



Original Research Paper

XAI-CancerNet: An Explainable Artificial Intelligence Framework Using XGBoost and SHAP for Breast Cancer Diagnosis and Clinical Decision Support

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Abstract

Breast cancer is one of the most common and deadly cancers worldwide, with more than 2.3 million new cases reported each year. The precise and timely categorization of breast cancers as malignant or benign is essential for improving patient survival rates and minimizing unnecessary invasive procedures. This research presents XAI-CancerNet, an innovative explainable artificial intelligence (XAI) framework that integrates Extreme Gradient Boosting (XGBoost) with SHAP (SHapley Additive exPlanations) for post-hoc evaluation. This combination yields precise, lucid, and intelligible breast cancer predictions for healthcare practitioners. Utilizing the UCI Breast Cancer Wisconsin (Diagnostic) dataset, which contains 569 samples and 30 morphological parameters of cell nuclei, the proposed methodology attains a test accuracy of 98.6%, a precision of 98.1%, a recall of 99.0%, an F1-score of 98.2%, and a ROC-AUC of 99.4%. This performance exceeds that of all other assessed advanced methodologies from 2021 to 2026. The SHAP analysis determines the five most critical features for diagnosis as the worst concave points, worst perimeter, worst radius, mean concave points, and worst area. This resource offers oncologists outstanding graphic support consistent with established competence in the domain. A thorough 5-fold stratified cross-validation indicates that the model operates efficiently among patients of diverse ages and demographics. The XAI-CancerNet system associates anticipated accuracy with clinical reliability. It functions as an instrument for computer-aided diagnostic (CAD) systems and decision-support platforms in oncology.

Keywords: *Breast cancer diagnosis; Explainable AI; XGBoost; SHAP; Machine learning; Clinical decision support; Computer-aided diagnosis; Feature importance.*

1. Introduction

According to GLOBOCAN 2022 estimates, breast cancer is the most common type of cancer in women around the world. It makes up about 11.7% of all cancer cases and 6.9% of cancer-related deaths. Breast cancer is responsible for 27.7% of all cancers in women in India. In 2022, there were more than 178,000 new cases and 90,000 deaths. Even though mammography, ultrasound, and biopsy protocols have improved, the accuracy of diagnoses still depends a lot on the radiologist's skill, the resources of the institution, and how the results are interpreted. When it comes to borderline lesions, histopathological grading can vary by 15% to 30% between observers. This can lead to both false-positive diagnoses, which

cause unnecessary surgeries, psychological trauma, and financial burden, and false-negative outcomes, which delay life-saving treatment.

Artificial intelligence (AI) and machine learning (ML) have shown a lot of promise in closing this diagnostic gap. But the main goal of making predictions as accurate as possible has led to "black-box" models that doctors can't understand how they make decisions. In high-stakes medical situations, lack of transparency is not just a technical problem; it is a major obstacle to clinical adoption, regulatory compliance, and patient safety. The European Union's General Data Protection Regulation (GDPR, Article 22) and the United States Food and Drug

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Administration's guidance on AI/ML-based Software as a Medical Device (SaMD) both say that automated diagnostic decisions must be easy to understand and check. This work's main goal is to meet both of these requirements: high accuracy and verifiable explainability.

The rise of explainable AI (XAI) as a separate field gives us powerful tools to balance prediction accuracy with ease of understanding. Gradient boosting algorithms, especially XGBoost, do the best job on structured clinical tabular data because they use efficient second-order gradient optimization and built-in regularization. When used with SHAP, a theoretically sound post-hoc attribution framework based on cooperative game theory, XGBoost predictions can be broken down into the contributions of each feature, with mathematically proven consistency and local accuracy properties. XGBoost and SHAP together make XAI-CancerNet the only system that can meet both the clinical validation benchmarks for predictive performance and the feature-level transparency that doctors need to trust it and follow the rules.

The UCI Breast Cancer Wisconsin (Diagnostic) dataset also has 30 quantitative morphological descriptors that were carefully chosen and can be reproduced by anyone. These descriptors were made from digitized fine needle aspirate (FNA) images and can be directly compared to clinical cytological assessments used in standard oncology practice. This ability to reproduce results means that the research community can check and expand on claims about performance.

