# Automatic Diagnosis of Breast Cancer in Histopathologic Images Based on Convolutional AutoEncoders and Reinforced Feature Selection

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**ABSTRACT:**
Breast cancer is one the most ubiquitous types of cancer which affect a considerable number of women around the globe. It is a malignant tumor, whose origin is in the glandular epithelium of the breast and causes serious health-related problems for patients. Although there is no known way of curing this disease, early detection of it can be very fruitful in terms of reducing the negative ramifications. Thus, accurate diagnosis of breast cancer based on automatic approaches is demanded immediately. Computer vision-based techniques in the analysis of medical images, especially histopathological images, have proved to be extremely performant. In this paper, we propose a novel approach for classifying malignant or non-malignant images. Our approach is based on the latent space embeddings learned by convolutional autoencoders. This network takes a histopathological image and learns to reconstruct it and by compressing the input into the latent space, we can obtain a compressed representation of the input. These embeddings are fed to a reinforcement learning-based feature selection module which extracts the best features for distinguishing the normal from the malicious images. We have evaluated our approach on a well-known dataset, named BreakHis, and used the K-Fold Cross Validation technique to obtain more reliable results. The accuracy, achieved by the proposed model, is 96.8% which exhibits great performance.

**KEYWORDS:** Breast Cancer Detection, Convolutional Autoencoders, Feature Selection, Reinforcement Learning, Histopathology

## 1. INTRODUCTION

Cancer is a group of illnesses in which the body's cells congregate to create lumps known as malignant tumors [1]. These cells proliferate across the surrounding tissues, expand uncontrollably, and suffocate the healthy cells [2]. From ancient times to the present, cancer has been one of the most serious illnesses to endanger human health. According to a study done in 2018, there will be an estimated 18.1 million new cases of cancer added to the projected 9.6 million cancer cases already present in the world [3].

The prevalence of breast cancer (BC) is rising progressively in both industrialized and developing nations (considered the second most common cancer among women). According to the Nottingham score, the evaluation of nuclear pleomorphism, tubule



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development, and the mitotic count is used to grade BC [4]. Epithelial cell nuclei in a healthy breast are homogeneous in size and shape [5]. Malignant epithelial cell nuclei, however, take on a non-uniform, darker, and bigger shape. The term "nuclear pleomorphism" refers to this change. The percentage of cancerous cells that form tubules in a typical duct structure is represented [6]. One of the most crucial proliferation parameters, the mitotic count, provides crucial diagnostic data needed for BC histological grading [7].

Using image processing and machine learning approaches, quick tumor identification and diagnosis may now significantly improve the accuracy of a BC diagnosis [8]. Clinical illness diagnosis, treatment evaluation, and the detection of problems in several human organs, including the eye, lungs, brain, breast, and stomach, all depend heavily on medical imaging [9]. Medical imaging is a variety of methods used to examine the human body in order to identify, monitor, or cure diseases [10].

The histopathologic diagnosis continues to be the gold standard for cancer diagnosis despite significant advances in medical science [11]. Images taken under a microscope of the tissues used to study illness are known as histopathological images [12]. Because of the nature of histological pictures and the sharp increase in labor, this task takes a long time, and the results could be influenced by the pathologist's subjective judgment.

