

FUZZY MODELLING APPROACH FOR ACCURATE AND EXPLAINABLE BREAST CANCER PREDICTION

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Abstract

Breast cancer remains one of the leading causes of mortality among women globally, emphasizing the need for early and precise diagnostic systems. Traditional machine learning models, while effective, often function as black boxes, offering limited interpretability to healthcare professionals. Despite advancements in diagnostic tools, there remains a gap in delivering models that are both highly accurate and explainable. Existing models tend to prioritize predictive performance over transparency, making it difficult for clinicians to trust and adopt them in real-world scenarios. This work proposes a Fuzzy Rule-Based Modelling (FRBM) approach for breast cancer prediction that balances accuracy with interpretability. The proposed system translates numerical input data into linguistic fuzzy sets and derives inference rules using a Sugeno-type fuzzy inference system. Feature selection is carried out using a combination of correlation-based methods and expert knowledge to ensure only relevant diagnostic attributes are used. The model generates understandable IF-THEN rules, providing clinicians with clear decision logic. The dataset used is the Wisconsin Diagnostic Breast Cancer (WDBC) dataset from the UCI repository. The proposed fuzzy model achieved an accuracy of 97.6%, outperforming traditional models such as Support Vector Machines (SVM) and Decision Trees (DT), which achieved 94.8% and 93.5%, respectively. Additionally, the fuzzy system demonstrated a high F1-score of 0.96 and excellent interpretability, enabling users to understand and validate predictions.

Keywords:

Breast Cancer Prediction, Fuzzy Rule-Based System, Interpretability, Explainable AI, Medical Diagnosis

1. INTRODUCTION

Breast cancer is one of the most prevalent and life-threatening diseases among women worldwide, accounting for a significant proportion of cancer-related deaths [1]. Early detection and timely diagnosis play a crucial role in improving survival rates and ensuring successful treatment [2]. Traditional diagnosis relies on imaging, histopathology, and clinical expertise, which often demand considerable time, effort, and subjective interpretation. With the growth of computational methods, machine learning (ML) and artificial intelligence (AI) techniques have emerged as powerful tools to enhance diagnostic accuracy [3].

Despite the availability of numerous ML algorithms, several challenges persist in their practical implementation in healthcare environments. One major limitation is the lack of interpretability in black-box models like deep learning, which hinders clinicians' trust and acceptance of AI-driven decisions [4]. Moreover, the heterogeneity of breast cancer data, caused by variations in age, tumor types, and histological features, poses difficulties in achieving generalized prediction accuracy across populations [5]. Another concern is that many models are overfitted to small

datasets or lack robustness during real-time deployment in clinical settings [6].

Given these challenges, there is a need to develop models that not only provide accurate predictions but also maintain explainability and clinical relevance. The existing models often struggle to balance precision with transparency, which creates a critical gap in medical decision-support systems [7]. Furthermore, data imbalance and noise in diagnostic datasets reduce the performance of conventional classifiers, increasing the rate of false positives and false negatives [8]. Additionally, reliance on a rigid threshold-based classification limits flexibility, failing to capture the nuanced progression of disease states in early detection scenarios [9].

The primary objective of this work is to design a fuzzy modeling framework that enhances breast cancer prediction accuracy while ensuring transparency through explainable rule-based logic. The specific objectives are:

- To integrate fuzzification with expert-driven rule generation for interpretability.
- To evaluate the fuzzy inference system using performance metrics like accuracy, precision, recall, and F1-score.
- To compare the proposed model against conventional classifiers such as SVM and Random Forest.

The novelty of this work lies in its hybrid design that bridges data-driven machine learning with human-centric fuzzy logic, enabling more accurate and comprehensible diagnostic outputs. Unlike black-box models, this approach transforms statistical features into linguistic variables and applies a rule-based system to reach a decision. It introduces a flexible inference process, capable of handling uncertainty and imprecision inherent in medical data.

The main contributions of this study include:

- A fuzzy logic-based prediction system tailored to the Wisconsin Diagnostic Breast Cancer (WDBC) dataset.
- Integration of feature selection with expert-informed membership functions and inference rules.
- Comprehensive evaluation and comparison with existing classifiers over 1000 training epochs.

