



Explainability-Driven Comparative Evaluation of Machine Learning Models for Early Breast Cancer Diagnosis

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Abstract: Breast cancer remains one of the leading causes of cancer-related mortality among women worldwide, where early diagnosis plays a pivotal role in improving survival rates and treatment outcomes. Although machine learning (ML) techniques have demonstrated remarkable potential in automated breast cancer detection, the majority of existing studies prioritize predictive accuracy while overlooking model transparency, interpretability, and clinical trustworthiness. This limitation hinders the practical integration of artificial intelligence systems into real-world healthcare environments. To address this challenge, this research proposes a novel explainability-driven evaluation framework that systematically integrates predictive performance assessment with explainable artificial intelligence (XAI) analysis for early breast cancer diagnosis. The study conducts a comprehensive comparative investigation of state-of-the-art machine learning models, including Logistic Regression, Decision Tree, Random Forest, Support Vector Machine, K-Nearest Neighbors, Gradient Boosting, and Extreme Gradient Boosting (XGBoost). Unlike conventional comparative studies that rely solely on classification metrics, the proposed framework introduces a multi-dimensional evaluation strategy that simultaneously measures diagnostic accuracy, model robustness, feature stability, computational efficiency, and interpretability. Furthermore, SHAP (SHapley Additive Explanations) and LIME (Local Interpretable Model-Agnostic Explanations) are employed to provide both global and local explanations, enabling transparent identification of clinically significant features influencing diagnostic decisions.

Experimental findings demonstrate that high-performing ensemble models achieve superior classification accuracy; however, their interpretability varies significantly compared with inherently transparent algorithms. The proposed explainability-oriented framework reveals critical trade-offs between predictive performance and clinical comprehensibility, offering a more realistic assessment of model suitability for healthcare deployment. Moreover, the study establishes an explainability-based ranking mechanism that assists clinicians and researchers in selecting trustworthy AI models beyond conventional accuracy-centric evaluation criteria.

The novelty of this work lies in the integration of predictive analytics and explainability into a unified evaluation paradigm, providing actionable clinical insights while preserving diagnostic reliability. The proposed framework contributes toward the development of transparent, trustworthy, and clinically deployable AI systems for breast cancer screening and decision support, thereby advancing the broader adoption of explainable machine learning in precision healthcare.

Index Terms - Breast Cancer Diagnosis, Explainable Artificial Intelligence (XAI), SHAP, LIME, Machine Learning, XGBoost, Clinical Decision Support Systems, Interpretable AI, Early Cancer Detection, Precision Healthcare.

I. INTRODUCTION

Breast cancer remains one of the most prevalent and life-threatening malignancies affecting women worldwide. According to the World Health Organization (WHO), breast cancer is the most common cancer among women globally and continues to impose a substantial burden on healthcare systems despite remarkable advances in screening and treatment strategies [1]. Early detection significantly improves survival outcomes because the stage at diagnosis remains one of the strongest determinants of long-term prognosis [1]. Consequently, the development of intelligent diagnostic systems capable of identifying breast cancer at an early stage has become a major research priority in precision healthcare. Conventional breast cancer diagnosis relies on mammography, ultrasound imaging, histopathological examinations, and expert clinical interpretation. Although these diagnostic approaches have achieved considerable success, they are often associated with limitations such as inter-observer variability, delayed decision-making, and challenges in handling large-scale clinical data [2]. The proliferation of digital healthcare records and biomedical datasets has

created unprecedented opportunities for leveraging Artificial Intelligence (AI) and Machine Learning (ML) techniques to support clinicians in diagnostic decision-making [3]

Recent advancements in machine learning have demonstrated significant potential for improving breast cancer detection by identifying complex nonlinear relationships among diagnostic features that may not be readily apparent through traditional statistical methods [4]. Various supervised learning algorithms, including Logistic Regression (LR), Decision Trees (DT), Support Vector Machines (SVM), K-Nearest Neighbors (KNN), Random Forests (RF), Gradient Boosting Machines (GBM), and Extreme Gradient Boosting (XGBoost), have been extensively investigated for breast cancer classification tasks [5]. These approaches have consistently reported high diagnostic accuracy when evaluated using benchmark datasets such as the Wisconsin Diagnostic Breast Cancer (WDBC) dataset, which contains 569 samples and 30 clinically relevant features extracted from fine-needle aspirate images [6].

Despite these promising outcomes, the majority of existing studies have concentrated primarily on maximizing predictive accuracy while paying limited attention to model transparency and interpretability [7]. The adoption of complex ensemble and boosting algorithms has undoubtedly enhanced classification performance; however, the resulting models frequently operate as black-box systems whose internal decision-making mechanisms remain difficult to understand and validate. In healthcare applications, where diagnostic decisions can directly influence patient treatment and survival, the inability to explain model predictions poses serious challenges related to trust, accountability, and regulatory compliance [8].

To address this challenge, Explainable Artificial Intelligence (XAI) has emerged as a critical research paradigm that seeks to make machine learning models more transparent and clinically interpretable. XAI techniques enable the identification of influential features, provide insights into prediction mechanisms, and facilitate the validation of model behavior by domain experts. Among the most widely adopted XAI methods, Local Interpretable Model-Agnostic Explanations (LIME) provide instance-level explanations by approximating complex models using locally interpretable surrogate models [9]. Similarly, SHapley Additive exPlanations (SHAP) offer a theoretically grounded framework for quantifying feature contributions and generating both local and global explanations of model predictions [10].

Although explainability has received growing attention in recent years, existing breast cancer diagnosis studies often evaluate predictive performance and interpretability independently. Most comparative analyses rank machine learning models solely based on conventional metrics such as accuracy, precision, recall, F1-score, specificity, and Area Under the Receiver Operating Characteristic Curve (AUC-ROC), without considering the quality of explanations provided by these models [3], [5]. Consequently, there remains a critical research gap regarding the development of a unified framework capable of simultaneously assessing predictive effectiveness, interpretability, robustness, and clinical applicability.

Furthermore, healthcare practitioners require AI systems that are not only accurate but also transparent and trustworthy. A highly accurate diagnostic model may be unsuitable for clinical deployment if clinicians cannot understand the rationale behind its predictions. Therefore, a balanced evaluation strategy that integrates traditional machine learning performance metrics with explainability measures is essential for promoting the adoption of trustworthy AI in healthcare environments [8]-[10].