Hitherto, a variety of machine learning and deep learning-based algorithms have been put forward for detecting malignant samples in histopathologic images [13]. In [14], Spanhol et al. trained a distinct version of the AlexNet CNN model using a collection of pixel components from HPIs. These pieces, which are 32*32 and 64*64 in size, were created utilizing sliding window and randomization techniques. According to the magnification factor, the best accuracy for binary categorization (malignant and benign) was between 80 and 90 percent. Additionally, two distinct CNN models were created by Bayramoglu et al. [15] to forecast two classes (binary classification). While multi-classification accuracy fluctuated between 80 and 83 percent, binary classification accuracy fluctuated between 82 and 85 percent. Furthermore, Wei et al. [16] introduced a CNN model for binary classification called BiCNN that has three convolutional layers and three pooling layers. The BiCNN model's performance was contrasted with that of pre-trained CNN models like VGGNet and AlexNet. Pre-trained CNN models were surpassed by the BiCNN model, which had accuracy levels between 97.56 and 97.97 percent. In addition, CNN and Bidirectional Long Short Term Memory (BiLSTM) models were utilized for binary classification by Budak et al. [17]. Both the CNN model and the Bi-LSTM model underwent independent training for the tasks of deep feature extraction and classification. For various magnification factors, this hybrid model achieved accuracy scores between 93.61 percent and 96.32 percent. Li et al. [18] introduced a deep learning model for breast cancer diagnosis that is based on the CNN model and uses an end-to-end learning procedure. With this model, the categorization accuracy was 90.0 percent. To improve classification performance, Thuy et al. [19] suggested a hybrid deep learning model including VGG16 and VGG19 CNN models and a generative adversarial network (GAN). On the 2-class BreakHis dataset, this technique has a classification accuracy of 98.1 percent.

In this paper, we propose an approach based on Convolutional AutoEncoders (CAEs) and reinforcement learning-based feature selection for diagnosing breast cancer from histopathological images. Our approach does not need any special preprocessing step except for normalization. In addition to this, a dataset collected from real subjects in hospitals has been gathered to train and evaluate the proposed pipeline. Overall, in this work, our contributions are fourfold as follows:

1. A robust approach for diagnosing breast cancer is proposed in which the power of CAEs is utilized.
2. A feature selection module based on reinforcement learning is integrated with the object of optimizing the bottleneck feature vector generated by the CAE.
3. A dataset of 60000 samples has been collected from real hospitals and this adds to the reliability of the results.
4. Our proposed approach achieves competitive results, compared with the previous works.

The rest of the paper is outlined as follows: Section 2 explicates the details of the proposed methodology. Section 3 contains our results and experimental setup. Section 4 includes the conclusion.

## 2. MATERIALS AND METHODS

### 2.1. Overview

An overview of the proposed methodology is depicted in Fig. 1. As is seen in Fig. 1, the input batch of images, after being preprocessed, is fed into the model and the model learns to reconstruct the original image. This way, the bottleneck vector is a representation that can be used to be classified. Our proposed method contains a feature selection stage, where we utilize the power of RL to select the best elements in the feature vector.

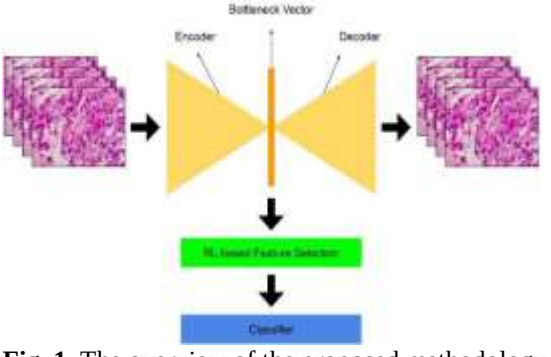


**Fig. 1.** The overview of the proposed methodology.

### 2.2. Dataset

In this study, we have used a dataset containing 60000 samples in two classes, namely normal and cancerous. The samples are collected from three well-known health centers in Iraq, namely Saint Raphael (Al Rahibat) Hospital and Ibn Al-Bitar Hospital. Fig. 2 demonstrates some samples from the dataset from the two classes.

