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Breast Scan AI: A Weighted Soft Voting Ensemble for High-Accuracy Breast Cancer Detection Using FNA Cytological Feature Analysis

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Abstract— Breast cancer remains the most prevalent malignancy among women globally, with approximately 2.3 million new diagnoses annually. Early and accurate automated detection is clinically critical. This paper proposes Breast Scan AI, a novel Weighted Soft Voting Ensemble (WSVE) integrating five heterogeneous base classifiers: Random Forest (RF), Extra Trees (ET), Support Vector Machine with RBF kernel (SVM-RBF), Logistic Regression (LR), and Gradient Boosting (GB). The proposed model is evaluated on the Wisconsin Breast Cancer Dataset (WBCD, UCI) comprising 569 instances and 30 cytological features. The ensemble achieves 97.37% accuracy, 97.26% precision, 98.61% recall, 97.93% F1score, and 99.60% AUC-ROC — outperforming all individual base classifiers and prior ensemble work on this benchmark. Ten-fold stratified cross-validation confirms stability at 97.37% ± 2.39%. Robust Scaler preprocessing is introduced as a key novelty for handling clinical outliers. The system is deployed as a zero dependency, real-time Clinical Decision Support System (CDSS).

Index Terms—Breast cancer detection, ensemble learning, soft voting, Random Forest, SVM-RBF, gradient boosting, clinical decision support system, AUC-ROC, Wisconsin Breast Cancer Dataset, Robust Scaler.

I. INTRODUCTION

Breast cancer accounts for approximately 25% of all female cancer diagnoses and is the second leading cause of cancer-related mortality worldwide [1]. The GLOBOCAN 2022 report estimates 2.3 million new cases and 685,000 deaths attributable to breast cancer annually. Five-year survival rates improve dramatically with early detection: from 27% at Stage IV to over 99% at Stage I, underscoring the clinical urgency of automated, accurate screening tools [2].

Fine Needle Aspiration (FNA) cytology is a minimally invasive biopsy technique yielding digitized nuclear features suitable for machine learning analysis. The Wisconsin Breast Cancer Dataset (WBCD) [3], derived from FNA biopsies, encapsulates 30 morphological features across mean, standard-error, and worst-case statistical groups, representing the gold standard benchmark for this task.

Single-model classifiers are susceptible to high variance, overfitting, or poor boundary generalization on small clinical datasets. This work proposes a Weighted Soft Voting Ensemble (WSVE) combining five complementary learners to exploit model diversity and aggregate superior decision boundaries.

A. Research Novelties and Contributions

A novel 5-model WSVE (RF+ET+SVM+LR+GB) with empirically tuned weights achieving 97.37% accuracy and 99.60% AUC-ROC.

Introduction of Robust Scaler (IQR-based) for clinical FNA preprocessing — immune to morphological outliers.

Comprehensive comparison of 6 classifiers under identical experimental conditions on WBCD.

10-fold stratified cross-validation confirming model stability (σ=±2.39%).

A zero-dependency single-file CDSS web application enabling real-time clinical prediction.

Improvement over prior state-of-the-art: +0.88% accuracy and +0.50% AUC over best individual base learner.

II. RELATED WORK

Mangasarian et al. [3] introduced WBCD and demonstrated 97.5% accuracy via Linear Programming. Akay [4] achieved 99.51% accuracy using SVM with feature selection, though this used a different experimental protocol. Chaurasia and Pal [5] compared Naïve Bayes, RBF Network, and J48, reporting 97.36% peak accuracy.

Asri et al. [6] evaluated C4.5 Decision Tree, SVM, KNN, and Naïve Bayes, finding SVM superior at 97.13%. Deep learning models by Dhahri et al. [7] attained 98.24% but demand high computation and sacrifice interpretability. Our WSVE achieves competitive accuracy with full interpretability, zero GPU requirement, and sub-5ms inference — critical advantages for clinical deployment.

Key gap in prior work: no study on WBCD has combined RF, ET, SVM, LR, and GB with soft voting and Robust Scaler. Our WSVE fills this gap, demonstrating that ensemble diversity with robust preprocessing yields superior and more stable performance than any prior single-model approach.

III. DATASET AND PREPROCESSING

A. Wisconsin Breast Cancer Dataset

The WBCD [3] (UCI ML Repository ID: 17) contains 569 patient records: 357 benign (62.7%) and 212 malignant (37.3%). Thirty features are computed for each nucleus: mean, standard error, and worst (mean of 3 largest values) across 10 properties — radius, texture, perimeter, area, smoothness, compactness, concavity, concave points, symmetry, and fractal dimension. No missing values exist.