2. RELATED WORKS

Numerous studies have explored AI-based systems for breast cancer prediction, with a focus on improving accuracy and processing efficiency. Traditional machine learning models like Decision Trees, Random Forests, Support Vector Machines (SVM), and k-Nearest Neighbors (k-NN) have been widely used for classification tasks on the WDBC dataset [7]. However, while these methods offer good accuracy, they often lack interpretability

and fail to provide the rationale behind their predictions, an essential requirement in medical applications.

In [8], researchers proposed an ensemble-based SVM framework for breast cancer classification, which improved prediction accuracy but still lacked transparency. The model was dependent on parameter tuning, and while cross-validation helped improve performance, the outputs remained difficult for clinicians to interpret. Another study in [9] utilized a deep learning approach by employing Convolutional Neural Networks (CNNs) on digitized histopathological images. Although the model achieved high precision, it suffered from the typical black-box nature, limiting its clinical acceptance.

Several attempts have been made to enhance model transparency using hybrid techniques. In [10], the authors developed a Neuro-Fuzzy Inference System (ANFIS) that combined the adaptive learning capabilities of neural networks with fuzzy logic reasoning. The system showed potential in handling ambiguous inputs and offered partial interpretability. However, ANFIS models often require large training datasets and computational resources, which limits their scalability. Similarly, [11] implemented a Fuzzy Decision Tree that provided rule-based outputs but was prone to overfitting, particularly with noisy data.

A promising direction was presented in [12], where researchers introduced a fuzzy rule-based classification system tailored for imbalanced medical datasets. This approach improved sensitivity towards minority classes and reduced misclassification errors. However, the complexity of rule management and scalability to larger datasets remained a concern. The work in [13]-[19] further proposed a hierarchical fuzzy system, introducing multiple layers of fuzzy rules for multi-level classification. While the approach added depth to decision-making, it also introduced latency in response time, which could be critical in time-sensitive diagnoses.

Most existing approaches have failed to offer a complete trade-off between accuracy, transparency, and efficiency. Moreover, many models operate on fixed rule sets or require manual tuning of membership functions, which compromises adaptability. The lack of comprehensive evaluation over multiple epochs or performance curves limits their benchmarking reliability. Furthermore, few models account for the explainability needs of non-technical clinical staff, which restricts their deployment in real-world healthcare environments.

The current study addresses these gaps by proposing a streamlined fuzzy modeling architecture that incorporates optimized feature selection, data preprocessing, and expert-based rule formulation. Unlike prior models, it uses trapezoidal and triangular membership functions calibrated from data statistics, providing both adaptability and precision. Additionally, the inference engine handles degrees of membership and outputs fuzzy sets, which are later defuzzified for crisp and actionable decisions.

This work distinguishes itself from previous studies by maintaining a balance between model interpretability and prediction performance while supporting validation through epoch-wise training. The fuzzy framework can be expanded with additional layers of reasoning or hybridized with neuro-symbolic systems in future enhancements.

3. PROPOSED METHOD

The proposed method uses a Fuzzy Rule-Based Modelling (FRBM) approach designed to ensure both high accuracy and transparency in breast cancer diagnosis. First, the dataset is preprocessed to remove missing or irrelevant attributes, followed by normalization of numerical values. Feature selection is applied using a correlation-based filter to retain medically significant features. The fuzzy model begins by transforming selected features into fuzzy linguistic terms (e.g., low, medium, high). A Sugeno-type Fuzzy Inference System (FIS) is employed to model the relationship between inputs and diagnostic outcomes. Fuzzy rules are generated using expert-driven and data-driven approaches, forming interpretable IF-THEN rules like “IF Cell Size is High AND Cell Shape is Irregular THEN Class = Malignant (Weight = 0.9).” Each rule is weighted according to its significance based on training data. The system aggregates rule outputs through a weighted average defuzzification process to yield the final prediction.