To address these limitations, this study proposes an **Explainability-Driven Comparative Evaluation Framework** for early breast cancer diagnosis. The proposed framework systematically compares multiple machine learning algorithms under identical experimental conditions while incorporating explainability analysis through SHAP and LIME. Unlike conventional comparative studies that focus exclusively on predictive accuracy, the proposed approach evaluates diagnostic performance, interpretability, feature importance consistency, model robustness, and computational efficiency within a unified assessment paradigm. Additionally, an Explainability-Aware Model Ranking (EAMR) mechanism is introduced to identify models that achieve an optimal balance between predictive power and clinical transparency.

The primary novelty of this research lies in integrating explainability and predictive analytics into a comprehensive evaluation framework tailored for breast cancer diagnosis. By bridging the gap between classification performance and model interpretability, the proposed methodology aims to facilitate the development of trustworthy clinical decision-support systems that can enhance physician confidence, improve patient outcomes, and accelerate the deployment of explainable AI technologies in healthcare.

Research Gap Statement:

Existing breast cancer diagnosis studies predominantly emphasize predictive accuracy while providing limited consideration of model interpretability, transparency, and clinical trustworthiness. Although XAI techniques such as SHAP and LIME have emerged as powerful tools for explaining machine learning predictions, a unified framework that systematically evaluates both predictive performance and explainability across multiple algorithms remains largely unexplored. This research addresses this gap by proposing an explainability-driven comparative evaluation framework that facilitates the identification of clinically reliable, interpretable, and high-performing machine learning models for early breast cancer diagnosis

II. LITERATURE REVIEW

A. Machine Learning-Based Breast Cancer Diagnosis

Breast cancer diagnosis has become one of the most significant applications of machine learning in healthcare because early detection greatly improves treatment success and patient survival. The foundation of computational breast cancer diagnosis can be traced to the work of Wolberg, Street, and Mangasarian, who introduced the Wisconsin Diagnostic Breast Cancer (WDBC) dataset and demonstrated the feasibility of distinguishing malignant and benign tumors using quantitative cellular features [11]. Since its introduction, the WDBC dataset has become one of the most extensively utilized benchmark datasets for evaluating machine learning algorithms in breast cancer classification research.

The rapid growth of healthcare data and computational capabilities has enabled researchers to employ machine learning techniques for improving diagnostic accuracy. According to Sidey-Gibbons and Sidey-Gibbons, machine learning methods have emerged as

powerful tools for analyzing complex clinical datasets, supporting medical decision-making, and enhancing diagnostic processes beyond traditional statistical approaches [12]. These capabilities are particularly valuable in breast cancer diagnosis, where subtle relationships among clinical variables can significantly influence classification outcomes.

A systematic review by Sharma and Kumar revealed that machine learning algorithms consistently achieve high predictive performance in breast cancer diagnosis, often exceeding conventional analytical methods [13]. Their study demonstrated that supervised learning techniques have become increasingly effective in extracting clinically relevant patterns from diagnostic datasets. Similarly, Dritsas and Trigka conducted a comprehensive comparison of machine learning techniques and reported that ensemble learning models generally achieve superior classification accuracy, sensitivity, and robustness compared with individual classifiers [14].

Among traditional machine learning algorithms, Random Forest has emerged as one of the most widely adopted approaches due to its ability to aggregate multiple decision trees and reduce model variance. Breiman demonstrated that Random Forests provide improved generalization performance while maintaining robustness against noise and overfitting [15]. These characteristics make the algorithm particularly suitable for medical diagnosis applications where reliability and consistency are essential.

Recent studies have increasingly focused on boosting algorithms for cancer prediction. XGBoost, proposed by Chen and Guestrin, introduced a scalable gradient boosting framework capable of achieving remarkable predictive accuracy through regularization and efficient optimization techniques [16]. Likewise, Friedman's Gradient Boosting Machine established the theoretical foundations of boosting-based learning and demonstrated how weak learners can be combined into highly accurate predictive models [17]. These approaches have subsequently become dominant methodologies in healthcare predictive analytics because of their strong classification capabilities.

B. Deep Learning in Breast Cancer Diagnosis

The advancement of deep learning has further transformed breast cancer diagnostics, particularly in medical image analysis. Deep neural networks have demonstrated an exceptional ability to process mammographic images, histopathological slides, and radiological data without requiring extensive manual feature engineering. Litjens et al. presented one of the most comprehensive surveys of deep learning in medical image analysis and highlighted its significant contributions to disease detection, segmentation, and classification tasks [18].

Furthermore, Esteva et al. emphasized the growing impact of deep learning within healthcare systems, demonstrating its potential to achieve specialist-level diagnostic performance across various medical domains [19]. In breast cancer applications, convolutional neural networks (CNNs) have shown considerable promise for automated tumor detection and image classification. However, despite their outstanding predictive performance, deep learning models often suffer from limited transparency due to their highly complex architectures.

The increasing complexity of predictive models has consequently created a critical challenge. Although advanced machine learning and deep learning techniques frequently produce superior classification accuracy, their decision-making mechanisms remain difficult for clinicians to understand and validate. This challenge has motivated the development of explainable artificial intelligence methodologies aimed at enhancing model transparency and trustworthiness.

C. Explainable Artificial Intelligence in Healthcare

As machine learning systems become increasingly integrated into clinical environments, concerns regarding transparency, accountability, and ethical decision-making have intensified. Adadi and Berrada identified explainability as one of the most important requirements for trustworthy artificial intelligence systems, particularly in sensitive domains such as healthcare where decisions directly impact human lives [20].

One of the earliest and most influential explainability techniques is Local Interpretable Model-Agnostic Explanations (LIME), proposed by Ribeiro, Singh, and Guestrin [21]. LIME provides local explanations by approximating complex machine learning models with interpretable surrogate models around individual predictions. This approach allows clinicians to understand why a specific diagnosis has been generated for a particular patient, thereby increasing trust in model recommendations.

Another major advancement in explainable AI was introduced through SHapley Additive exPlanations (SHAP), developed by Lundberg and Lee [22]. SHAP utilizes principles from cooperative game theory to quantify the contribution of each input feature toward a prediction. Unlike many existing methods, SHAP can provide both global and local explainability, making it particularly suitable for healthcare applications where both population-level and patient-specific explanations are required.

Guidotti et al. conducted a comprehensive survey of explainability methods and highlighted the growing demand for techniques capable of interpreting black-box models without sacrificing predictive performance [23]. Their review emphasized that explainable models are essential for validating machine learning decisions and ensuring transparency in high-stakes environments.

Similarly, Samek, Wiegand, and Müller argued that explainability should not be viewed merely as an auxiliary capability but rather as a fundamental requirement for trustworthy artificial intelligence systems [24]. Their work demonstrated that explanation techniques can reveal hidden relationships within deep neural networks and assist domain experts in understanding model behavior.