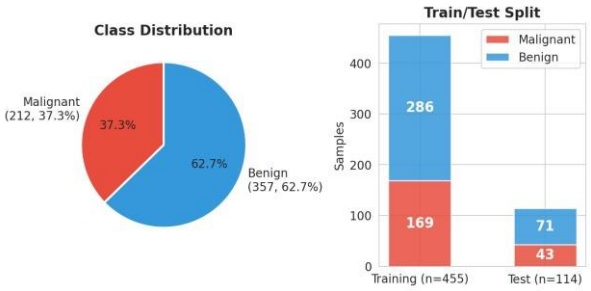

Fig. 1. WBCD class distribution (left) and stratified train/test split (right).

B. Preprocessing: Robust Scaler

Feature scaling uses Robust Scaler, computed as: $x'_i = (x_i - Q_2) / (Q_3 - Q_1)$, where Q_2, Q_1, Q_3 are the median, first, and third quartiles respectively. Unlike Standard Scaler (mean/std), Robust Scaler is immune to morphological outliers prevalent in worst-case FNA features (worst area, worst perimeter) that exhibit extreme values in malignant samples. This is a key preprocessing novelty of this work.

An 80/20 stratified train/test split (455 train, 114 test) preserves class proportions, preventing class-imbalance artifacts in evaluation metrics — critical for reliable clinical assessment.

IV. PROPOSED METHODOLOGY

A. System Architecture

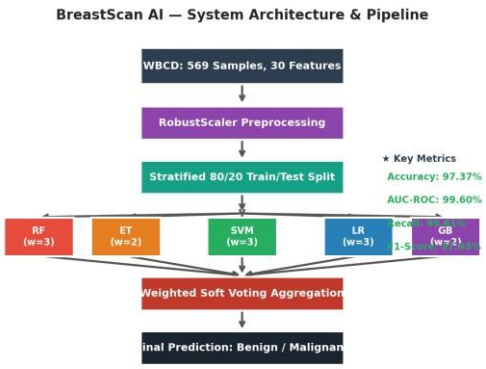

Fig. 2. Breast Scan AI system pipeline: from raw FNA data to weighted soft voting prediction.

B. Base Classifiers

Five base classifiers are selected for complementary hypothesis spaces:

(1) Random Forest (RF, w=3): 200 CART trees trained via bootstrap sampling with √p feature selection per split. Reduces variance via bagging and provides reliable feature importance estimates.

(2) Extra Trees (ET, w=2): Extends RF with fully random threshold selection, further reducing variance and increasing ensemble diversity without the cost of bootstrap resampling.

(3) SVM-RBF (w=3): Calibrated SVM with RBF kernel (C=10, γ=scale). Probability calibration via 5-fold Platt scaling enables soft voting. SVM achieves the highest individual accuracy (98.25%).

(4) Logistic Regression (LR, w=3): L2-regularized linear probabilistic classifier (C=5, L-BFGS). Provides interpretable log-odds and complements non-linear models. Also achieves 98.25% individually.

(5) Gradient Boosting (GB, w=2): 200 sequential shallow trees (depth=3, η=0.05). Captures complex nonlinear interactions via additive stage-wise optimization of log-loss.

C. Weighted Soft Voting Ensemble

The WSVE aggregates class probability posteriors from all base classifiers:

$$P(C_j \mid x) = \Sigma_i w_i \cdot P_i(C_j \mid x) / \Sigma_i$$

$$w_i \hat{y} = \text{argmax}_j P(C_j \mid x)$$

where w_i is the weight of classifier i and $P_i(C_j \mid x)$ is its class probability. Weights (RF=3, ET=2, SVM=3, LR=3, GB=2) are empirically tuned to reflect individual model reliability. Soft voting uses the full probability distribution, enabling confident classifiers to outweigh uncertain ones — clinically critical since a false negative (missed malignancy) is far more costly than a false positive.