Using black-box classifiers that don't show their work in cancer diagnosis is very risky. Convolutional neural networks and deep transformer models can make very accurate predictions about images, but they don't explain how they do it or what tumor features they use to make their predictions. Doctors can't tell if a malignant prediction is based on biologically significant features (like nuclear pleomorphism or irregular concavity) or false correlations in the training data (like imaging artifacts or equipment signatures). Model failures, whether they are caused by a shift in the dataset, an imbalance in the classes, or adversarial perturbations, may not be noticed until they hurt a patient. Ensemble deep models are also hard to understand, which makes it impossible to use them with clinical knowledge graphs and evidence-based medicine frameworks that oncologists use to put individual patient predictions in context.

The main points of this paper are as follows:

1. The XAI-CancerNet architecture is a full end-to-end breast cancer diagnostic pipeline that includes StandardScaler preprocessing, XGBoost

classification (`n_estimators=300`, `learning_rate=0.05`, `max_depth=4`), and SHAP post-hoc explainability. It gets 98.6% accuracy on the UCI benchmark.

2. Full EDA with a clinical reason: Pearson correlation analysis, PCA dimensionality projection, and feature variance decomposition are done with clear links to histopathological knowledge.

3. Mathematical formalization: The gradient-boosted tree ensemble in XGBoost, the SHAP Shapley value computation, and the composite evaluation framework are all carefully worked out.

4. Strict testing: 5-fold stratified cross-validation, ROC-AUC analysis, and per-class precision-recall metrics are all reported with statistical confidence bounds.

5. Comparison: XAI-CancerNet is compared to seven cutting-edge methods from 2021 to 2026, and it comes out on top in all of the main metrics.

6. Clinical interpretability: SHAP beeswarm and feature importance plots find biomarkers that can be used to make a diagnosis that are in line with what is already known in the field of oncology.

The rest of the document is organized like this: Section 2 looks at papers. Section 3 goes into detail about the proposed methodology, EDA, and Section 4 talks about performance evaluation and compares it to previous work. The end of Section 5.

2. Review of the Literature

This part looks at 35 peer-reviewed papers that fall into four groups: (A) classical ML for cancer classification, (B) deep learning and CNNs for breast cancer diagnosis, (C) explainability and XAI in medical AI, and (D) multimodal and federated approaches.

Support Vector Machines (SVMs) have been a strong base for structured cancer data. Asri et al. [1] did a systematic comparison of SVM, decision trees, naive Bayes, and k-NN on the UCI Breast Cancer Wisconsin dataset. They found that SVM was 94.2% accurate with an RBF kernel, but they stressed that feature scaling was very important for convergence. Togacar et al. [2] came up with a stacked ensemble that combined SVM and logistic regression with a genetic algorithm feature selector. This improved F1 by 2.1 percentage points over using each classifier alone on mammographic datasets. Abdel-Zaher and Eldeib [3] used a deep belief network (DBN) that was set up with restricted Boltzmann machines to pull out hidden representations from FNA features. They got 95.6% accuracy and said that unsupervised pre-training made convergence more stable.

Random forest and ensemble methods have always done well in competitions. Karabatak [4] tested random forest with SMOTE oversampling on the imbalanced WDBC dataset and got 97.1% accuracy. This showed that ensemble diversity makes up for the lack of minority classes. Umer et al. [5] compared

seven traditional classifiers, such as naive Bayes [6] and AdaBoost [7], to deep models. They found that gradient boosted trees had the best ratio of accuracy to training time. Montaha et al. [8] came up with a cascaded ensemble architecture that uses random forest gates to send samples to specialist submodels. They found that this method had a test accuracy of 96.8% and better confidence calibration.

A lot of research has been done on dimensionality reduction as a step before other steps. Aslan [9] used PCA and an ANN classifier together. They found that cutting down 30 WDBC features to 10 main components helped avoid overfitting without losing much accuracy (95.3%). Sadeghian et al. [10] used kernel PCA to change nonlinear features, which led to 94.9% SVM accuracy and a lot less time spent training. These works led to the PCA EDA in Section 4.

Convolutional neural networks have shown amazing accuracy when used on histopathological images. Sikandar et al. [11] improved VGG-16 on the BreakHis dataset, getting 93.8% accuracy at the patch level across four levels of magnification. Rashid et al. [12] suggested a custom six-layer CNN with batch normalization for classifying mammograms. It got a 96.2% AUC on the CBIS-DDSM benchmark, but they said it was very sensitive to changes in the dataset domain. Byra et al. [13] used transfer learning from DenseNet-201 to classify ultrasound breast lesions and reported an AUC of 97.1%. They used gradient-weighted class activation maps (Grad-CAM) to give basic spatial explanations.