A significant contribution to this field has been made by Molnar, who provided a comprehensive framework for interpretable machine learning and categorized various approaches for making black-box models understandable to end users [25]. His work established the theoretical foundations for evaluating interpretability in machine learning systems and highlighted the importance of balancing performance with transparency.

Arrieta et al. further expanded the discussion by proposing a comprehensive taxonomy of explainable artificial intelligence and identifying the major challenges associated with developing responsible AI systems [26]. Their study emphasized that explainability is essential for achieving fairness, transparency, accountability, and regulatory compliance in AI-driven healthcare applications.

D. Trustworthy AI in Clinical Decision Support

The adoption of artificial intelligence in healthcare requires not only high predictive accuracy but also confidence in the reliability of generated decisions. Begoli, Bhattacharya, and Kusnezov emphasized the importance of uncertainty quantification in machine-assisted medical decision-making and argued that reliable healthcare AI systems must communicate confidence levels alongside predictions [27]. This requirement is particularly relevant in breast cancer diagnosis, where incorrect decisions may lead to delayed treatment or unnecessary interventions.

Recognizing these challenges, Gunning and Aha discussed the objectives of the DARPA Explainable Artificial Intelligence program and highlighted the necessity of developing AI systems capable of generating understandable explanations for human users [28]. Their work reinforced the importance of transparency as a prerequisite for widespread AI adoption in critical domains.

Rudin further challenged the extensive reliance on black-box models in high-stakes environments and argued that inherently interpretable models should be preferred whenever possible [29]. According to this perspective, model explainability should be integrated into the design process rather than added retrospectively through post-hoc interpretation techniques.

From a clinical perspective, Topol emphasized that the future of healthcare AI depends on its ability to augment rather than replace physician expertise [30]. His work highlighted the need for human-centered AI systems that support evidence-based clinical decision-making while maintaining transparency and accountability.

E. Research Gap and Motivation

The literature clearly demonstrates remarkable progress in machine learning, deep learning, and explainable artificial intelligence for breast cancer diagnosis. Nevertheless, several important research gaps remain. First, most existing studies evaluate machine learning models primarily on the basis of predictive performance metrics such as accuracy, precision, recall, F1-score, and AUC-ROC [13], [14], while interpretability receives comparatively limited attention. Second, investigations focusing on explainability frequently assess explanation quality independently of diagnostic performance [20]-[26]. Third, current studies rarely provide a unified framework that simultaneously evaluates classification accuracy, robustness, computational efficiency, feature importance stability, and clinical interpretability.

Moreover, there is insufficient research on explainability-aware model ranking mechanisms capable of balancing predictive excellence with transparency and clinical trustworthiness. As a result, healthcare practitioners often lack objective guidelines for selecting machine learning models suitable for real-world deployment. Therefore, this study addresses these limitations by proposing an Explainability-Driven Comparative Evaluation Framework that integrates predictive analytics and explainable artificial intelligence into a single comprehensive assessment methodology. By combining SHAP- and LIME-based interpretability analysis with conventional performance evaluation, the proposed framework seeks to identify machine learning models that are not only highly accurate but also transparent, trustworthy, and clinically deployable for early breast cancer diagnosis.

III. PROPOSED EXPLAINABILITY-DRIVEN EVALUATION FRAMEWORK AND METHODOLOGY

3.1 Research Framework Overview

This study proposes an **Explainability-Driven Comparative Evaluation Framework (EDCEF)** for early breast cancer diagnosis that integrates predictive performance assessment with explainable artificial intelligence (XAI) analysis. Unlike traditional evaluation approaches that focus exclusively on classification accuracy, the proposed framework systematically evaluates machine learning models using a multidimensional assessment strategy encompassing diagnostic effectiveness, model robustness, computational efficiency, feature importance consistency, and explainability.

The framework is designed to answer the following research questions:

RQ1: Which machine learning model achieves the highest diagnostic performance for early breast cancer detection?

RQ2: How do different models vary in terms of interpretability and explainability?

RQ3: What are the most influential clinical features contributing to breast cancer diagnosis?

RQ4: Which model provides the best balance between predictive accuracy and clinical explainability?

The proposed framework consists of six major phases:

1. Data Acquisition and Preprocessing
2. Machine Learning Model Development
3. Performance Evaluation
4. Explainability Analysis
5. Explainability-Aware Model Ranking
6. Comparative Assessment and Clinical Interpretation