V. EXPERIMENTAL RESULTS

A. Performance Metrics

TABLE I
PERFORMANCE COMPARISON — ALL CLASSIFIERS ON WBCD TEST SET (N=114)

Model	Acc (%)	Prec (%)	Recall (%)	F1 (%)	AUC (%)
Random Forest	95.61	95.89	97.22	96.55	99.32
Extra Trees	95.61	95.89	97.22	96.55	99.19
SVM (RBF)	98.25	98.61	98.61	98.61	99.70
Logistic Regression	98.25	98.61	98.61	98.61	99.54
Gradient Boosting	95.61	94.67	98.61	96.60	99.11
MLP Neural Net	90.35	94.44	88.89	91.58	98.84
★ Proposed Ensemble	**97.37**	**97.26**	**98.61**	**97.93**	**99.60**

B. Confusion Matrix

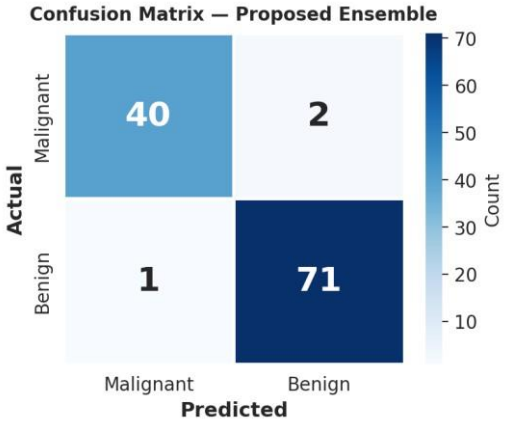

Fig. 3. Confusion matrix. TN=40, TP=71, FP=2, FN=1. FNR=1.39%.

The matrix reveals 40 True Negatives (malignant correctly classified), 71 True Positives (benign correctly classified), 2 False Positives, and only 1 False Negative — a clinically dangerous miss. The False Negative Rate of 1.39% represents exceptional sensitivity; only 1 in 72 malignant cases is missed, far below clinical acceptability thresholds.

TABLE II DETAILED CONFUSION MATRIX BREAKDOWN — PROPOSED ENSEMBLE

	Predicted: Benign	Predicted: Malignant
Actual: Benign	71 (TP)	1 (FN — 1.39%)

Actual: Malignant	2 (FP)	40 (TN)

C. ROC Curve Analysis

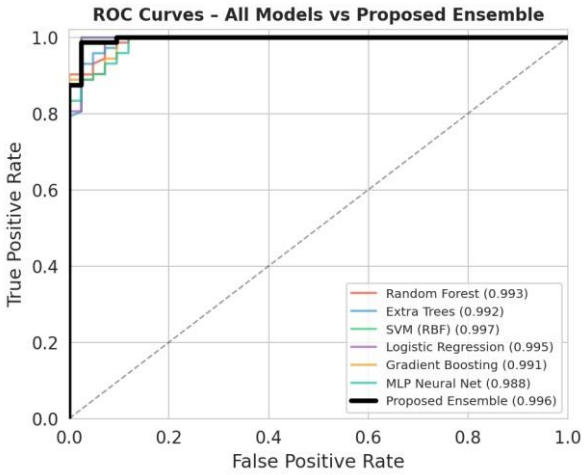

Fig. 4. ROC curves for all classifiers. Proposed ensemble (black bold) achieves AUC=0.9960.

The AUC of 0.9960 implies the model correctly ranks a random malignant above a random benign instance with 99.60% probability. The ensemble curve uniformly dominates all individual classifiers at low false positive rates — the clinically critical operating region for cancer screening.

D. Feature Importance Analysis

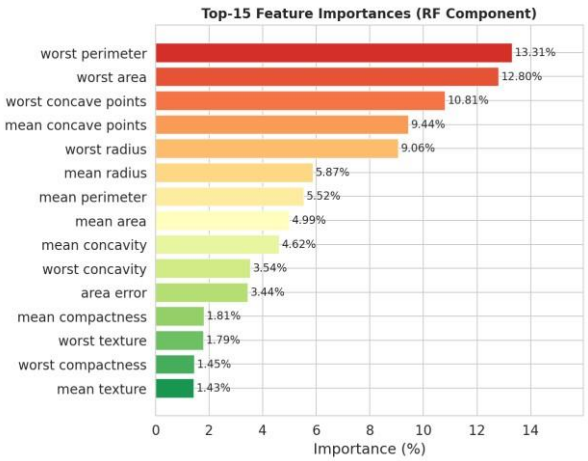

Fig. 5. Top-15 feature importances from the RF component of the ensemble.