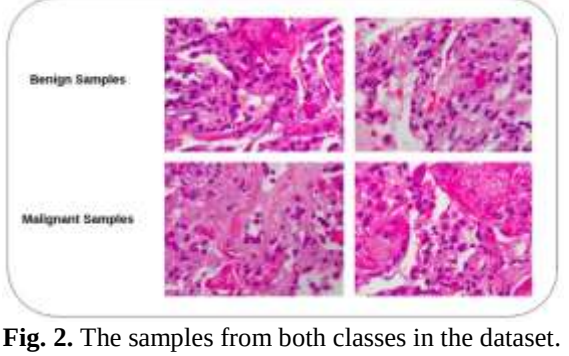


**Fig. 2.** The samples from both classes in the dataset.

Using specialized cameras and a microscope, together with an automated computerized process, it is possible to acquire histopathology pictures [20]. The biopsy specimen is embedded in wax and stained with one or more dyes in order to examine the different architecture and components of tissues under a microscope [21]. Pathologists utilize staining techniques to separate cellular components for structural as well as component viewing of tissue for diagnosis [22]. There are five steps in it, and each one has the potential to impact the final image's quality. Fixing: Chemical fixation is used to preserve biological tissue samples. There are several methods of fixation, but formaldehyde or glutaraldehyde solution fixation is the method that is most frequently used in the biomedical area to safeguard the cells. To avoid tissue autolysis and putrefaction, this crucial stage is tissue preparation; Processing: Dehydration and clearing are the two key steps in tissue processing, which is a vital stage. Dehydration is used to remove water from the viscous tissue and replace it with an alcohol solution that hardens it. This procedure aids in cutting extremely thin slices of the material. Clearing entails removing the dehydrator using a substance that serves as both the embedding paraffin and the dehydrating agent's solvent. This procedure is crucial because perfect microscopic analysis requires the correct orientation of the tissue; Sectioning: This procedure is necessary to produce ultra-thin slices of tissue samples that are sufficient to enable clear observation of the microstructure characterization of the cells using microscopy techniques. Afterward, transfer the ultra-thin slices of the sample on a fresh glass slide; Staining: Staining the tissue and mounting it on the slide are the last steps in preparing it for light microscopy. Staining enhances the tissue's contracts and draws attention to some particular characteristics that would otherwise be virtually unnoticeable under the microscope. Although there are many other types of stains, H & E staining is the most used form for histology [23].

### 2.3. Convolutional AutoEncoders

Due to the remarkable performance of convolutional neural networks, researchers have proposed a variety of such models in various fields [24]-[25]-[26]-[27]-[28]. A particular kind of feedforward convolutional neural network called an autoencoder uses input and output to be identical [29]. They reduce the input's dimension before using this representation to recreate the output. The code, also known as the latent-space representation, is an efficient "summary" or "compression" of the input [30]. Encoder, code, and decoder are the three parts of an autoencoder. The input is compressed by the encoder, which also creates a code. The decoder then reconstructs the input exclusively using the code [31]. Convolutional AutoEncoders (CAEs) use the convolution operator to exploit this observation [32]. Rather than manually engineer convolutional filters, we let the model learn the optimal filters that minimize the reconstruction error [33]. These filters can then be used in any computer vision task. CAEs are the state of art tools for unsupervised learning of convolutional filters. Once these filters have been learned, they can be applied to any input to extract features [34]. These features can be used to do any task that requires a compact representation of the input, like classification [35]. The primary distinction between the conventional interpretation of CNN and CAE is the former's end-to-end training in the acquisition of filters and the combining of features with the goal of categorizing input [36]. The latter are merely taught filters that can extract information from the input and be used to rebuild it. Table 1 demonstrates the train, validation, and test distribution for the dataset.

**Table 1.** The distribution of train/validation and test sets.

| | Train | Validation | Test |
|---|---|---|---|
| Malignant | 19200 | 4800 | 6000 |
| Benign | 19200 | 4800 | 6000 |
| Number of samples | 38400 | 9600 | 12000 |

### 2.4. Feature Selection using Reinforcement Learning

The range of variables or characteristics that may be utilized to describe a specific predictor of interest keeps expanding exponentially as the cost of data gathering falls [37]. Therefore, the key to properly training a machine learning model is to select the most distinctive characteristics that decreases variance without endangering the bias of our models [38]. Finding these traits is also essential for optimal computing cost, predictability, and interpretability [39]. While statistical techniques like shrinkage, subset selection, and dimensionality reduction have been used to choose the best set of features, some other approaches in the literature have treated the task of feature selection as a search problem where each state in the search space is a potential feature subset [40].