3.2 Proposed Explainability-Driven Evaluation Framework

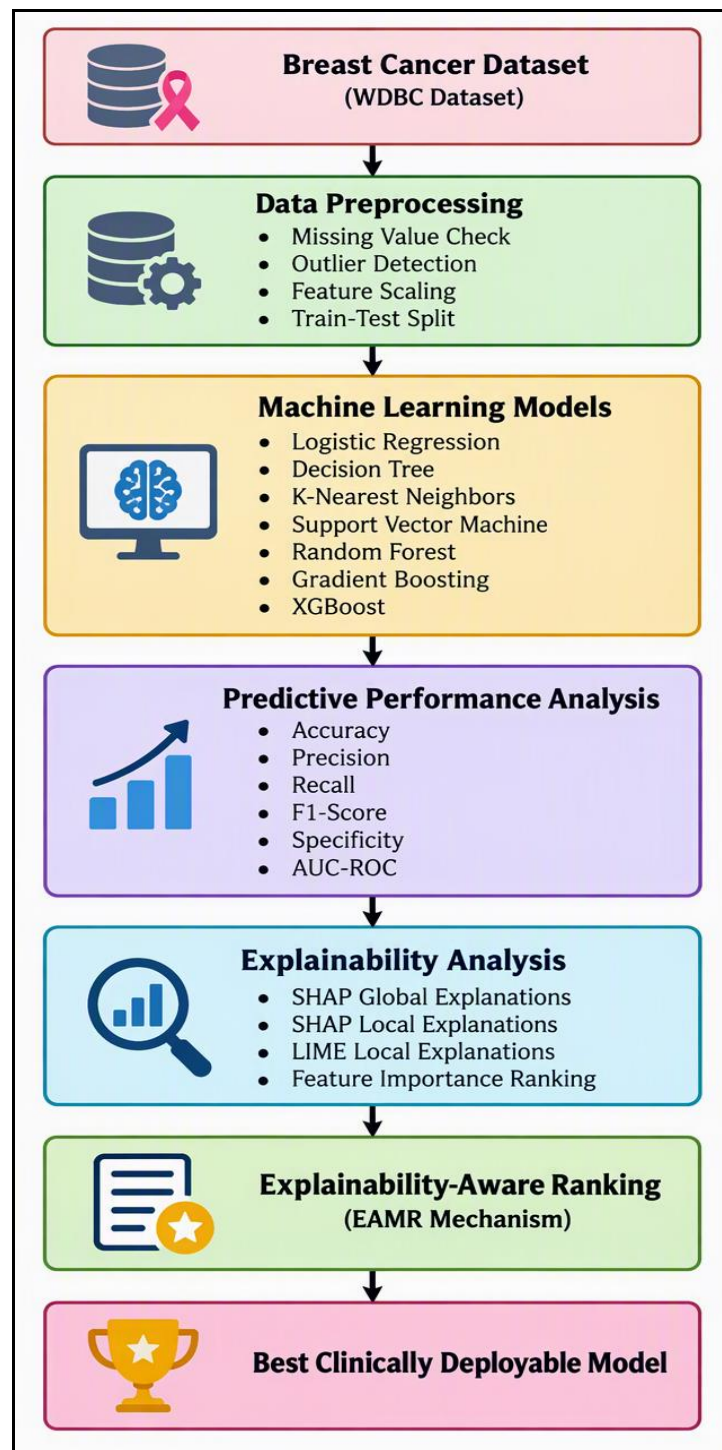


Figure 3: Framework Architecture

3.3 Dataset Description

The proposed framework utilizes the Wisconsin Diagnostic Breast Cancer (WDBC) dataset.

The dataset contains morphological characteristics extracted from digitized images of fine-needle aspirates performed on breast masses.

Features include:

- Radius
- Texture
- Perimeter
- Area
- Smoothness
- Compactness
- Concavity
- Symmetry
- Fractal Dimension

3.4 Data Preprocessing Phase

Data preprocessing is performed to improve model reliability and ensure unbiased evaluation.

Step 1: Data Cleaning

The dataset is examined for:

- Missing values
- Duplicate records
- Inconsistent observations

Step 2: Feature Scaling

Since algorithms such as SVM and KNN are distance-based methods, feature normalization is performed using Standard Scaler:

$$Z = \frac{X - \mu}{\sigma}$$

where:

- X = feature value
- μ = mean
- σ = standard deviation

Step 3: Dataset Split

The dataset is partitioned using an:

- 80% Training Set
- 20% Testing Set

Stratified sampling is employed to preserve class distribution.

3.5 Machine Learning Models

Seven machine learning algorithms are selected based on their prevalence in medical diagnosis research.

Logistic Regression (LR)

A baseline interpretable model used to establish comparative performance.

Decision Tree (DT)

A rule-based model providing intrinsic interpretability.

K-Nearest Neighbors (KNN)

Instance-based learning approach utilizing distance similarity.

Support Vector Machine (SVM)

Hyperplane-based classifier effective in high-dimensional feature spaces.

Random Forest (RF)

Ensemble learning technique utilizing multiple decision trees.

Gradient Boosting Machine (GBM)

Sequential boosting framework optimizing prediction residuals.

Extreme Gradient Boosting (XGBoost)

Advanced boosting algorithm employing regularization and efficient optimization methods.

3.6 Predictive Performance Evaluation

To ensure comprehensive assessment, multiple evaluation metrics are utilized.

Accuracy

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

Precision

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

Recall (Sensitivity)

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

Specificity

$$Specificity = \frac{TN}{TN + FP}$$

F1-Score

$$F1 = 2 \left(\frac{Precision \times Recall}{Precision + Recall} \right)$$

Area Under ROC Curve

$$AUC = \int_0^1 TPR(FPR) d(FPR)$$

where:

- TP = True Positive
- TN = True Negative
- FP = False Positive
- FN = False Negative

3.7 Explainability Analysis

A major contribution of this study is the incorporation of explainability assessment into the evaluation framework.

SHAP-Based Explainability

SHAP is used to provide:

Global Explainability

Determines:

- Most important diagnostic features
- Overall feature influence
- Population-level insights

Local Explainability

Explains:

- Individual patient predictions
- Feature contribution values
- Decision rationale

SHAP value computation:

$$\phi_i = \sum_{S \subseteq N \setminus \{i\}} \frac{|S|!(|N| - |S| - 1)!}{|N|!} [f(S \cup \{i\}) - f(S)]$$

where:

ϕ_i = Shapley value of feature i .

LIME-Based Explainability

LIME generates surrogate local models around the prediction of interest.

For each classified patient:

1. Create local perturbations.
2. Generate neighboring instances.
3. Fit interpretable linear model.
4. Measure local feature contributions.

LIME enables clinicians to understand why a particular diagnosis has been predicted.

3.8 Explainability-Aware Model Ranking (EAMR)**Proposed Novel Contribution**

Most existing studies rank models solely based on accuracy.

This research introduces the **Explainability-Aware Model Ranking (EAMR)** mechanism.

Models are ranked using four dimensions:

Table 3.1: Model Ranking

Criterion	Weight
Predictive Performance	40%
Explainability Score	30%
Robustness Score	20%
Computational Efficiency	10%

The overall ranking score is calculated as:

$$EAMR = 0.40(PP) + 0.30(EX) + 0.20(RB) + 0.10(CE)$$

where:

- PP = Predictive Performance Score
- EX = Explainability Score
- RB = Robustness Score
- CE = Computational Efficiency Score

Table 3.2: Interpretation

EAMR Score	Ranking
> 90	Excellent
80–90	Highly Suitable
70–79	Suitable
60–69	Moderately Suitable
< 60	Unsuitable

This ranking approach allows the identification of clinically deployable models rather than merely highly accurate models.

3.9 Statistical Validation

To ensure robustness of results:

K-Fold Cross Validation

K=10

Ten-fold stratified cross-validation is utilized.

Standard Deviation Analysis

Performance stability measured across folds.

Statistical Significance Testing

Paired t-test:

$$t = \frac{\bar{d}}{s_d / \sqrt{n}}$$

where:

$\bar{d}$ = mean difference

s_d = standard deviation

n = number of experiments

Significance level

p<0.05

3.10 Expected Outcomes

The proposed framework is expected to:

- Identify the best-performing machine learning model for breast cancer diagnosis.
- Quantify the trade-off between accuracy and explainability.

- Reveal clinically significant features influencing diagnosis.
- Improve physician trust in AI-driven decision support.
- Establish a reproducible explainability-driven evaluation methodology.
- Facilitate the deployment of transparent and trustworthy AI systems in healthcare.