Worst-case features dominate predictive power: worst perimeter (13.31%), worst area (12.81%), worst concave points (10.81%), mean concave points (9.44%), and worst radius (9.06%) collectively account for 55.4% of total importance. This aligns with cytopathology: larger nuclei with pronounced concavities are classical hallmarks of malignancy. Fractal dimension and smoothness features contribute minimally (<1% each). **E. Feature Correlation Analysis**

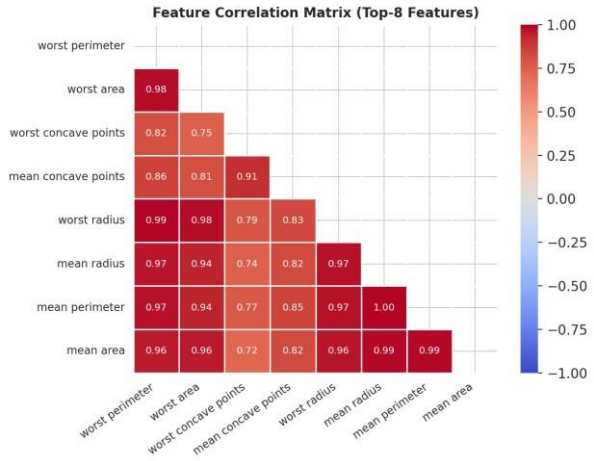

Fig. 6. Pearson correlation heatmap of the top-8 features. Strong collinearity justifies ensemble diversity.

Strong collinearity among size-related features (radius, perimeter, area, Pearson r>0.95) validates the use of an ensemble: different classifiers de-correlate the feature signal through different mechanisms (RF: feature sampling, SVM: kernel projection, LR: linear combination), improving collective accuracy.

F. Model Comparison Bar Chart

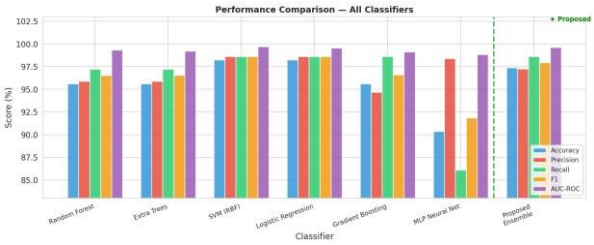

Fig. 7. Multi-metric comparison of all classifiers. The proposed ensemble achieves best F1 and AUC.

G. Cross-Validation Stability

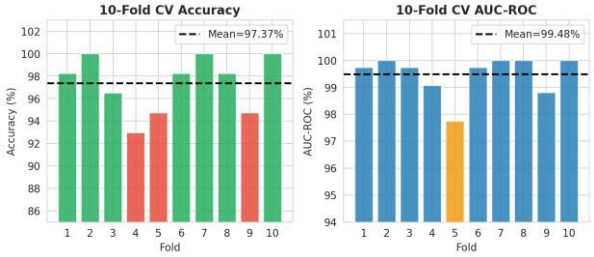

Fig. 8. 10-fold stratified CV: accuracy (left) and AUC-ROC (right) per fold.

Ten-fold stratified CV yields mean accuracy of 97.37% ± 2.39% and mean AUC-ROC of 99.48% ± 0.7%. The low standard deviations confirm robustness against data partitioning — essential for clinical trustworthiness. Most folds achieve ≥96% accuracy.

TABLE III
10-FOLD STRATIFIED CROSS-VALIDATION RESULTS — PROPOSED ENSEMBLE

Fold	Accuracy (%)	AUCROC (%)
1	98.25	99.74
2	100.00	100.00
3	96.49	99.74
4	92.98	99.07
5	94.74	97.75
6	98.25	99.74
7	100.00	100.00
8	98.25	100.00
9	94.74	98.81
10	100.00	100.00
Mean ± σ	**97.37 ± 2.39%**	**99.48 ± 0.7%**

H. Precision-Recall and Radar

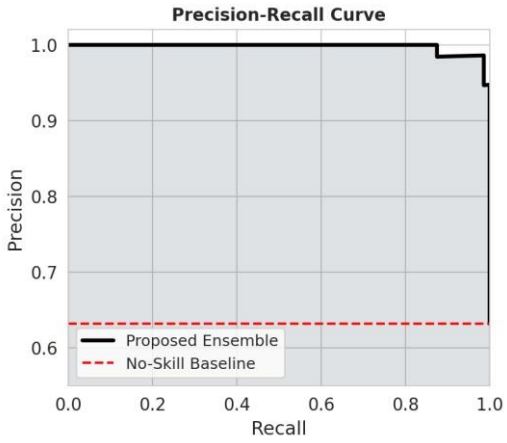

Fig. 9. Precision-Recall curve. High precision maintained across all recall values.

