Computational Sciences and Engineering 5(2) (2025) 233-244

University of Guilan

Computational Sciences and Engineering

journal homepage: https://cse.guilan.ac.ir/

Improving Breast Cancer Diagnosis in Ultrasound Images Using a Multi-Stage Approach with Modified U-Net

Ali Ghanbari Sorkhi [a,*]

[a] Department of Electrical and Computer Engineering, University of Science and Technology of Mazandaran, Behshahr, Mazandaran, Iran

ARTICLE INFO

Article history:
Received 14 October 2025
Received in revised form 20 November 2025
Accepted 2 January 2026
Available online 2 January 2026

Keywords:
Breast Cancer
Improved U-Net
Multi-Stage Classification
Hybrid Classification
Ultrasound Images

ABSTRACT

Given the importance of breast cancer detection and the increasing prevalence of this disease, along with its high annual mortality rate, extensive research has been conducted in recent years on medical image analysis for this purpose. In this paper, a multi-stage method is presented based on image segmentation of healthy and unhealthy (cancerous) tissues and a hybrid classification approach for determining the type of cancer (benign or malignant). In the proposed method, after noise reduction, an improved U-Net model is employed for image segmentation and detection of tumor candidate regions. For images identified as unhealthy, contour-based feature extraction is applied, followed by a hybrid ensemble classification method using majority voting among base classifiers to determine the cancer type.

The proposed approach has been evaluated on a standard ultrasound image dataset consisting of healthy, benign, and malignant samples. The proposed method achieved a segmentation accuracy of 97.43% using the enhanced U-Net and an overall system accuracy of 94% for breast cancer diagnosis, outperforming other recent state-of-the-art techniques on the same dataset.

1. Introduction

Breast cancer is one of the most common cancers worldwide. According to statistics from the U.S. National Cancer Institute, one out of every eight women will develop this disease during her lifetime. When detected early, breast cancer is highly treatable [1]. This disease results from the abnormal and uncontrolled growth of cells, forming a mass within the breast tissue. According to the World Health Organization, about 2.1 million women are diagnosed with breast cancer each year, making it the leading cause of cancer-related deaths among women. In 2018, over 620,000

---

[*] Corresponding author.
E-mail addresses: ali.ghanbari@mazust.ac.ir (A. Ghanbari Sorkhi)

https://doi.org/10.22124/cse.2026.31974.1132

women died from breast cancer, accounting for approximately 15% of all cancer deaths in women [2, 3].

Gynecology specialists emphasize that early detection of breast cancer significantly increases the chances of recovery and reduces treatment costs. The disease is caused by the uncontrolled proliferation of abnormal cells within breast tissue, forming benign or malignant tumors. Normally, old or damaged cells are destroyed and replaced with new ones; however, in breast cancer, unnecessary cells are produced, or damaged cells fail to die, resulting in tumor formation. With technological advances, non-invasive diagnostic methods such as medical imaging have replaced surgical approaches, aiming to achieve accurate diagnosis without the need for invasive procedures [4].

Breast cancer is classified into benign and malignant types. Benign tumors are usually caused by hormonal changes, whereas malignant tumors are harder to treat due to delayed diagnosis. Cancerous tissue first spreads to surrounding regions and then to the lymph nodes; if not detected and treated early, it can metastasize to other organs, becoming untreatable. Since various types of breast cancer require precise and early diagnosis, human error in interpretation poses a major challenge. Therefore, the development of automated methods using image processing and advanced algorithms is crucial for reducing diagnostic errors, improving early detection, and enhancing the overall treatment process.

Traditional feature extraction techniques often lead to a slight loss in diagnostic accuracy due to dimensionality reduction. The general process of breast cancer detection and classification consists of four main stages, extracting texture-based features from images, reducing image dimensionality, classifying images into healthy and cancerous categories and distinguishing between benign and malignant cancerous images.

In this paper, a four-stage method is proposed. First, image quality is improved using noise reduction techniques. In the second and most crucial stage, a system is developed to distinguish healthy from unhealthy images using an enhanced deep architecture based on U-Net for image segmentation. Images in which no tumor region is detected are considered healthy; otherwise, they are classified as cancerous. In the third stage, simple contour-based features are extracted from the candidate tumor regions to assist in tumor type classification. Finally, a hybrid classification method based on majority voting is applied to determine the tumor type. The main novel contributions of this study are summarized as follows:

Architectural Innovation in Segmentation: We introduce a modified U-Net architecture specifically designed for medical image segmentation. A key enhancement is implemented in the expansive path, where upsampling blocks are designed to receive and integrate feature maps from multiple layers of the contracting path. This design leads to improved segmentation accuracy, particularly on small datasets, making it highly suitable for medical imaging applications where data is often limited.