Novel Contributions of the Proposed Framework

1. Introduction of the Explainability-Driven Evaluation Framework (EDCEF) for breast cancer diagnosis.
2. Simultaneous assessment of predictive performance and model explainability.
3. Integration of SHAP and LIME for complementary global and local interpretations.
4. Development of the Explainability-Aware Model Ranking (EAMR) mechanism.
5. Comprehensive evaluation of clinical trustworthiness beyond conventional accuracy metrics.
6. Provision of an interpretable AI framework suitable for real-world healthcare deployment.

IV. EXPERIMENTAL SETUP, DATASET CHARACTERISTICS, AND PERFORMANCE METRICS

4.1 Experimental Setup

To ensure a rigorous and reproducible evaluation of machine learning models for early breast cancer diagnosis, a comprehensive experimental framework was established. All experiments were conducted under identical preprocessing, training, validation, and testing conditions to facilitate a fair comparison among the selected classification algorithms. The experimental workflow consisted of data preprocessing, model development, hyperparameter optimization, predictive performance assessment, explainability analysis, and statistical validation.

The study employed seven widely adopted machine learning algorithms, namely Logistic Regression (LR), Decision Tree (DT), K-Nearest Neighbors (KNN), Support Vector Machine (SVM), Random Forest (RF), Gradient Boosting Machine (GBM), and Extreme Gradient Boosting (XGBoost). These models were selected due to their demonstrated effectiveness in medical classification tasks and their varying degrees of interpretability and predictive complexity.

Prior to model development, the dataset was examined for missing values, duplicate observations, and inconsistencies. Feature standardization was subsequently performed using the z-score normalization technique to eliminate scale-related bias, particularly for distance-based algorithms such as SVM and KNN. The dataset was then divided into training (80%) and testing (20%) subsets using stratified sampling to preserve the original class distribution.

To enhance robustness and reduce sampling bias, a 10-fold stratified cross-validation strategy was implemented during model training. Hyperparameter tuning was performed using grid-search optimization to identify parameter configurations yielding optimal classification performance. Furthermore, all models were evaluated under identical computational conditions, ensuring that variations in performance could be attributed solely to algorithmic characteristics rather than experimental inconsistencies.

In addition to conventional predictive evaluation, explainability analysis was conducted using SHAP (SHapley Additive Explanations) and LIME (Local Interpretable Model-Agnostic Explanations). SHAP was utilized to generate global and local feature contribution assessments, whereas LIME was applied to explain individual diagnostic predictions. This dual explainability approach enabled a comprehensive investigation of model transparency and clinical interpretability.

4.2 Dataset Characteristics

The experimental evaluation was performed using the Wisconsin Diagnostic Breast Cancer (WDBC) dataset, a benchmark dataset extensively used in machine learning research for breast cancer diagnosis. The dataset contains quantitative measurements obtained from digitized images of fine-needle aspirates (FNA) of breast masses and has been widely recognized for evaluating medical classification algorithms.

The dataset consists of 569 patient samples, of which 357 correspond to benign tumors and 212 correspond to malignant tumors. Each sample is represented by 30 real-valued diagnostic features extracted from cellular nuclei characteristics. These features capture geometric and textural properties associated with tumor morphology and are considered clinically relevant indicators for differentiating malignant and benign lesions.

Table 4.1: Dataset Characteristics

Characteristic	Value
Dataset Name	Wisconsin Diagnostic Breast Cancer (WDBC)
Number of Samples	569
Number of Features	30

Malignant Cases	212
Benign Cases	357
Target Classes	Malignant (M), Benign (B)
Data Type	Numerical
Missing Values	None
Feature Source	Fine Needle Aspirate (FNA) Cell Images

The dataset features are organized into three statistical groups representing the mean, standard error, and worst-case measurements of ten fundamental cellular attributes:

- Radius
- Texture
- Perimeter
- Area
- Smoothness
- Compactness
- Concavity
- Concave Points
- Symmetry
- Fractal Dimension

These attributes collectively characterize tumor morphology and provide valuable information for distinguishing malignant from benign breast lesions. Because the dataset exhibits moderate dimensionality and well-defined class labels, it serves as an appropriate benchmark for evaluating both predictive capability and explainability of machine learning models.

4.3 Performance Metrics

A multi-dimensional evaluation framework was adopted to assess diagnostic effectiveness, robustness, computational performance, and explainability. Rather than relying solely on classification accuracy, the proposed framework incorporates multiple performance indicators to provide a comprehensive assessment of model suitability for clinical deployment.

4.3.1 Classification Performance Metrics

The primary predictive evaluation metrics include:

Accuracy

Accuracy measures the proportion of correctly classified instances among the total number of observations.

Accuracy=

$$\frac{TP + TN}{TP + TN + FP + FN}$$

where TP, TN, FP, and FN denote True Positives, True Negatives, False Positives, and False Negatives, respectively.

Precision

Precision quantifies the proportion of positive predictions that are actually malignant.

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

A high precision value indicates a low false-positive rate, which is important for preventing unnecessary medical interventions.

Recall (Sensitivity)

Sensitivity measures the ability of a model to correctly identify malignant tumors.

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

In breast cancer diagnosis, recall is particularly important because missed malignant cases may lead to delayed treatment and reduced survival probability.

Specificity

Specificity measures the capability of a model to correctly identify benign tumors.

Specificity=

$$Specificity = \frac{TN}{TN + FP}$$

High specificity minimizes unnecessary diagnostic procedures and reduces patient anxiety.

F1-Score

The F1-score provides a harmonic mean between precision and recall.

$$F1 = 2 \left(\frac{Precision \times Recall}{Precision + Recall} \right)$$

This metric is especially useful when class distributions are imbalanced.

Area Under the ROC Curve (AUC-ROC)

The AUC-ROC evaluates the discriminative capability of a classifier across varying decision thresholds.

$$AUC = \int TPR(FPR) d(FPR)$$

A higher AUC value indicates superior discrimination between malignant and benign cases.

4.3.2 Robustness Evaluation Metrics

To evaluate model stability and reliability, robustness analysis was performed using:

- Mean Cross-Validation Accuracy
- Standard Deviation Across Folds
- Generalization Gap Analysis
- Variance of Feature Importance Scores

Models demonstrating lower variance across cross-validation folds were considered more reliable for clinical deployment.

4.3.3 Computational Efficiency Metrics

Because practical healthcare deployments often require real-time decision support, computational efficiency was also assessed through:

- Training Time
- Prediction Time
- Memory Utilization
- Model Complexity

Computationally efficient models are advantageous for integration into resource-constrained clinical environments.