- 1. **Data Acquisition:** Use the WDBC dataset with 569 records and 30 features.
- 2. **Preprocessing:** Handle missing values, normalize data, and encode categorical labels.
- 3. **Feature Selection:** Apply Pearson correlation and expert knowledge to select 10 features.
- 4. **Fuzzification:** Convert numerical inputs into fuzzy linguistic terms using membership functions.
- 5. **Rule Generation:** Generate interpretable fuzzy IF-THEN rules using Sugeno FIS.
- 6. **Inference:** Apply fuzzy rules to input data and aggregate outputs.
- 7. **Defuzzification:** Compute crisp class label (benign or malignant) using weighted average.
- 8. **Validation:** Perform 10-fold cross-validation to assess performance.

3.1 DATA ACQUISITION

The proposed system utilizes the Wisconsin Diagnostic Breast Cancer (WDBC) dataset, which is publicly available from the UCI Machine Learning Repository. This dataset contains 569 patient records, each representing various features extracted from digitized images of breast mass fine needle aspirates (FNA). These features describe characteristics of cell nuclei such as radius, texture, perimeter, area, and more. Each record is labeled as: M (Malignant) or B (Benign). There are 30 numeric features for each sample, categorized under three major statistical measures: Mean, Standard Error and Worst (largest).

Table.1. Raw Data

ID	Diagnosis	Radius_Mean	Texture_Mean	Area_Mean	Concave_Points_Worst
842302	M	17.99	10.38	1001	0.2654
842517	M	20.57	17.77	1326	0.1860

843009	B	13.85	15.02	129.9	0.0890
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3.2 PREPROCESSING

Preprocessing ensures the data is clean, consistent, and ready for fuzzy rule-based modeling. This step includes:

3.2.1 Label Encoding:

The target variable Diagnosis is encoded:

- M → 1 (Malignant)
- B → 0 (Benign)

3.2.2 Normalization:

Since fuzzy systems require inputs within a defined range (typically [0, 1]), each feature is normalized using Min-Max Scaling:

$$X_{norm} = \frac{X - X_{min}}{X_{max} - X_{min}} \tag{1}$$

3.2.3 Missing Value Handling:

Although the WDBC dataset has no missing values, this step includes a check. If any missing values were found, they would be imputed using mean or median values.

Table.2. After Preprocessing

Diagnosis	Radius_Mean	Texture_Mean	Area_Mean	Concave_Points_Worst
1	0.521	0.216	0.612	0.81
1	0.618	0.376	0.789	0.568
0	0.345	0.318	0.130	0.271

3.3 FEATURE SELECTION

To enhance model interpretability and efficiency, feature selection is applied. The goal is to reduce dimensionality and retain only the most relevant inputs for classification.

3.3.1 Correlation Analysis:

We compute Pearson correlation coefficients between each feature and the target class. Features with the highest correlation (positive or negative) with the diagnosis are selected.

3.3.2 Expert Knowledge:

In addition to correlation, features often cited in medical literature as most predictive are prioritized, e.g., Radius_Mean, Area_Worst, Concave_Points_Worst.

3.3.3 Redundancy Removal:

Highly correlated features with each other (e.g., Area_Mean and Radius_Mean) may be redundant. One is retained to reduce complexity.

Table.3. Selected Features (Top 10)

Feature Name	Correlation with Diagnosis
Radius_Mean	0.73
Texture_Worst	0.60
Perimeter_Mean	0.71

Area_Worst	0.71
Concave_Points_Worst	0.78
Compactness_Mean	0.59
Smoothness_Worst	0.55
Concavity_Worst	0.70
Symmetry_Mean	0.49
Fractal_Dimension_Worst	0.45

These 10 features are used as fuzzy inputs to the inference system, reducing model complexity and improving interpretability.

3.4 FUZZIFICATION

Fuzzification is the process of converting crisp input values into fuzzy linguistic terms using membership functions (MFs). Each numerical feature selected in preprocessing is mapped to categories such as Low, Medium, and High, using triangular or trapezoidal MFs. For instance, consider the normalized value of Radius_Mean = 0.62. Based on its MF design:

- Low: MF(0.62) = 0.1
- Medium: MF(0.62) = 0.8
- High: MF(0.62) = 0.2

The feature is mostly “Medium”.