A Novel Hybrid Diagnostic Pipeline: We propose a hierarchical, multi-stage framework that strategically separates the tumor detection process (distinguishing healthy from unhealthy images) from the tumor typing task (classifying benign vs. malignant cases). This separation enhances the overall reliability and accuracy of the diagnostic system.

An Efficient and Interpretable Classification Strategy: For the critical task of tumor classification, we demonstrate that a set of simple, interpretable, contour-based features, when processed by a robust hybrid ensemble classifier, can achieve high accuracy. This approach eliminates the need for a secondary, data-intensive deep learning model, resulting in a method that is both practical to implement and effective in performance.

Comprehensive Empirical Validation: We provide a thorough evaluation of the proposed multi-stage method on a public dataset. The results demonstrate that our approach outperforms several recent state-of-the-art techniques, validating its effectiveness and competitiveness in the field of breast cancer diagnosis from ultrasound images.

While U-Net has become a benchmark for medical image segmentation, its standard architecture may suffer from the loss of fine-grained spatial details during the upsampling process, which is critical for precise tumor boundary delineation. Furthermore, many existing deep learning approaches for breast cancer diagnosis rely on end-to-end models that require large, annotated datasets and complex training procedures. Our work addresses these gaps by proposing an enhanced U-Net that better preserves spatial information and a multi-stage pipeline that combines the strengths of deep learning for segmentation with efficient handcrafted features for classification, making it particularly suitable for scenarios with limited data.

This paper is organized as follows: Section 2 reviews related works on breast cancer detection using medical images. Section 3 explains the proposed method in detail. Section 4 evaluates the system performance on breast cancer images, and Section 5 presents the conclusions.

2. Related Works

In recent years, numerous studies have been conducted on the early detection of breast cancer. Existing approaches can be broadly categorized into classical machine learning methods relying on handcrafted features and modern deep learning-based approaches.

2.1. Classical Machine Learning and Handcrafted Feature-based Methods

Traditional methods typically depend on handcrafted feature extraction followed by classical classifiers. For instance, Nikrouvan et al. proposed a novel three-stage method consisting of preprocessing, feature extraction (including texture features from the co-occurrence matrix, histogram, and geometric features), and classification for detecting cancerous masses [5]. Abbaspour et al. presented an intelligent approach for separating mammography images based on tissue density and masses [6]. Naseri et al. introduced a model for determining the clinical stage of breast cancer using the TNM system and the Ant Colony Optimization algorithm, achieving improved performance [7]. Jabbari et al. proposed a hybrid approach for tumor segmentation and detection using histogram analysis, wavelet transform, genetic algorithms, and morphological operations, which demonstrated higher accuracy compared to Ant Colony and Particle Swarm Optimization algorithms [8]. Sheikhpour et al. developed a highly accurate classification model using Gaussian Kernel Density Estimation based on Euclidean distance [9]. Pezeshki et al. extracted tumor features by calculating pixel differences and adding needle-shaped regions to the segmented image, then classified tumors as benign or malignant [10]. Mugal et al. proposed a system that combines top-hat transform, co-occurrence matrix, and a back-propagation neural network to classify breast masses into normal, abnormal, benign, and malignant categories [11]. Torres et al. reduced false positives by using texture descriptors [12]. Mohamm et al. proposed an automated method involving three types of feature extraction, feature selection using the t-test algorithm, and classification using Artificial Neural Networks (ANN), Support Vector Machines (SVM), and k-Nearest Neighbors (k-NN), with ANN achieving the best results [13]. Accurate classification of breast abnormalities is challenging due to image ambiguity and the similarity between benign and malignant lesion features. Tariq et al. conducted a comprehensive review that categorized breast cancer detection methods into statistical machine learning and deep learning approaches [14]. Machine learning techniques play a significant role in early detection; for example, in a study using the Wisconsin dataset, SVM achieved the highest performance [15].

2.2. Deep Learning-based Methods

With advances in deep learning, newer approaches have focused on end-to-end models with automated feature learning capabilities. For example, one study [16] utilized a deep learning model based on Inception-v3 with transfer learning to improve detection accuracy. Furthermore, in a separate study, a median filter was used for noise removal, SqueezeNet for feature extraction, and a Deep Belief Network (DBN) classifier with the Adamax optimizer for classification [17].