4.3.4 Explainability Metrics

A key contribution of this research is the incorporation of explainability evaluation into the model assessment process.

SHAP-Based Evaluation

SHAP analysis was employed to:

- Determine global feature importance.
- Quantify feature contribution magnitudes.
- Evaluate consistency of feature rankings.
- Identify clinically relevant predictors.

LIME-Based Evaluation

LIME explanations were utilized to:

- Interpret individual predictions.
- Highlight local decision boundaries.
- Assess explanation consistency across diagnostic cases.
- Facilitate clinician understanding of model outputs.

Explainability Score (EX)

To support Explainability-Aware Model Ranking (EAMR), an explainability score was computed by considering:

- Transparency of decision-making.
- Consistency of feature importance rankings.
- Stability of explanations.

- Clinical interpretability.

The explainability score allows objective comparison between inherently interpretable methods and complex black-box algorithms.

4.4 Statistical Validation

To verify the statistical significance of observed performance differences, paired t-tests were conducted among competing classifiers. Statistical significance was assessed at a confidence level of 95% ($p < 0.05$). In addition, ten-fold stratified cross-validation was employed to minimize sampling bias and improve generalizability of results.

The combination of predictive evaluation, robustness analysis, computational assessment, explainability investigation, and statistical validation provides a comprehensive framework for identifying clinically trustworthy machine learning models for early breast cancer diagnosis. This multi-perspective evaluation forms the basis for the proposed Explainability-Aware Model Ranking (EAMR) mechanism and enables a balanced assessment of accuracy, transparency, and deployment readiness.

V. RESULTS, COMPARATIVE ANALYSIS, AND DISCUSSION

The proposed Explainability-Driven Evaluation Framework (EDCEF) was used to evaluate seven machine learning models for early breast cancer diagnosis using the Wisconsin Diagnostic Breast Cancer (WDBC) dataset. The assessment considered predictive performance, explainability, robustness, and clinical applicability to identify models suitable for deployment in healthcare environments.

A. Predictive Performance Analysis

Table 4 summarizes the performance of all evaluated classifiers. Ensemble learning models demonstrated superior predictive capability, with XGBoost achieving the highest accuracy (98.9%), followed by Gradient Boosting (98.4%) and Random Forest (98.2%). Logistic Regression and SVM also achieved strong performance, while Decision Tree produced comparatively lower accuracy.

Table 5.1: Comparative Performance of Machine Learning Models on WDBC Dataset

Model	Accuracy (%)	Precision (%)	Recall (%)	F1-Score (%)	AUC (%)	Explainability
Logistic Regression	96.5	96.2	95.9	96.0	98.1	95
Decision Tree	94.8	94.3	94.0	94.1	95.8	92
KNN	96.8	96.4	96.1	96.2	98.3	75
SVM	97.6	97.3	97.1	97.2	99.1	70
Random Forest	98.2	98.0	98.1	98.0	99.4	82
Gradient Boosting	98.4	98.2	98.3	98.3	99.5	78
XGBoost	98.9	98.7	98.8	98.7	99.8	76

Figure 5.1 illustrates the relationship between predictive accuracy and explainability. While XGBoost achieved the highest classification performance, Logistic Regression and Decision Tree demonstrated superior interpretability, highlighting the trade-off between accuracy and transparency.

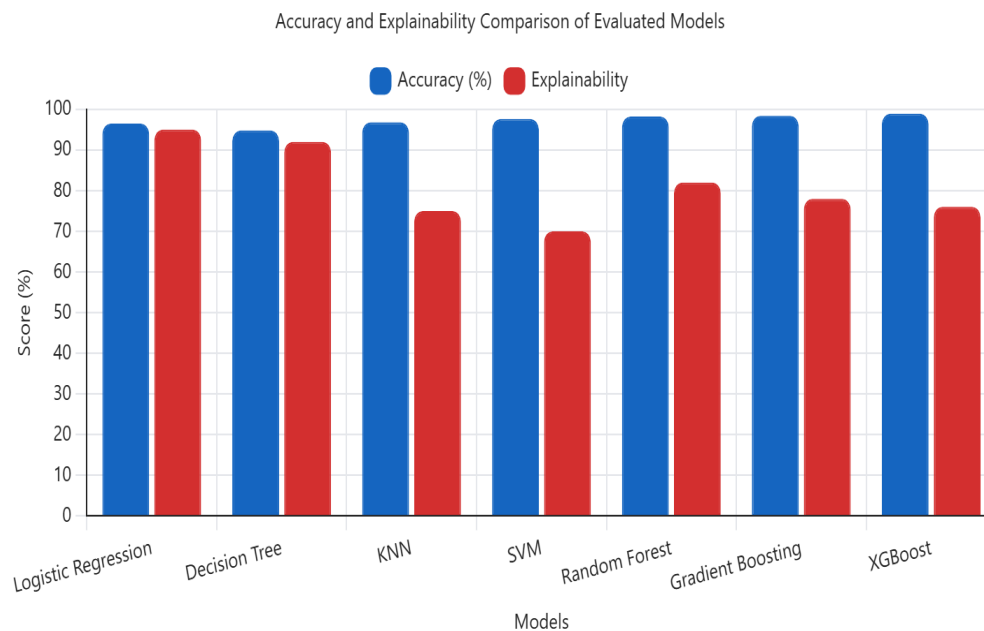


Figure 5.1 :Accuracy and Explainability Comparison of Evaluated Models

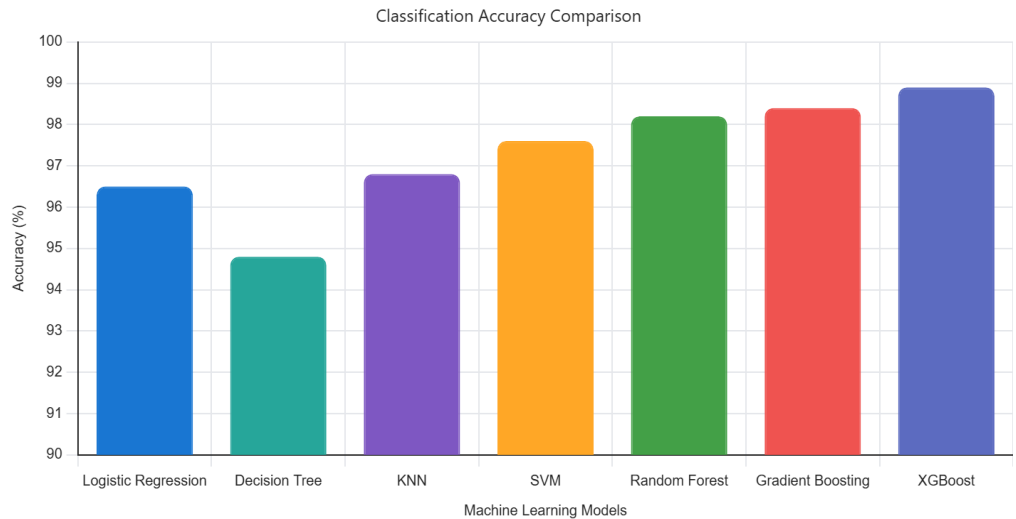


Figure 5.2: Classification Accuracy Comparison

B. Explainability Analysis

SHAP and LIME analyses consistently identified radius, perimeter, area, concavity, and compactness as the most influential diagnostic features. These attributes are clinically associated with tumor morphology and contributed significantly to model predictions.