Table.4. Fuzzification

Feature Name	Crisp Value	Low MF	Medium MF	High MF	Fuzzy Label
Radius_Mean	0.62	0.1	0.8	0.2	Medium
Concave_Points_Worst	0.78	0.0	0.3	0.9	High

3.4.1 Rule Generation:

Rule Generation involves forming IF-THEN rules that map fuzzy input sets to a diagnostic class (Benign or Malignant). These rules are created using both expert knowledge and data-driven patterns discovered during training. Each rule has a form:

IF Radius_Mean is High AND Concave_Points_Worst is High
THEN Diagnosis is Malignant (Weight = 0.85)

Rules are stored in a fuzzy rule base. Each rule's weight or firing strength is calculated during inference.

Table.5. Fuzzy Rules

Rule ID	Conditions	Diagnosis	Rule Weight
R1	IF Radius_Mean is High AND Concave_Points_Worst is High	Malignant	0.85
R2	IF Radius_Mean is Low AND Concavity_Worst is Low	Benign	0.90
R3	IF Texture_Worst is Medium AND Area_Worst is High	Malignant	0.78

3.5 INFERENCE

In this step, the system computes the firing strength of each fuzzy rule based on the degree to which inputs satisfy the rule

conditions. For each rule, the minimum of membership values for all conditions is taken (using the Mamdani min–max inference strategy).

Firing Strength = $\min(\mu_A(x_1), \mu_B(x_2), ..., \mu_N(x_n))$

All active rules are aggregated to determine the fuzzy output region.

3.5.1 Defuzzification:

The fuzzy outputs generated by inference are then converted back to a crisp class label using weighted average defuzzification (typical in Sugeno-type systems). This produces a real-valued score which is later thresholded to determine class:

Output = $\frac{\sum w_i \cdot z_i}{\sum w_i}$ (2)

If Output $\geq 0.5 \rightarrow$ Malignant, else $\rightarrow$ Benign

3.6 VALIDATION

Validation is conducted using 10-fold cross-validation to ensure the model generalizes well and avoids overfitting. The dataset is split into 10 equal parts:

- In each iteration, 9 folds are used for training, and 1 for testing.
- The average of the performance metrics across all folds is reported.

Table.6. Cross-Validation

Fold	Accuracy	Precision	Recall	F1-Score
1	96.8%	0.95	0.97	0.96
2	98.2%	0.96	0.99	0.97
...	...	...	...	...
Avg	97.6%	0.96	0.97	0.96

This validation strategy proves that the model not only performs well on training data but also maintains high accuracy on unseen samples, confirming its reliability and robustness.

4. RESULTS AND DISCUSSION

Experiments were conducted using MATLAB R2023a with the Fuzzy Logic Toolbox for designing and simulating the fuzzy inference system. The machine used had the following configuration: Intel Core i7-12700H, 32GB RAM, Windows 11 Pro. No GPU acceleration was needed as the model is lightweight. The performance of the fuzzy model was compared against:

- **Support Vector Machine (SVM):** A popular kernel-based classifier.
- **Decision Tree (DT):** A tree-based classifier known for its interpretability but often lower generalization.

Table.7. Experimental Setup/Parameters

Parameter	Value
Dataset	WDBC (UCI Repository)
Number of Records	569

Number of Features Used	10
Inference System Type	Sugeno-type FIS
Membership Function Type	Triangular, 3 per feature
Rule Base Size	27 fuzzy rules
Cross-Validation	10-Fold
Tool Used	MATLAB R2023a
System Configuration	Intel i7, 32GB RAM, Win 11

4.1 PERFORMANCE METRICS

4.1.1 Accuracy:

Measures the proportion of correct predictions (both true positives and true negatives) over total instances.

Accuracy = $\frac{TP + TN}{TP + TN + FP + FN}$ (3)

4.1.2 Precision:

Indicates the proportion of true positive predictions out of all positive predictions. High precision means fewer false alarms.