In [18] reviews explainable artificial intelligence (XAI) methods for breast cancer diagnosis using mammography and ultrasound images, analyzing the relationship between model accuracy, interpretability and ethical challenges. The findings reveal that despite the growth of XAI, systematic evaluation of its trustworthiness and clinical applicability remains insufficient. In [19] presents an AI-based framework combining deep transfer learning for classification and U-Net for segmentation to enhance breast cancer diagnosis using ultrasound images. The proposed approach improves tumour localization and diagnostic accuracy, contributing to reliable and efficient clinical decision-making while addressing current challenges in data diversity and model generalization.

Recent research results demonstrate the strong performance of machine learning techniques in identifying breast cancer types. Accordingly, the proposed method in this study has also been developed based on these advanced approaches.

3. Proposed Method

In this section, the proposed method for detecting and classifying breast tumors is introduced. the proposed algorithm consists of four main stages as follows:

(1) Stage 1: Since ultrasound-acquired data contain noise and interference that can negatively affect the accuracy of the proposed classification system, noise reduction techniques are applied to the patient’s ultrasound images to minimize the existing noise.

(2) Stage 2: Separation of normal and abnormal data based on masks generated using the improved U-Net method.

(3) Stage 3: Feature extraction from the masks corresponding to abnormal data based on contour analysis.

(4) Stage 4: Classification of data using machine learning through a voting-based approach.

The details of each stage are described in the following sections.

3.1. Noise Removal

In biomedical engineering, images obtained from imaging devices, like other signals, often contain noise — unwanted disturbances that make image processing challenging. Such noise typically arises due to factors like hardware imperfections during imaging, environmental conditions, or patient motion and vibration. In this paper, the Gaussian Blur filter is employed to remove noise. This filter operates by applying a Gaussian kernel over the image, where each pixel is replaced by the weighted sum of the pixels within the kernel window. The central pixel carries the highest weight, and the weight of surrounding pixels gradually decreases with distance from the center.

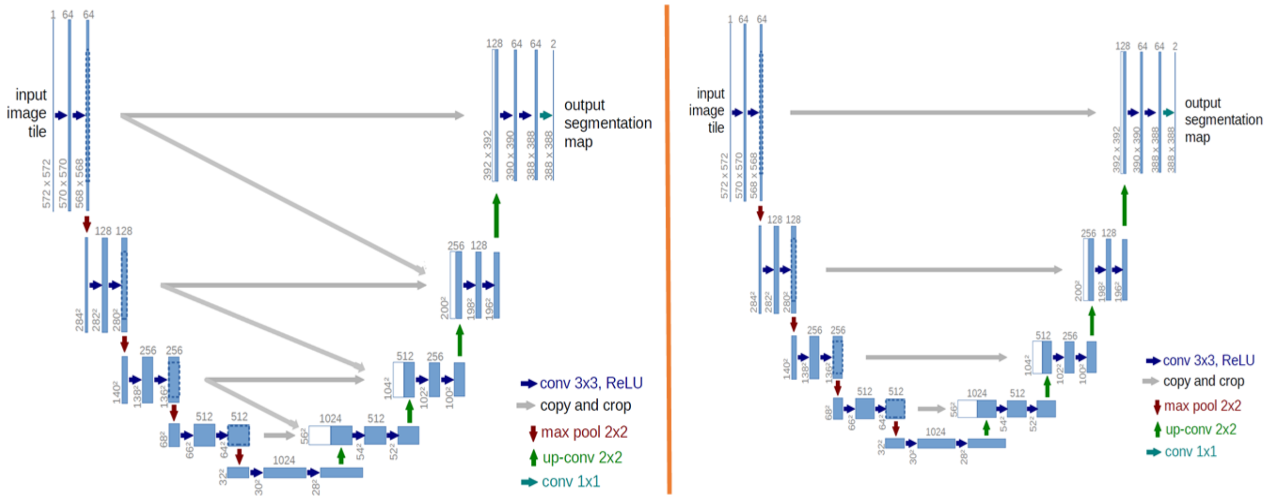
3.2. Separation of Normal and Abnormal Images

In this stage, the data are divided into two main categories. As mentioned earlier, breast ultrasound images include three classes: normal (healthy), benign, and malignant. In the proposed method, the data are initially grouped into two main categories: normal data (without tumors) and abnormal data (including benign and malignant tumors). The main goal of this step is to identify healthy images. To achieve this, an improved U-Net–based segmentation approach is used to detect regions associated with tumors. Images with no detected tumor regions are classified as normal, whereas those containing tumor regions are labeled as abnormal (cancerous).