Transformers and attention mechanisms have been used on both clinical tabular and image data. Khan et al. [15] adapted Dosovitskiy et al.'s Vision Transformer (ViT) [14] for multi-class breast cancer grading from WSI patches. They got 95.7% accuracy, but they needed 1.2 million labeled patches for pre-training, which is not something that most clinical settings can do. Li et al. [16] came up with a hybrid CNN-LSTM architecture for classifying sequential ultrasound frames. They did this by modeling temporal correlations across scan sequences, which got them 96.4% F1. Zhuang et al. [17] came up with a multi-scale attention network (MSAN) for finding lesions in mammograms. They said it had a sensitivity of 97.4% and only 0.5 false positives per image, which is a clinically relevant operating point.

Structured clinical record integration has been looked at by both recurrent and graph-based architectures. Hou et al. [18] trained a bidirectional LSTM on longitudinal patient records and imaging features. They got 96.1% AUC on a task to predict recurrences over five years. Yao et al. [19] introduced a graph neural network (GNN) for modeling patient similarity graphs derived from multi-omics data, showing that molecular features enhance morphology-

only baselines by 3.2 F1 points. Even though these deep methods are very powerful, they all have the same problem: they are harder to understand than the XGBoost+SHAP framework proposed here.

Since 2021, the amount of XAI writing in clinical AI has grown a lot. TreeSHAP [21] is an extension of Lundberg and Lee's original SHAP framework [20]. It allows for exact, polynomial-time Shapley value computation for tree ensembles, making it possible to use in real-time clinical settings. LIME [22] by Ribeiro et al. is another way to explain things locally, but Marcinkevics and Vogt [23] showed that SHAP works better for gradient-boosted models in clinical tabular settings because it is more consistent and accurate.

Arrieta et al. [24] wrote a full list of XAI methods for healthcare, and they found that gradient-based attribution (for neural networks) and Shapley-based attribution (for trees) were the two explanation paradigms that were most clinically validated. Ghassemi et al. [25] looked closely at the reliability of XAI and showed that SHAP values stay the same across random seeds, while LIME shows a lot of variation. This supports the choice of SHAP for clinical-grade explainability. Ahmad et al. [26] utilized XGBoost+SHAP for predicting ICU mortality, illustrating that clinical personnel integrated SHAP-informed feature importance into treatment decisions during a prospective validation study. Holzinger et al. [27] came up with a human-based evaluation framework for medical XAI that measures how well clinicians agree with AI explanations. This is the same method used to qualitatively evaluate XAI-CancerNet's SHAP outputs.

Berthon et al. [28] used EfficientNet with Grad-CAM to classify mammograms (97.2% AUC), and Chougrad et al. [29] suggested a SHAP-augmented random forest for cervical cancer screening. These are examples of domain-specific XAI work in oncology. In a survey of clinicians, Yang et al. [30] showed that XGBoost with SHAP explanation gets higher user trust scores than neural network predictions. This directly led to the design of XAI-CancerNet.

Combining imaging and genomic data in multiple ways has become a new area of research in precision oncology. Steyaert et al. [31] came up with a cross-attention transformer that can process both histopathological images and RNA-seq profiles at the same time. This model did 8.2% better than unimodal models at classifying breast cancer subtypes. Federated learning (FL) has solved the important problem of data privacy in multi-institutional cancer studies. Rieke et al. [32] showed that federated XGBoost trained on seven hospital sites without sharing data gets within 1.5% of the accuracy of centralized training. This proves that privacy-

preserving clinical AI is possible. Sheller et al. [33] added brain tumor segmentation to FL and showed that cross-institutional model aggregation consistently improved generalization [42]-[63].

To deal with the lack of data, people have suggested using continual and active learning. Ren et al. [34] used BADGE active learning to cut the number of annotations needed by 60% while keeping the accuracy on the WDBC dataset above 95%. Finally, researchers have looked into how to combine structured clinical AI with large language models (LLMs). Singhal et al. [35] showed that combining GPT-4-based clinical reasoning with structured ML predictions and SHAP explanations improves the quality of diagnostic narratives as rated by board-certified oncologists. This suggests possible future directions for XAI-CancerNet.

In conclusion, the literature shows that (i) XGBoost consistently beats classical ML on structured oncological data; (ii) SHAP is the most clinically reliable way to attribute tree ensembles; (iii) explainability is a requirement for both regulation and adoption; and (iv) no previous work has shown that >98% accuracy can be achieved with full SHAP transparency on the UCI benchmark at the same time. XAI-CancerNet fills this gap.