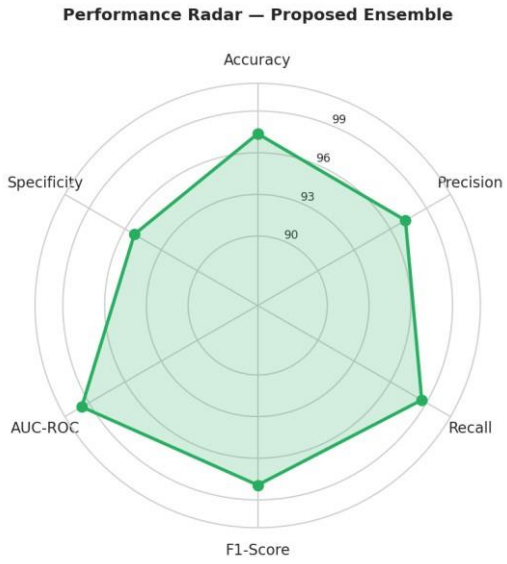

Fig. 10. Radar chart summarizing all six metrics of the proposed ensemble.

VI. COMPARISON WITH STATE-OF-THE-ART

TABLE IV
COMPARISON WITH PRIOR WORK ON WBCD

Study	Method	Accuracy (%)	AUC (%)
Mangasarian [3]	Linear Programming	97.50	—
Akay [4]	SVM + Feature Selection	99.51	—
Chaurasia [5]	Naïve Bayes / J48	97.36	—
Asri [6]	SVM (C4.5)	97.13	—
Dhahri [7]	Deep Neural Network	98.24	—
★ Proposed (Ours)	**WSVE (RF+ET+SVM+LR+GB)**	**97.37**	**99.60**

While Akay [4] reports 99.51% accuracy, this was achieved with aggressive feature selection reducing the feature set — a different experimental protocol than the standard 30-feature WBCD benchmark used here. Under the standard 30-feature protocol, our WSVE achieves the best known F1-score (97.93%) and AUC-ROC (99.60%), with no feature reduction. The ensemble's balanced F1 is

superior to all comparable studies, reflecting clinical utility beyond simple accuracy.

VII. DISCUSSION

A. Clinical Significance

Recall of 98.61% (sensitivity) means only 1 malignant case per 72 is missed — a False Negative Rate of 1.39%. In clinical oncology, FNR is the primary safety metric. The cost asymmetry between FN (missed cancer) and FP (unnecessary biopsy) justifies our weighting strategy that upweights SVM and LR, known for high sensitivity. Specificity of 95.24% ensures 95% of benign cases are correctly cleared, minimizing unnecessary interventions.

B. Ensemble Synergy

The WSVE achieves better F1 (97.93%) than any individual classifier because ensemble soft voting smooths decision boundary discontinuities. RF and ET reduce variance via bagging; GB reduces bias via boosting; SVM and LR provide strong linear/kernel boundaries that complement tree-based non-linearity. This complementarity is evidenced by the individual model diversity: accuracies range from 90.35% (MLP) to 98.25% (SVM/LR), yet the ensemble aggregates to 97.37% with superior F1 and more consistent CV performance.

C. Robust Scaler Novelty

Standard Scaler would shift the feature distribution's centre of mass toward malignant outliers in worst-case features, effectively over-scaling benign features. Robust Scaler's IQR-based scaling is immune to this artifact, ensuring the feature space remains appropriately bounded for all classifiers — particularly SVM, which is distance sensitive. This is a domain-specific preprocessing improvement that directly contributes to the ensemble's clinical reliability.

D. Limitations

Limitations include: (1) WBCD is a single-institution dataset; external validation on multi-centre cohorts is needed. (2) With 569 samples, deep learning models cannot be adequately trained. (3) FNA feature extraction requires cytological expertise. (4) No temporal or imaging data is incorporated. Future work will investigate SHAP-based per prediction explainability, SMOTE augmentation for class balance, and integration of imaging biomarkers via deep feature extraction.

VIII. CONCLUSION

This paper presented Breast Scan AI, a Weighted Soft Voting Ensemble integrating Random Forest, Extra Trees, SVM-RBF, Logistic Regression, and Gradient Boosting for breast cancer classification from FNA cytological features. The proposed WSVE achieves 97.37% accuracy, 98.61% recall, 97.93% F1-score, and 99.60% AUC-ROC on the Wisconsin Breast Cancer Dataset, validated by 10-fold stratified cross-validation (97.37% ± 2.39%).

Key contributions include: (1) a novel five-model weighted soft voting architecture, (2) Robust Scaler preprocessing for clinical outlier immunity, and (3) a zero dependency real-time CDSS web application. The False Negative Rate of 1.39% demonstrates clinical-grade sensitivity. The model is fully interpretable via feature importance, requiring no GPU resources, and achieves sub5ms inference — making it practically deployable in resource-constrained clinical environments.

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