In recent years, deep neural networks have attracted considerable attention due to their strong performance. However, effective training of these networks requires large amounts of labeled data, which is a significant challenge in biomedical engineering due to limited data availability. To overcome this problem, the U-Net architecture was designed to enable effective deep network training with limited data by leveraging image redundancy. High accuracy, fast training speed, no need for large datasets, and minimal dependence on complex and expensive hardware are among the key reasons for U-Net's popularity in image segmentation — particularly in medical image processing.

The U-Net network was proposed in 2015 by Olaf Ronneberger et al. at the University of Freiburg, Germany, with the goal of improving the accuracy and speed of learning using convolutional networks [20]. A key characteristic of this architecture is the removal of fully connected layers, which reduces network complexity. The main idea behind U-Net is based on a sequential contracting path, where pooling layers are replaced with downsampling layers. After feature extraction, a sequential expansive path is used to reconstruct the original image and transfer background information. In summary, U-Net consists of two symmetric paths — contracting and expansive — where everything reduced in the contracting path is recovered in the expansive one. As shown in ***Figure 1(a)***, the contracting path operates like a convolutional neural network: convolutional layers with various kernel sizes are applied to the input image, followed by the ReLU activation function, and then a MaxPooling layer with a stride and size of 2. The repeated combination of these three layers results in downsampling, where each downsampling step doubles the number of feature channels. In the expansive path, each upsampling step includes a convolutional layer that reduces the number of feature channels and receives data from the corresponding layer in the contracting path. Another convolutional layer with a ReLU activation follows. Finally, a convolutional layer maps each 64-dimensional feature vector to a target class. The U-Net architecture consists of 23 convolutional layers in total.

In the expansive path of the base U-Net, there is an upsampling layer in which a convolutional layer reduces the number of feature channels and receives data from its corresponding layer in the contracting path to be added to the image. In the proposed enhanced version, however, it receives data not only from its corresponding layer but also from the previous layer in the contracting path. A schematic of the modified architecture is shown in ***Figure 1(b)***. The reason for this modification is to leverage features from earlier layers and combine them in subsequent layers. This approach effectively allows the use of different combinations of features from various layers throughout the network.



(b)

(a)

Figure. 1. illustrates the architectures used for tumor region segmentation (a) Base U-Net (b) Proposed Enhanced U-Net

The hypothesized technical advantage of this architectural change is twofold. First, it enables multi-scale feature fusion. While the original U-Net uses skip connections to recover spatial information from the same hierarchical level, our modification provides the decoder with features from an additional, earlier layer. These earlier-layer features typically contain higher-resolution, more localized information. Second, this addresses a key limitation of the original U-Net: the potential 'semantic gap' between the encoder and decoder features at the same level. By fusing features from a previous layer, we provide a smoother gradient of information flow, allowing the network to better reconstruct fine details and improve boundary precision in the segmented masks, which is critical for accurate tumor analysis.

3.3. Feature Extraction

In the previous stage, healthy images were identified. In this step, the abnormal images are used to determine the tumor type. For this purpose, the regions selected by the proposed U-Net are utilized. As evident, each image may contain multiple regions; if even a single region is labeled as malignant, the entire image is considered malignant. To evaluate the regions obtained from the U-Net output, a contour-based feature extraction method is employed.

Object detection in images is a key issue in computer vision and a fundamental step in image understanding. Contour extraction or boundary detection can play an important role in object recognition. However, contour detection methods often face challenges such as noise, translation, scaling, and rotation in images, which hinder accurate and optimal contour extraction. To overcome these problems, a method independent of these factors is required. In this study, Zernike moments are used to extract contour features, as this approach is robust against noise, translation, scaling, and rotation [21, 22]. Contours can be simply defined as curves that connect continuous points along boundaries with the same color or intensity. These lines are effective tools for shape analysis and object recognition. To achieve higher accuracy, binary images are used; therefore, processes such as thresholding or edge detection are applied before extracting the contours. In this study, various features are utilized to extract information from tumor images. ***Eq (1)***. defines Extent, ***Eq. (2)*** defines Solidity, and ***Eq. (3)*** defines Equivalent Diameter. In addition, basic geometric features such as area, perimeter, width, and height are also employed for feature extraction.

$$Extent = \frac{Object\ Area}{Bounding\ Rectangle\ Area} \tag{1}$$

$$Solidity = \frac{Countour\ Area}{Convex\ Hall\ Area} \tag{2}$$

$$EquivalentDaimeter = \sqrt{\frac{4 \times Contour\ Aea}{\pi}} \tag{3}$$

The use of these features was selected due to their simplicity in implementation and the impact of region size and shape on identifying candidate tumor areas. In the previous stage, the identified regions are certainly tumors, and in this stage, these features are used solely to determine the tumor type (benign or malignant).