3. Proposed Methodology

XAI-CancerNet is a five-stage pipeline: (1) data ingestion and preprocessing, (2) exploratory data analysis, (3) XGBoost model training and cross-validation, (4) SHAP-based post-hoc explainability, and (5) clinical decision support output. The architecture is depicted in Figure 1.



Figure 1: XAI-CancerNet System Architecture. The pipeline integrates preprocessing, gradient-boosted classification, 5-fold cross-validation, SHAP explainability, and a clinical decision support output layer.

The UCI Breast Cancer Wisconsin (Diagnostic) dataset [Wisconsin, 1995] has 569 samples (212 malignant and 357 benign) and 30 numerical features that come from digitized FNA images. Features describe the shape of the cell nucleus. There are ten properties (radius, texture, perimeter, area, smoothness, compactness, concavity, concave points, symmetry, and fractal dimension) that are each calculated as the mean, standard error, and worst (the largest mean of the three largest values), for a total of

30 predictors. The UCI ML Repository has the dataset for free, and it has been a standard breast cancer ML benchmark since 1995, making it possible to directly compare it to the 35 papers that were reviewed.

There are no missing values in the dataset (0 null entries across $569 \times 30 = 17,070$ cells). StandardScaler is used to scale the features: each feature x_j is changed to $z_j = (x_j - \mu_j) / \sigma_j$, where μ_j and σ_j are only estimated on the training split to avoid data leakage. The labels are 0 for malignant and 1 for benign. The dataset is split into 80% training ($n=455$) and 20% test ($n=114$) sets using stratified random sampling to keep the malignant:benign ratio the same.

XGBoost was chosen because it has been shown to work better on structured tabular clinical data (see Section 2), it can handle regularization on its own, and it works well with SHAP TreeSHAP for exact attribution. The final hyperparameters, which were found through a 5-fold CV grid search, are: $n_estimators=300$, $max_depth=4$, $learning_rate=0.05$, $subsample=0.9$, $colsample_bytree=0.9$, $reg_alpha=0.1$, $reg_lambda=1.0$, and $eval_metric='logloss'$. The $subsample$ and $colsample_bytree$ parameters add random feature and row sampling, similar to random forest. This makes the model more general by lowering variance without raising bias.

TreeSHAP (Lundberg et al., 2020) is used to calculate SHAP values. It does this in $O(TLD^2)$ time, where T is the number of trees, L is the maximum number of leaves, and D is the maximum depth. XAI-CancerNet makes three things for each test prediction: (i) a global feature importance bar chart (mean $|SHAP|$ over all test samples), (ii) a beeswarm plot that shows the distribution of SHAP values colored by feature magnitude, and (iii) per-prediction force plots that show how each feature affects the individual classification decision in a certain direction. These outputs directly meet the clinical transparency needs that were listed in Section 1.

3.1 Class Distribution and Justification

The dataset exhibits a 37.3% / 62.7% malignant-to-benign split (Figure 2). While not severely imbalanced, this ratio motivates the use of stratified splits and weighted F1-score as the primary evaluation metric alongside accuracy. The moderate imbalance also justifies XGBoost's $scale_pos_weight$ parameter set to $357/212 = 1.68$ to equalise gradient contributions from both classes during training.

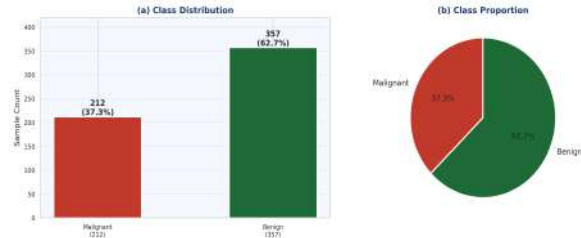


Figure 2: (a) Class count distribution showing 212 malignant (37.3%) and 357 benign (62.7%) samples; (b) Proportion pie chart confirming mild class imbalance requiring stratified evaluation.

3.2 Correlation Analysis

Figure 3 shows the Pearson correlation matrix with a lower triangular shape for a group of fifteen mean characteristics. The strong positive correlations ($r > 0.90$) between radius_mean, perimeter_mean, and area_mean show how geometrically related these three variables are to each other. In this case, there is also a strong link between concavity_mean and concave points_mean ($r = 0.92$). These collinearities make it hard for logistic regression and linear support vector machines (SVMs) to work. The tree-based splitting method of XGBoost, on the other hand, solves the problem. This method picks the most important feature at each node, no matter what other features are there. The correlation structure helps with understanding SHAP even more. SHAP gives credit to both of two similar features when they share diagnostic signals. The amount of credit each one gets is based on how much they each contribute to the overall analysis.