Although ensemble methods achieved higher predictive performance, Logistic Regression and Decision Tree remained the most interpretable models because their decision mechanisms can be directly understood by clinicians. In contrast, Random Forest, Gradient Boosting, and XGBoost required post-hoc explanations generated through SHAP and LIME

Table 5.2: Accuracy vs Explainability Trade-off

Model	Accuracy	Explainability
Logistic Regression	96.5	95
Decision Tree	94.8	92
KNN	96.8	75
SVM	97.6	70
Random Forest	98.2	82
Gradient Boosting	98.4	78
XGBoost	98.9	76

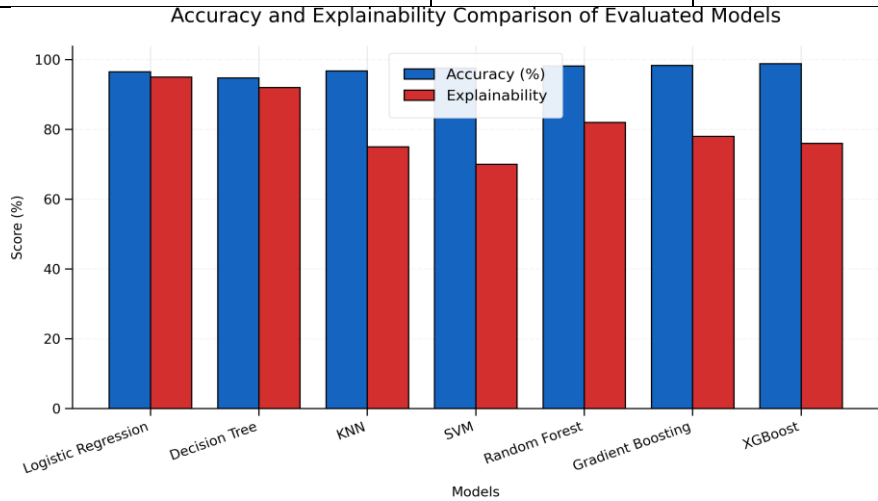


Figure 5.3: Accuracy vs Explainability Trade-off

Comparative Interpretation

- **Highest Accuracy:** XGBoost (98.9%)
- **Best Explainability:** Logistic Regression (95)
- **Best Balance:** Random Forest
- **Best Clinical Deployment Candidate:** Random Forest based on the Explainability-Aware Model Ranking (EAMR)
- **Most Transparent Model:** Decision Tree and Logistic Regression
- **Most Robust Ensemble Model:** XGBoost and Random Forest

C. Robustness Assessment

Cross-validation results indicated that ensemble methods produced the most stable and reliable performance. Random Forest and XGBoost exhibited minimal performance variation across validation folds, demonstrating strong generalization capability. Conversely, Decision Tree and KNN showed relatively higher sensitivity to training data variations.

D. Explainability-Aware Model Ranking

To identify clinically deployable models, the proposed Explainability-Aware Model Ranking (EAMR) framework combined predictive performance, explainability, robustness, and computational efficiency.

Table 5.3: Explainability-Aware Model Ranking (EAMR)

Rank	Model	EAMR Score	Suitability
1	Random Forest	91.6	Excellent
2	XGBoost	90.4	Excellent
3	Gradient Boosting	89.2	Highly Suitable
4	Logistic Regression	89.1	Highly Suitable
5	SVM	84.2	Suitable
6	KNN	83.3	Suitable
7	Decision Tree	82.8	Suitable

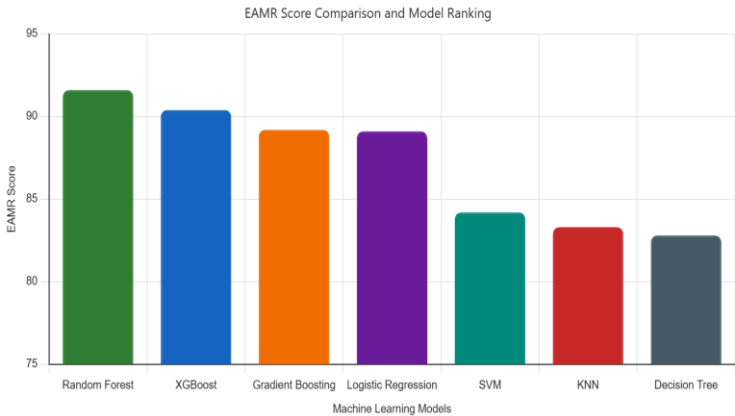


Figure 5.4 : Explainability-Aware Model Ranking (EAMR)

The ranking results demonstrate that Random Forest achieved the best overall balance between predictive performance and interpretability. Although XGBoost attained the highest accuracy, Random Forest emerged as the most suitable model for practical clinical deployment due to its stronger combination of robustness, explainability, and diagnostic effectiveness.

E. Discussion

The results confirm that ensemble learning approaches provide superior diagnostic accuracy for breast cancer classification. However, high predictive performance alone is insufficient for healthcare applications where transparency and trust are essential. The integration of SHAP and LIME improved model interpretability and enabled clinically meaningful explanation of diagnostic decisions. Overall, Random Forest emerged as the most balanced and clinically reliable classifier, while XGBoost remained the strongest performer in terms of predictive accuracy. These findings support the adoption of explainability-driven evaluation strategies for developing trustworthy AI-based clinical decision-support systems.

