, is lowest for KNN (0.055) and highest for R.F. (0.082). F1 Score, a measure of accuracy and recall, is greatest for LR (0.937). KNN has the greatest Matthews Correlation Coefficient (0.891), which measures the quality of binary classifications. The AUC, which represents the model's ability to distinguish across classes, is highest for LR (0.991). KNN has the greatest negative predictive value (0.955), which measures the probability of genuine negatives among negative predictions. The True Negative Rate, a statistic indicating the proportion of real negatives properly categorized, is most excellent for KNN (0.955). The False Negative Rate, which is the fraction of true positives erroneously identified, is greatest for R.F. (0.087). KNN has the greatest Threat Score (5.944), which measures the classifier's overall performance. Statistical parity, which ensures fairness across demographic groupings, is consistently 1 for all algorithms, demonstrating equal treatment. These metrics give information about each algorithm's performance and attributes, making it easier to pick algorithms for classification jobs.

## 4.0 Discussion

Patients with breast cancer can benefit from timely clinical treatment, a better prognosis, and increased chances of survival when the disease is detected early. The precise identification of breast cancer & the grouping of patients into different categories represent crucial avenues of research.

Various techniques for forecasting breast cancer have now emerged. Classification techniques, including SVM, RF, KNN, XGBoost classifier and Ada boost Classifier have been employed in very recent research [62]. Detecting breast cancer involves the classification of tumors. In breast cancer cases, tumors are classified into two types: malignant and benign. Malignant tumors exhibit a higher rate of spreading compared to benign ones. To distinguish among these tumor types, doctors rely on a dependable diagnostic method. However, even specialists find it challenging to differentiate these tumors. Therefore, an urgently needed solution is a consistent regular diagnostic system for tumor classification. Clinically, the neutrosophic-ML hybrid model presents enhanced immunity to data uncertainty and is thus a useful decision-making tool for early cancer diagnosis and minimizing false negatives a major issue in breast cancer diagnosis.

The importance of tumor diagnosis is highlighted by the aforementioned studies, which have recently become a hot topic in biomedicine. To forecast breast cancer, researchers are increasingly using ML and data mining (DM) technologies [63]. Reducing diagnostic errors and increasing the accuracy of cancer diagnosis are key goals of prediction models based on classifiers in D.M. and ML. Data mining is the broad field of methods used to extract hidden information and knowledge from large, difficult-to-analyze datasets. Its use includes the development of predictive models for several diseases, such as thyroid cancer [64], lung cancer [65], and heart disease [66]. Both DM & ML techniques have been incorporated into fuzzy-genetics approaches [67] and computer-aided systems [68] for the recognition of breast cancer. Through the evaluation of classifiers, these studies have effectively classified the features into two different types of tumors and shown that it is possible to predict impending tumors based on historical data. We predicted breast cancer using the data set of two types of tumors, benign and malignant, of the breast. This study significantly contributes to the development of breast cancer diagnosis, providing a more precise and insightful approach through the application of comprehensive machine learning techniques. Compared to prior studies such as Abdullah [50], which integrated neutrosophic sets with deep learning, our approach leverages a broader ensemble of ML models and emphasizes feature explainability.