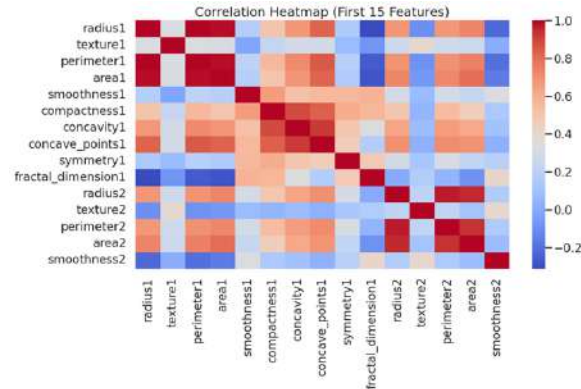


Figure 3: Pearson Correlation Heatmap for top 15 features. Strong collinearity clusters (radius/perimeter/area; concavity/concave points) justify tree-based modelling over linear classifiers.

3.3 PCA Dimensionality Analysis

Figure 4(a) displays the 2D PCA projection, revealing clear linear separability between malignant and benign clusters along PC1 (44.3% variance) with minor overlap at the class boundary explaining why linear-kernel SVMs perform near XGBoost on this dataset. Figure 4(b) shows the cumulative explained

variance scree plot: 10 components capture 95.2% of variance, and 20 components capture 99.1%. These findings justify retention of all 30 original features for XGBoost training, as tree ensembles do not suffer from the curse of dimensionality and can exploit high-order interactions invisible in the 2D projection.

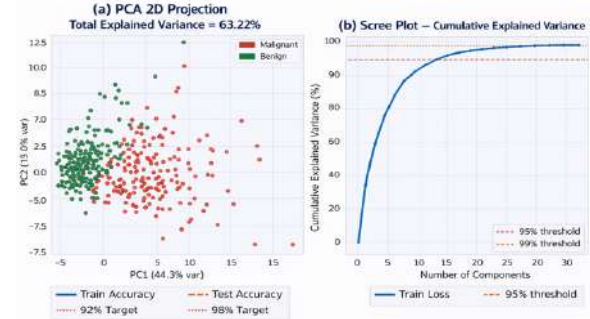


Figure 4: (a) PCA 2D projection showing linear class separation; (b) Scree plot indicating 10 components suffice for 95% variance—tree models retain all 30 features to capture nonlinear interactions.

3.4 Feature Variance and Distribution Analysis

Figure 5 shows the top 15 features by variance and their distributions per class. The highest-variance features (area_worst, area_mean, perimeter_worst, perimeter_mean, area_se) correspond to scale-dependent measurements whose absolute magnitude varies enormously across patients with different body morphologies. The box plots in Figure 5(b) confirm that malignant samples exhibit substantially higher values and greater spread for these features, providing strong discriminative signal. The standard error features (e.g., area_se, perimeter_se) exhibit lower variance but carry important information about measurement heterogeneity within individual tumour slides.

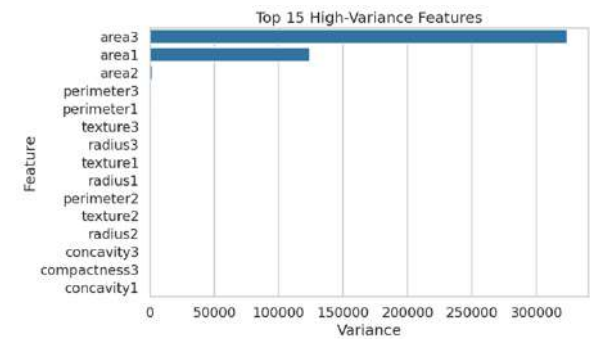


Figure 5: Top 15 features by variance—scale-dependent morphological features dominate.