Inspired by [41], using the Reinforcement Learning technique, where the state space consists of all conceivable subsets of the features and action is any feature that is included in the model, we attempt to address the feature selection problem. The amount of features that are missing from the model affects the action space for each state [42]. By doing so, we may avoid having an excessively sparse state space, decrease the search space for the next optimal action, and speed up computation [43]. The scoring accuracy of the machine learning algorithm used to assess the prediction strength of the present state determines the reward function [44]. The reward is defined as erquation1:

$$R_f = Accuracy_{t+1} - Accuracy_t \quad (1)$$

Based on the reward received and the value of the state when it was previously visited, we applied the Temporal Difference (TD) method to evaluate the state's worth [45]. The formulation of this issue allows it to work with a high-dimensional feature space and is strong enough to handle any non-linear relationships between the predictors and the response variable. For the purpose of determining the state value for each chosen subset, we employed the Support Vector Machines (SVM) classifier [46]. SVM exhibits strong behavior across a wide range of learning tasks. Additionally, they are completely automated, therefore classifier parameter adjustment is not necessary. SVM classifiers also work well in high-dimensional spaces and are particularly resilient to difficulties with non-linear classification [47].

## 3. EXPERIMENTAL RESULTS

### 3.1. Experimental Setup

This subsection includes all the mediums used in implementing the proposed methodology. We used Python 3.10 as the programming language and Pytorch 1.10 as the deep learning framework. The Central Processing Unit (CPU) of the machine we used for training is core i7, 3.8 GHz and its Graphical Processing Unit (GPU) is GeForce RTX 1050. Additionally, the learning rate for training the autoencoder is 0.004 with a batch size of 64. The model is trained for 55 epochs and the optimizer used in the implementation is Adam.

Furthermore, Table 2 shows the architecture of the CAE used in this study. Table 2 contains both the architecture convolutional encoder of the model and its decoder part.

**Table 2.** The CAE that was used in this study.

| Network | Layer Type | Parameters | Non-Linear Activation Function |
|---|---|---|---|
| Input | Input | 480 | - |
| Encoder | Conv | 64 | ReLU |
| | Pooling | 32 | - |
| | Conv | 16 | ReLU |
| | Pooling | 8 | - |
| Decoder | Conv | 8 | ReLU |
| | Upsampling | 16 | - |
| | Conv | 32 | ReLU |
| | Upsampling | 64 | - |

### 3.2. Classification metrics

We have used the metrics introduced in Table 3. for evaluating our proposed approach. These metrics are used in order to prove the efficacy of a classifier in machine learning.

Fig. 3 demonstrates a Confusion Matrix (CM), which includes 4 important entities named True Positive (TP), True Negative (TN), False Positive (FP), and False Negatives (FN). TP is the number of malignant samples that are classified correctly. TN is the number of benign samples that are classified correctly. FP is the number of samples that are actually benign but classified as malignant and FN is the number of benign samples that are classified as malignant.

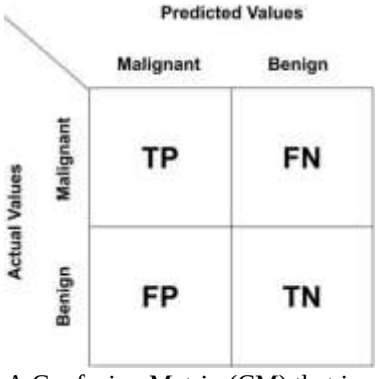


**Fig. 3.** A Confusion Matrix (CM) that is used for evaluating classifiers

**Table 3.** The metrics used for evaluating our proposed method.

| Metric | Calculation |
|---|---|
| Accuracy | $\frac{TP+TN}{TP+FP+FN+TN}$ |
| Precision | $\frac{TP}{TP+FP}$ |
| Recall | $\frac{TP}{TP+FN}$ |
| F1-Score | $\frac{2\times Precision\ \times Recall}{Precision+Recall}$ |

### 3.3. Classification results

This section includes the results achieved by the proposed classifier based on the metrics introduced in section 3.2. Fig. 4 and Table 4 detail the CM and the results obtained by our proposed algorithm.