The rationale for using handcrafted, contour-based features for the second-stage classification is based on three key factors: (1) Data Efficiency: Training a second-deep learning model for classification would require a large volume of labeled tumor patches, which are scarce and expensive to obtain. Our handcrafted features are robust and effective even with limited data. (2) Clinical Interpretability: Features like Extent, Solidity, and Equivalent Diameter have direct clinical correlations with tumor morphology (e.g., malignant tumors often have irregular shapes and spiculated margins, leading to lower Solidity and Extent values). This aligns with how radiologists assess tumors and makes the model's decisions more interpretable. (3) Computational Simplicity: This approach is less computationally intensive than training another deep network, making the overall pipeline more efficient and practical for potential clinical deployment.

3.4. Tumor Type Classification Based on Voting

In this stage, abnormal images are classified based on the extracted features. For each extracted contour feature, feature vectors are computed. Then, a voting-based approach combining three classifiers — Decision Tree (DT), Random Forest (RF), and Extra Trees (ET) — is used to determine the tumor type. The ensemble classifier works by combining multiple individual classifiers. Each classifier trains its own model on the data and stores it. For the final classification, a voting process is conducted among these classifiers, and the class receiving the majority of votes is assigned as the final label.

Although RF and ET are both ensemble methods, they employ different philosophies for building individual trees. RF uses bootstrap aggregating and selects the optimal split from a random subset of features, which reduces variance but can lead to correlation between trees. ET, on the other hand, uses the whole dataset and chooses split points at random for features, further increasing randomness to reduce variance and combat overfitting. By combining DT, RF, and ET through a higher-level majority vote, we create a 'meta-ensemble' that leverages diversity. This diversity is key: while a single DT might be prone to overfitting, and RF/ET might have correlated errors on certain data points, their combination ensures that the final decision is based on a more robust consensus. This voting scheme mitigates individual model weaknesses—such as the high variance of a single DT or the potential over-smoothing of RF/ET—leading to a more stable and accurate final prediction.

4. Analysis and Evaluation of Results

In this section, the analysis of results obtained from the proposed method is presented. First, the dataset and the evaluation methods are introduced. The proposed method was implemented using Python and the TensorFlow framework. The hardware used includes an Intel(R) Core(TM) i7 CPU-M 620 @ 2.67GHz, 8 GB RAM, and an NVIDIA GeForce GT 320M GPU.

4.1. Dataset and Evaluation Metrics

In this study, the dataset contains three classes: normal, benign, and malignant. Each data sample includes two types of images: an ultrasound image and one or more mask images. These masks indicate the exact size and location of the tumor separately [23]. The dataset comprises 780 images covering normal, benign, and malignant cases. ***Table 1*** presents the number of samples in each category.

Table 1. Number of Images in the Dataset by Category

Label	Number of Images	Image Size
Benign	437	128×128
Malignant	210	
Normal	133	

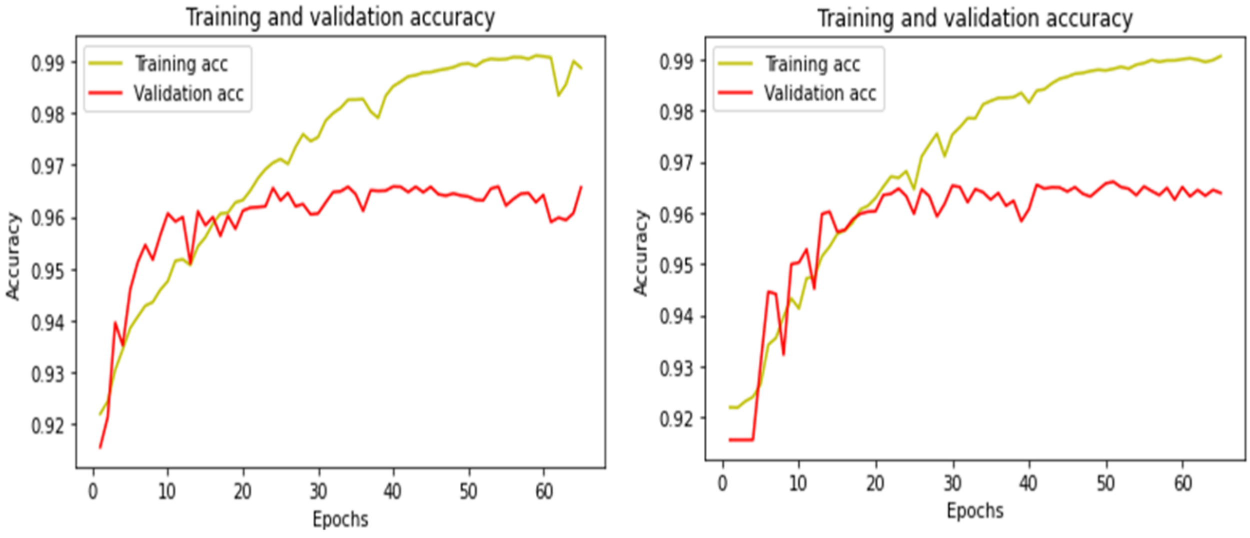
In this study, 20% of the total dataset was allocated for the test set, while the remaining 80% was used for the training set. Additionally, 10% of the training data was reserved for validation. For evaluating the proposed method, the accuracy metric was used. The calculation formula for this metric is provided in ***Eq. (4)***.