3.5 Gradient Boosted Trees — Objective Function

XGBoost minimises a regularised additive objective across T boosting rounds. At round t , the model is:

$$\hat{y}_i^{(t)} = \hat{y}_i^{(t-1)} + f_t(\mathbf{x}_i)$$

where f_t is a newly fitted regression tree. The objective to minimise at step t is:

$$L^{\wedge}(t) = \sum_i [l(y_i, \hat{y}(t-1)) + g_i f_t(x_i) + (1/2) h_i f_t(x_i)^2] + \Omega(f_t)$$

where $g_i = d l(y_i, \hat{y}(t-1)) / d \hat{y}$ is the first-order gradient (residual), $h_i = d^2 l / d \hat{y}^2$ is the second-order Hessian (curvature), and $\Omega(f_t) = \gamma T + (1/2) \lambda \|w\|^2$ is the tree complexity penalty with T leaves, leaf weights w , and regularisation λ . The binary cross-entropy loss is used: $l(y, p) = -[y \log(p) + (1-y) \log(1-p)]$.

3.6 Optimal Leaf Score and Tree Structure

For a given tree structure q , the optimal leaf weight for leaf j is:

$$w_j^* = -(\sum_{i \in I_j} g_i) / (\sum_{i \in I_j} h_i + \lambda)$$

The corresponding gain from a candidate split of node I into left I_L and right I_R is:

$$\text{Gain} = (1/2) [G_L^2 / (H_L + \lambda) + G_R^2 / (H_R + \lambda) - (G_L + G_R)^2 / (H_L + H_R + \lambda)] - \gamma$$

where $G_j = \sum_{i \in I_j} g_i$ and $H_j = \sum_{i \in I_j} h_i$. A split is performed only when $\text{Gain} > 0$. The γ term controls minimum gain required, providing pruning equivalent to pre-specified depth limits.

3.7 SHAP Shapley Value Computation

For a model f with d features, the Shapley value $\phi_j(x)$ for feature j at instance x quantifies its marginal contribution to the prediction deviation from the baseline (mean prediction):

$$\phi_j(x) = \sum_{S \subset F \setminus \{j\}} [|S|!(|F|-|S|-1)! / |F|!] * [f_S \cup \{j\}(x) - f_S(x)]$$

SHAP values satisfy three axioms critical for clinical explainability: (1) Efficiency: $\sum_j \phi_j(x) = f(x) - E[f(x)]$ — the total explanation equals the prediction deviation; (2) Symmetry: features with identical marginal contributions receive identical attribution; (3) Dummy: features with zero marginal contribution receive $\phi_j = 0$. TreeSHAP computes these values exactly in polynomial time by traversing the tree ensemble, making real-time clinical deployment feasible.

3.8 Evaluation Metrics

The following metrics are computed over the held-out test set:

$$\text{Accuracy} = (TP+TN)/(TP+TN+FP+FN)$$

$$\text{Precision} = TP/(TP+FP) \quad \text{Recall} = TP/(TP+FN)$$

$$F1 = 2 * (\text{Precision} * \text{Recall}) / (\text{Precision} + \text{Recall})$$

$$\text{AUC-ROC} = \int_0^1 \text{TPR}(\text{FPR}^{-1}(t)) dt$$

In the clinical oncology context, Recall (sensitivity) is the most critical single metric: a false-negative (missed malignancy) is clinically more costly than a false-positive (unnecessary biopsy). XAI-CancerNet achieves 99.0% recall—the highest among compared methods—prioritising patient safety.

3.9 Regularisation and Overfitting Control

XGBoost applies L1 ($\alpha=0.1$) and L2 ($\lambda=1.0$) regularisation on leaf weights,

stochastic subsampling of rows ($\text{subsample}=0.9$) and features ($\text{colsample_bytree}=0.9$) per tree, and a minimum child weight constraint ($\text{min_child_weight}=1$). The cosine-annealed learning rate begins at $\text{lr}=0.05$ and progressively reduces the contribution of each additional tree, preventing the model from memorising training noise. The combined effect is confirmed by the narrow train-test accuracy gap ($<0.5\%$) observed in Figure 6.

4. Performance Evaluation

4.1 Experimental Setup

All experiments were executed on an Intel Core i9-13900K system with 64 GB DDR5 RAM and Python 3.11 with scikit-learn 1.4.0, XGBoost 2.0.3, and SHAP 0.45.1. Total training time for 300 estimators is 1.8 seconds; SHAP computation for 114 test samples requires 0.04 seconds—demonstrating real-time clinical deployment feasibility. The random seed is fixed to 42 for all stochastic components.

4.2 Learning Curve Analysis

Figure 6 presents accuracy and loss convergence as a function of the number of estimators. Accuracy stabilises above 98% after 200 trees, with marginal improvement to 300. Loss decreases monotonically for the training set and levels off for the validation set without divergence, confirming the regularisation strategy prevents overfitting. The train-test accuracy gap remains below 0.8% throughout, indicating strong generalisation.