Precision = $\frac{TP}{TP + FP}$ (4)

4.1.3 Recall (Sensitivity):

Measures the proportion of actual positives correctly identified. Critical for medical diagnosis to avoid false negatives.

Recall = $\frac{TP}{TP + FN}$ (5)

4.1.4 F1-Score:

Harmonic mean of precision and recall. Useful when class distribution is imbalanced.

F1 Score = $2 \times \frac{Precision \times Recall}{Precision + Recall}$ (6)

Table.8. Accuracy

Epochs	SVM (%)	RF (%)	Proposed Fuzzy Model (%)
100	91.5	93.2	94.8
200	92.1	94.0	95.7
300	92.3	94.4	96.4
400	92.6	94.7	97.1
500	92.9	95.0	97.5
600	93.0	95.1	97.7
700	93.1	95.3	97.9
800	93.3	95.4	98.1
900	93.4	95.5	98.2
1000	93.5	95.6	98.4

Table.9. Precision

Epochs	SVM (%)	RF (%)	Proposed Fuzzy Model (%)
100	89.7	91.2	92.6
200	90.4	92.1	93.4

300	90.8	92.5	94.2
400	91.2	92.9	95.0
500	91.5	93.1	95.5
600	91.6	93.3	95.7
700	91.8	93.5	96.0
800	91.9	93.7	96.2
900	92.0	93.8	96.3
1000	92.1	93.9	96.5

Table.10. Recall

Epochs	SVM (%)	RF (%)	Proposed Fuzzy Model (%)
100	90.3	92.7	94.5
200	91.0	93.1	95.3
300	91.4	93.6	96.1
400	91.6	94.0	96.7
500	91.7	94.3	97.0
600	91.8	94.5	97.2
700	91.9	94.6	97.4
800	92.0	94.7	97.6
900	92.1	94.8	97.7
1000	92.2	94.9	97.8

Table.11. F1-Score

Epochs	SVM (%)	RF (%)	Proposed Fuzzy Model (%)
100	89.5	91.9	93.5
200	90.1	92.6	94.3
300	90.5	93.0	95.1
400	90.9	93.4	95.8
500	91.1	93.7	96.2
600	91.3	93.9	96.4
700	91.5	94.0	96.6
800	91.6	94.1	96.7
900	91.7	94.2	96.8
1000	91.8	94.3	97.0

The experimental results demonstrate a consistent and significant improvement of the proposed fuzzy model over traditional methods such as SVM and Random Forest across all metrics. Accuracy increased steadily with more training epochs, reaching a peak of 98.4%. Precision and recall also showed robust improvements, ensuring that the model is not only detecting cancer accurately but doing so reliably across both classes. The high F1-score reflects the model's ability to balance precision and recall effectively, which is crucial in a medical diagnostic context where both false positives and false negatives must be minimized.

5. CONCLUSION

The proposed fuzzy modeling approach for breast cancer prediction offers a highly accurate, interpretable, and explainable solution compared to conventional machine learning models. By

incorporating linguistic variables and rule-based logic, the system provides transparent decision-making, which is vital in clinical settings. The model effectively utilizes key statistical features from the WDBC dataset, transforming them through fuzzification and inference into reliable diagnostic outputs. Its ability to outperform established methods like Support Vector Machines and Random Forests over multiple training epochs reflects its robustness and learning capacity. Notably, the model achieves an accuracy of 98.4%, precision of 96.5%, recall of 97.8%, and F1-score of 97.0%, all of which underscore its practical value in real-world applications. These gains are attributed to the intelligent feature selection, structured rule generation, and comprehensive fuzzy inference mechanism. Moreover, the system's explainability supports better understanding by medical professionals, reducing reliance on black-box algorithms. In future extensions, integrating hybrid fuzzy-neuro approaches or incorporating deep learning components with fuzzy layers could further enhance performance. Ultimately, this fuzzy model bridges the gap between predictive accuracy and explainability, offering a meaningful step forward in the development of trustworthy AI systems for early cancer detection and diagnosis.

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