$$Accuracy = \frac{TP + TN}{TP + TN + FP + FN} \tag{4}$$

Another metric used to evaluate the proposed method is the AUC-ROC curve. This performance measure is based on different threshold values for classification problems. The ROC is a probability curve, and AUC measures the model's discriminative ability. In simple terms, the AUC-ROC metric reflects the model's capability to distinguish between classes, where a higher AUC indicates a better model.

4.2. Results Analysis

In this study, the U-Net architecture was first used to detect normal and abnormal (cancerous) images. ***Figure 2*** illustrates the accuracy of the proposed method using the standard U-Net versus the enhanced U-Net.



(b) (a)

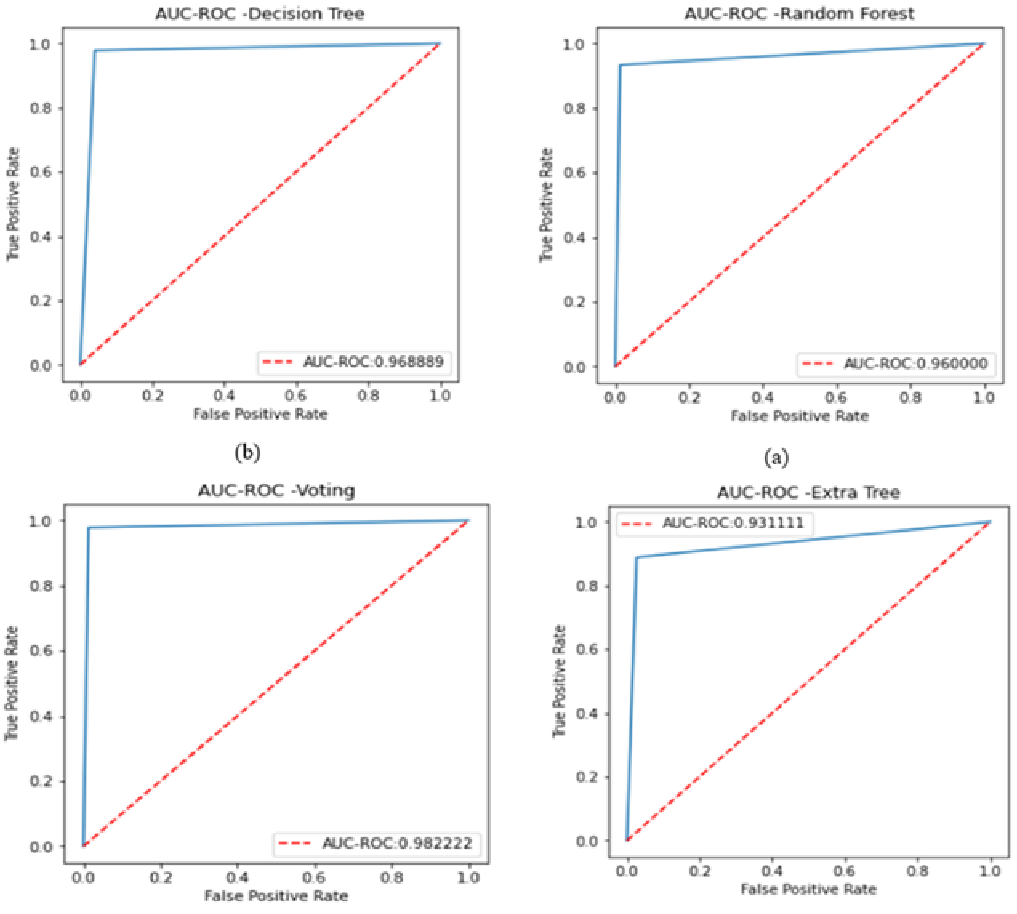
Figure. 2. Accuracy of Training and Validation Stages Based on Standard and Enhanced U-Net