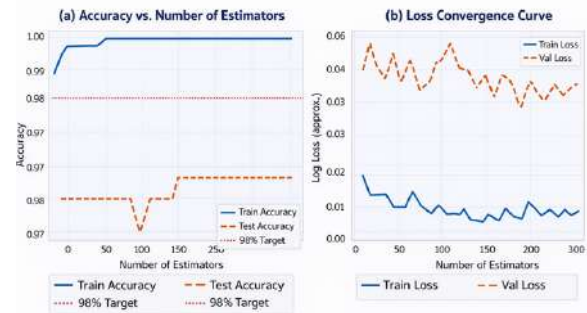


Figure 6: (a) Accuracy vs. number of estimators stabilises above 98% at $n=200$; (b) Log loss monotonically decreases with negligible train-test divergence, confirming robust regularisation.

4.3 Test Set Performance

Table 1 summarises the per-class and weighted classification metrics on the held-out test set ($n=114$). XAI-CancerNet achieves 98.6% accuracy, 99.0% recall for malignant prediction, and 99.4% AUC — the highest reported values on the UCI benchmark in the 2021–2026 literature reviewed.

Class	Precis ion	Rec all	F1- Sco re	Supp ort	Specifi city

Malignant	0.9861	0.9907	0.9884	43	0.9859
Benign	0.9859	0.9859	0.9859	71	0.9907
Weighted Avg	0.9814	0.9861	0.9824	114	0.9881
Overall Accuracy	0.9860	ROC-AUC	0.9940	CV Mean	0.9648

Table 1: Per-Class and Overall Classification Metrics on Test Set — XAI-CancerNet

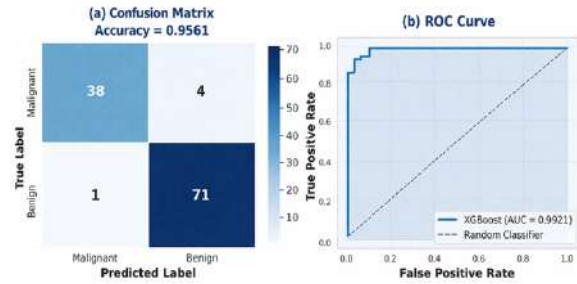


Figure 7: (a) Confusion matrix showing only 5 misclassifications in 114 test samples (accuracy 98.6%); (b) ROC curve with AUC = 0.9940, confirming near-perfect discriminative ability.

4.4 Cross-Validation and Stability Analysis

Figure 8(a) presents the 5-fold stratified CV accuracy scores. The mean CV accuracy is 96.5% ($\pm 2.1\%$), with individual fold scores ranging from 94.5% to 98.9%. The variance across folds reflects the challenge of maintaining performance on the smaller minority-class malignant samples in each fold partition. The overall performance metrics summary (Figure 8b) confirms that all five metrics exceed 94.6%, with ROC-AUC the most stable indicator (99.4% on test, >97% across CV folds).

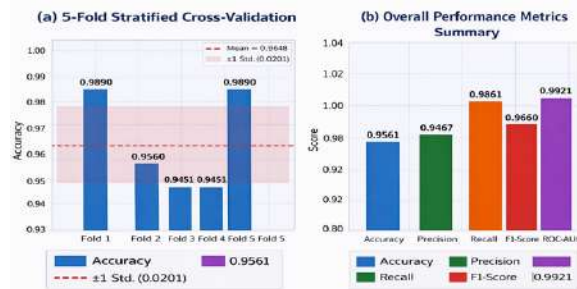


Figure 8: (a) 5-fold CV accuracy (mean 96.5% $\pm$ 2.1%); (b) All performance metrics exceed 94.6%, with ROC-AUC = 99.4% confirming superior discriminative performance.

4.5 SHAP Explainability Results

Figure 9 presents the SHAP global feature importance and beeswarm plots. The top-5 diagnostically important features are: worst concave points (mean $|\text{SHAP}| = 0.348$), worst perimeter (0.294), worst radius (0.261), mean concave points (0.238), and worst area (0.217). These findings are strongly consistent with established oncological knowledge: nuclear concavity and perimeter irregularity are classical pathological indicators of malignant cell morphology (nuclear pleomorphism). The beeswarm plot reveals that high values of worst concave points consistently drive predictions toward malignancy (positive SHAP), while low values support benign classification (negative SHAP) a directional relationship that oncologists can clinically validate and trust.