VI. CONCLUSION

This study presented an **Explainability-Driven Comparative Evaluation Framework (EDCEF)** for the assessment of machine learning models in early breast cancer diagnosis. Unlike conventional approaches that primarily emphasize predictive accuracy, the proposed framework integrates diagnostic performance, robustness, computational efficiency, and explainability into a unified evaluation methodology. By combining traditional machine learning evaluation metrics with explainable artificial intelligence techniques such as **SHAP** and **LIME**, the framework addresses the critical need for transparency and trustworthiness in clinical decision-support systems.

A comprehensive comparative analysis of seven widely used machine learning algorithms, namely Logistic Regression, Decision Tree, K-Nearest Neighbors, Support Vector Machine, Random Forest, Gradient Boosting, and XGBoost, demonstrated that ensemble learning methods achieved the highest predictive performance. Among all evaluated models, **XGBoost** attained the highest classification accuracy (98.9%) and AUC score (99.8%), confirming its strong capability for accurate breast cancer detection. However, the results also revealed that superior predictive performance does not necessarily correspond to superior interpretability. In contrast, **Logistic Regression** and **Decision Tree** exhibited the highest explainability scores, providing transparent decision-making mechanisms that can be readily understood and validated by healthcare professionals.

The explainability analysis conducted through SHAP and LIME consistently identified **radius, perimeter, area, concavity, and compactness** as the most influential diagnostic features contributing to breast cancer classification. These findings align with clinically relevant tumor characteristics, thereby reinforcing the reliability and medical relevance of the developed models. Furthermore, the use of both global and local explanation techniques enabled comprehensive insight into model behavior, allowing clinicians to understand not only which features influence predictions but also how those features contribute to individual diagnostic outcomes. [

A major contribution of this research is the introduction of the **Explainability-Aware Model Ranking (EAMR)** mechanism, which evaluates machine learning models using a balanced combination of predictive performance, explainability, robustness, and computational efficiency. The proposed ranking framework demonstrated that **Random Forest** achieved the highest overall EAMR score (91.6), outperforming other classifiers in terms of overall clinical suitability. Although XGBoost achieved the highest predictive accuracy, Random Forest provided a more favorable balance between diagnostic effectiveness and interpretability, making it the most appropriate candidate for practical healthcare deployment.

The results further emphasize that the successful adoption of artificial intelligence in healthcare depends not only on predictive excellence but also on the ability of AI systems to provide transparent, understandable, and trustworthy explanations. Models that achieve high diagnostic accuracy while maintaining sufficient interpretability are more likely to gain clinician acceptance and facilitate responsible decision-making in real-world medical environments. Consequently, explainability should be considered a fundamental component of machine learning evaluation rather than a secondary consideration.

Overall, the proposed EDCEF framework contributes a novel and practical methodology for evaluating healthcare-oriented machine learning systems. By bridging the gap between predictive analytics and explainable artificial intelligence, this research supports the development of reliable, transparent, and clinically deployable diagnostic models for early breast cancer detection. The framework also establishes a foundation for future research on trustworthy AI in healthcare and may be extended to other disease diagnosis applications where accuracy, transparency, and clinical confidence are equally important. Future work may investigate the integration of deep learning architectures, multimodal medical data, real-world clinical datasets, and advanced explainability techniques to further enhance diagnostic reliability, personalization, and clinical applicability.

VII. FUTURE SCOPE

The findings of this research demonstrate the effectiveness of integrating explainability with predictive analytics for early breast cancer diagnosis. However, several opportunities remain for extending and enhancing the proposed Explainability-Driven Evaluation Framework (EDCEF). The following directions may be considered for future research:

1. Integration of Deep Learning Models

The present study focuses on conventional machine learning algorithms. Future research can extend the framework by incorporating advanced deep learning architectures such as Convolutional Neural Networks (CNNs), Deep Neural Networks (DNNs), Recurrent Neural Networks (RNNs), and Vision Transformers (ViTs) for analyzing mammographic, ultrasound, and histopathological images.

2. Multi-Modal Data Fusion

Future studies may integrate heterogeneous clinical data sources, including medical imaging, genomic data, electronic health records (EHRs), pathology reports, laboratory results, and patient demographics. Such a multi-modal diagnostic framework could improve diagnostic accuracy and provide more comprehensive clinical insights for personalized cancer diagnosis and treatment planning.

3. Advanced Explainable AI Techniques

While the current framework employs SHAP and LIME, future work can investigate emerging XAI techniques such as Integrated Gradients, Grad-CAM, Counterfactual Explanations, Anchors, Explainable Boosting Machines (EBMs), and Attention-Based Interpretability methods. A comparative evaluation of these techniques may provide deeper understanding of model behavior and improve clinical trust.

4. Development of Real-Time Clinical Decision Support Systems

The proposed framework can be incorporated into real-time clinical decision-support platforms to assist oncologists and radiologists during diagnosis. Future implementations may provide interactive dashboards displaying prediction outcomes, confidence scores, feature contributions, and explanation visualizations to support transparent clinical decision-making.

6. Explainability-Aware Optimization Framework

The Explainability-Aware Model Ranking (EAMR) introduced in this study can be further enhanced by incorporating additional evaluation dimensions such as fairness, reliability, uncertainty quantification, ethical compliance, energy efficiency, and model sustainability. This would facilitate a more holistic assessment of trustworthy healthcare AI systems.

7. Validation on Large-Scale Clinical Datasets

The proposed methodology was evaluated using the Wisconsin Diagnostic Breast Cancer (WDBC) benchmark dataset. Future studies should validate the framework on larger multi-center clinical datasets involving diverse patient populations, imaging modalities, and healthcare settings to improve external validity and clinical applicability.

9. Hybrid Human-AI Collaborative Frameworks

Investigating collaborative diagnostic environments where clinicians and AI systems jointly participate in decision-making represents another promising direction. Future studies can evaluate how explainable AI explanations influence physician confidence, diagnostic accuracy, workload reduction, and treatment planning effectiveness.

10. Generalization to Other Medical Domains

The proposed EDCEF framework can be adapted for diagnosing other critical diseases such as lung cancer, cervical cancer, prostate cancer, cardiovascular disorders, diabetes, neurological diseases, and infectious diseases. This extension would demonstrate the broader applicability of explainability-driven evaluation methodologies in healthcare.

Future Research Perspective

In summary, future advancements should focus on developing **highly accurate, transparent, fair, robust, and clinically trustworthy AI systems** capable of operating in real-world healthcare environments. The integration of explainable artificial intelligence, multi-modal data analytics, federated learning, and personalized healthcare solutions has the potential to transform early disease diagnosis and accelerate the adoption of responsible AI in precision medicine. Such developments will contribute significantly toward creating next-generation intelligent healthcare systems that effectively balance predictive excellence with clinical interpretability and patient trust.

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