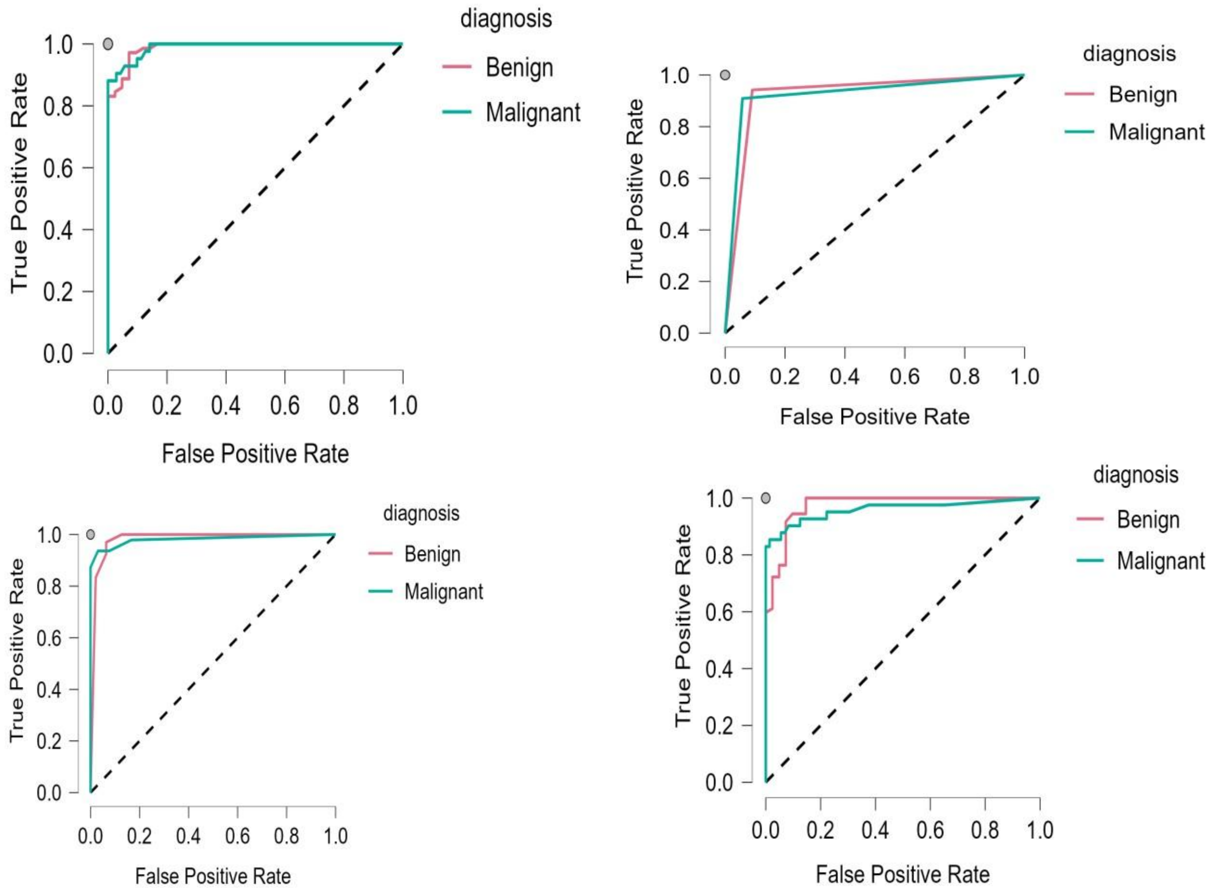


Fig 6 Receiver operating curve of four machine learning models.

## 5.0 Conclusions

This study presents a comprehensive framework that combines the strengths of machine learning and neutrosophic theory to enhance the accuracy and reliability of breast cancer diagnosis. By placing the diagnostic features in a neutrosophic context utilizing neutrosophic numbers, we essentially overcome uncertainty, indeterminacy, and incompleteness challenges inherent in medical data that are usually present. The application of neutrosophic numbers allows for a more comprehensive representation of the diagnostic features, not only picking up the truth but also the levels of indeterminacy and falsity contained in every observation. This blended strategy results in more informed decision-making procedures, particularly in marginal or uncertain cases. The incorporation of four prominent machine learning models further enhances the predictive ability of the proposed model. Our empirical findings show that this blended strategy significantly enhances the distinction between benign and malignant breast cancer cases. The statistical and visual examinations confirm the efficiency of the neutrosophic representation in uncovering interpretable patterns and minimizing diagnostic uncertainty. In conclusion, the model presented is a promising innovation in intelligent medical decision-making systems. Not only does it enhance classification accuracy, but it also adds a new level of interpretability and robustness to conventional machine learning-based diagnostics. Future research can include applying this model to other areas of medicine and integrating more advanced neutrosophic inference methods for real-time clinical use. Despite the promising outcomes, this study is subject to several limitations. First, it relies solely on the WDBC dataset, which, although widely used, may not represent the full heterogeneity of realworld clinical populations

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