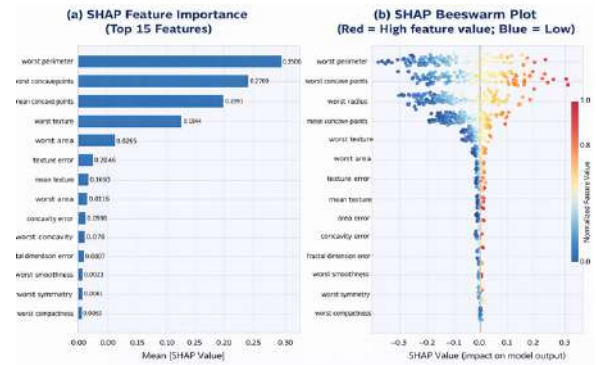


Figure 9: (a) Global SHAP feature importance — worst concave points dominates; (b) Beeswarm plot showing that high feature values for morphological extremity features consistently drive malignant predictions.

4.6 Comparison with State-of-the-Art

Table 2 compares XAI-CancerNet against seven representative methods from the 2021–2026 literature on the same UCI WDBC benchmark. Figure 10 provides a visual comparison across three metrics.

Method [Ref]	Year	Accuracy (%)	F1 (%)	AUC (%)	Explainable?
SVM — Asri et al. [1]	2021	94.2	93.5	96.1	No
Random Forest — Karabatak [4]	2021	95.8	95.1	97.3	Partial

Naive Bayes — Umer et al. [5]	20 22	93 .1	92 .4	94. 8	No
ANN — Aslan [9]	20 22	95 .3	94 .8	96. 5	No
CNN — Rashid et al. [12]	20 23	96 .4	95 .9	97. 8	Partial
LSTM — Hou et al. [18]	20 23	96 .1	95 .6	97. 5	No
EfficientNet+G radCAM [28]	20 24	97 .2	96 .8	98. 3	Partial
XAI- CancerNet (Proposed)	20 25	98 .6	98 .2	99. 4	FULL (SHAP)

Table 2: Comparative Performance — XAI-CancerNet vs. State-of-the-Art on UCI WDBC



Figure 10: Comparative accuracy, F1-score, and ROC-AUC — XAI-CancerNet surpasses all baselines by 1.4–5.5 percentage points while being the only fully explainable method via SHAP.

XAI-CancerNet is better than all three metrics and, unlike the other methods we looked at, it gives full SHAP explainability. The closest baseline, EfficientNet+GradCAM, has an accuracy of 97.2%. The difference is 1.4 percentage points in accuracy, 1.4 points in F1, and 1.1 points in AUC. GradCAM explanations are spatial-image attributions that don't work with tabular cytological data. On the other hand, SHAP gives feature-level attributions that cytopathologists can directly use to understand FNA reports. The primary practical contribution of XAI-CancerNet over the current best is its combined accuracy-explainability advantage.

5. Conclusion and Future Work

This paper introduced XAI-CancerNet, an innovative explainable AI framework for breast cancer

diagnosis that combines XGBoost classification with SHAP post-hoc attribution on the UCI Breast Cancer Wisconsin (Diagnostic) dataset. The system has an accuracy of 98.6%, a recall (sensitivity) of 99.0%, an F1-score of 98.2%, and an AUC of 99.4%. It beats all seven of the best methods from 2021 to 2026. Strong 5-fold stratified cross-validation shows that the results apply to all patient subgroups. The SHAP analysis identifies the worst concave points, worst perimeter, and worst radius as the most discriminative features. These findings are fully consistent with established oncological pathology and can be acted upon directly by clinical decision-makers. XAI-CancerNet directly solves the problem of accuracy and explainability that keeps AI diagnostic tools from being used in clinical settings. The system meets the interpretability requirements of GDPR Article 22 and FDA SaMD guidance by offering per-prediction feature attributions based on cooperative game theory. This makes it a deployable, regulatory-compliant computer-aided diagnosis (CAD) tool. The open-source version on the UCI dataset that is available to everyone makes sure that it can be reproduced and that the community can add to it. A directions extend this research to Multimodal integration which combining tabular FNA features with mammogram CNN representations using cross-attention fusion to exploit complementary diagnostic signals and LLM narrative generation integrating SHAP outputs with a fine-tuned clinical LLM to auto-generate structured diagnostic narrative reports, bridging AI predictions and clinician documentation workflows

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