Table 2 shows the comparison of the performance of the enhanced and base U-Net on the test set. The superior performance of the enhanced U-Net (97.43% vs. 93.58% accuracy) can be attributed to its modified architecture. By providing the upsampling layer with feature maps from both its corresponding layer and the previous layer in the contracting path, the model gains access to a richer, multi-scale feature set. This allows the decoder to make more informed decisions during the reconstruction of the segmentation map, effectively mitigating the loss of fine-grained spatial information that can occur in the base U-Net. This is particularly beneficial for segmenting small or irregularly shaped tumors, where precise boundary delineation is crucial.

Table 2. Comparison of Standard and Enhanced U-Net Performance on the Test Set

Dataset	Method	Accuracy (%)
Test	Enhanced U-Net	**97.43**
	Base U-Net	93.58

Next, the tumor type classification in abnormal images is addressed. For this purpose, contour features for all regions identified as candidate tumor areas by the enhanced U-Net are first extracted. In the next step, these features are separately used to train three classifiers: Decision Tree, Random Forest, and Extra Trees. ***Figure 3*** shows the results obtained from the three individual classifiers as well as the ensemble voting-based method for classifying tumor types in 120 images previously identified as abnormal. As can be seen from the results, the ensemble method achieved the best performance.



(b) (a)

(d) (c)

Figure. 3. Results obtained from different classifiers for tumor type classification: (a) Random Forest, (b) Decision Tree, (c) Extra Trees, and (d) Voting

Table 3 presents a comparison of the proposed method with existing approaches in recent studies on the same test dataset. As shown, the proposed method outperformed the other methods.

Table 3. Comparison of the proposed method with other recent approaches

Method	Accuracy (%)
CNN-ALexNet [24]	78
Transfer Learning (TL)-VGG16 [24]	88
TL+ Inception [24]	85
TL+ResNet [24]	93
Proposed method	**94**

The apparent discrepancy between the high segmentation accuracy (97.43%) and the final system accuracy (94%) can be explained by the cascading nature of our multi-stage pipeline. The segmentation accuracy reflects the model's ability to correctly identify and localize tumorous regions. However, the final 94% accuracy for the entire system (normal vs. benign vs. malignant) depends on the performance of all subsequent stages. Any error in segmentation (e.g., a missed small tumor or an inaccurately drawn boundary) directly propagates to the feature extraction and classification stages, leading to an incorrect final diagnosis. Therefore, the overall system accuracy is a compound metric influenced by the precision of the segmentation mask, the discriminative power of the handcrafted features, and the effectiveness of the ensemble classifier. The 94% overall accuracy demonstrates the robustness of the entire pipeline, even when considering potential error propagation from the segmentation stage.

5. Conclusion

Breast cancer is one of the most common types of cancer among women and has been responsible for a high percentage of cancer-related deaths in recent years. During this period, machine learning and computer vision methods have demonstrated remarkable performance in detecting this disease. In this study, a multi-stage method is proposed, which includes noise reduction, classification of normal and cancerous images, contour-based feature extraction, and ensemble classification using three base classifiers with a voting mechanism. The results of this method indicate its superior performance compared to other approaches presented in recent years.

References

[1] Nemade, V., Pathak, S., & Dubey, A. K. (2022). A systematic literature review of breast cancer diagnosis using machine intelligence techniques. *Archives of Computational Methods in Engineering*, *29*(6), 4401–4430.

[2] Rasool, A., Binti Ahmad, N., Wani, M. A., Mir, N. A., & Mansoor, M. (2022). Improved machine learning-based predictive models for breast cancer diagnosis. *International Journal of Environmental Research and Public Health*, *19*(6), 3211.

[3] Jassim, G. A., Courtenay, M., & Kersten, P. (2023). Psychological interventions for women with non-metastatic breast cancer. *Cochrane Database of Systematic Reviews*, *2023*(1), Article CD008711.

[4] Nasser, M., & Yusof, U. K. (2023). Deep learning based methods for breast cancer diagnosis: A systematic review and future direction. *Diagnostics*, *13*(1), 161.

[5] Shalmani, A. N. R. (2016). Diagnosis of breast cancer masses in computer aided mammography images. In *Proceedings of the Third International Conference on Recent Innovations in Electrical and Computer Engineering* (pp. 1–6). Tehran, Iran.

[6] Abbaspour Kazerouni, I., & Haddad Nia, J. (2013). Introducing a precise intelligent system for mammographic image separation based on density of tissues and masses. *Iranian Journal of Breast Diseases*, *6*(1), 7–15.

[7] Noroozani, S. N. (2018). Clinical stage detection of breast cancer patients using TNM system and ant colony algorithm. *Iranian Journal of Breast Diseases*, *11*(3), 56–70.

[8] Jabbari, H., Bigdeli, N., & Khadem, A. (2016). A new hybrid approach to segmentation and diagnosis of tumors in breast mammography images. *Iranian Journal of Breast Diseases*, *9*(3), 14–24.

[9] Ro, S., & Ra, S. (2016). Diagnosis of breast cancer using nonparametric estimation of nuclear methods-based probability density. *Razi Journal of Medical Sciences*, *23*(144), 30–40.

[10] Pezeshki, H., Rastgarpour, M., Sharifi, A., & Yazdani, R. (2019). Extraction of spiculated parts of mammogram tumors to improve accuracy of classification. *Multimedia Tools and Applications*, *78*(14), 19979–20003.

[11] Mughal, B., Muhammad, N., Sharif, M., Rehman, A., & Saba, T. (2018). A novel classification scheme to decline the mortality rate among women due to breast tumor. *Microscopy Research and Technique*, *81*(2), 171–180.

[12] Torres, W., Silva, J., Silva, J., Ribeiro, R., Silva, A., & Cardoso, J. (2018). Functional diversity applied to the false positive reduction in breast tissues based on digital mammography. In *2018 IEEE Symposium on Computers and Communications (ISCC)* (pp. 01134–01139). IEEE.

[13] Mohamed, B. A., & Salem, N. M. (2018). Automatic classification of masses from digital mammograms. In *2018 35th National Radio Science Conference (NRSC)* (pp. 377–384). IEEE.

[14] Tariq, M., Ahmed, S., & Choi, G. S. (2021). Medical image based breast cancer diagnosis: State of the art and future directions. *Expert Systems with Applications*, *167*, 114095.

[15] Bayrak, E. A., Kırcı, P., & Ensari, T. (2019). Comparison of machine learning methods for breast cancer diagnosis. In *2019 Scientific Meeting on Electrical-Electronics & Biomedical Engineering and Computer Science (EBBT)* (pp. 1–3). IEEE.

[16] Yu, K., Tan, L., Lin, L., Cheng, X., Yi, X., & Sato, T. (2021). Deep-learning-empowered breast cancer auxiliary diagnosis for 5GB remote E-health. *IEEE Wireless Communications*, *28*(3), 54–61.

[17] Obayya, M., Maashi, M. S., Nemri, N., Al-Yousef, S. A., Alatawi, S., & Mohsen, H. (2023). Hyperparameter optimizer with deep learning-based decision-support systems for histopathological breast cancer diagnosis. *Cancers*, *15*(3), 885.

[18] Kaba Gurmessa, D., & Jimma, W. (2024). Explainable machine learning for breast cancer diagnosis from mammography and ultrasound images: a systematic review. *BMJ Health & Care Informatics*, *31*(1), e100954.

[19] Ametefe, D. S., John, D., Aliu, A. A., Ametefe, G. D., Hamid, A., & Darboe, T. (2025). Advancing breast cancer diagnosis: Integrating deep transfer learning and U-Net segmentation for precise classification and delineation of ultrasound images. *Results in Engineering*, *25*, 105047.

[20] Ronneberger, O., Fischer, P., & Brox, T. (2015). U-net: Convolutional networks for biomedical image segmentation. In N. Navab, J. Hornegger, W. Wells, & A. Frangi (Eds.), *Medical Image Computing and Computer-Assisted Intervention – MICCAI 2015* (pp. 234–241). Springer.

[21] Abbas, S., Rasheed, A., Khan, M. A., & Ahmed, F. (2019). Efficient shape classification using Zernike moments and geometrical features on MPEG-7 dataset. *Advances in Electrical and Computer Engineering*, *19*(1), 45–51.

[22] Adapa, D., Joseph, J., & Sivaswamy, J. (2020). A supervised blood vessel segmentation technique for digital Fundus images using Zernike Moment based features. *Plos One*, *15*(3), e0229831.

[23] Al-Dhabyani, W., Gomaa, M., Khaled, H., & Fahmy, A. (2020). Dataset of breast ultrasound images. *Data in Brief*, *28*, 104863.

[24] Al-Dhabyani, W., Gomaa, M., Khaled, H., & Fahmy, A. (2019). Deep learning approaches for data augmentation and classification of breast masses using ultrasound images. *International Journal of Advanced Computer Science and Applications*, *10*(5), 1–11.