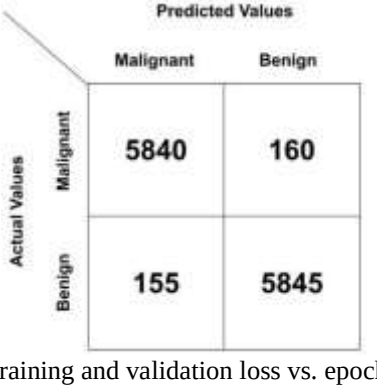


**Fig. 4.** Training and validation loss vs. epoch curve.

**Table 4.** Results achieved by the proposed methodology.

| Metric | Accuracy (%) | Recall (%) | Precision (%) | F1-Score (%) |
|---|---|---|---|---|
| Obtained Value | 97.38 | 97.32 | 97.41 | 97.35 |

Moreover, Fig. 5 illustrates the loss vs. epoch curve for training the autoencoder. Fig. 6 demonstrates the reconstructed images using the autoencoder for two samples.

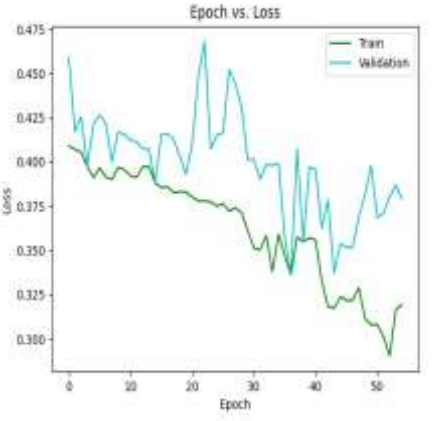


**Fig. 5.** Training and validation loss vs. epoch curve.

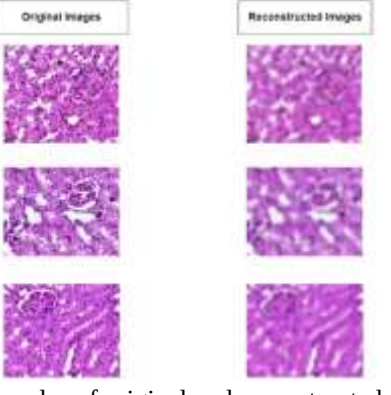


**Fig. 6.** Samples of original and reconstructed images using the proposed CAE.

Furthermore, Table 5 details comparison between our proposed methodology and other state-of-the-art research works. This comparison is done using the accuracy achieved by each methodology.

**Table 5.** Comparison between our proposed methodology and other research works

| Research | Accuracy (%) |
|---|---|
| [14] | 90.00 |
| [15] | 85.00 |
| [16] | 97.97 |
| [17] | 96.32 |
| [18] | 90.00 |
| [19] | 98.10 |
| Our proposed method | 97.38 |

Based on Table 5, the accuracy obtained by our proposed methodology is thoroughly competitive with the other works. This shows the reliable performance of the algorithm for classifying histopathological images.

Moreover, based on the F1-Score that is achieved by our proposed method, we can claim that the model has significant performance in recognizing both TP and TN samples within the dataset used in this study.

## 4. CONCLUSION

In this study, we have proposed an algorithm for atomizing the diagnosis procedure for breast cancer images. Our algorithm is able to analyze histopathological images without the demand for any special preprocessing step. Based on our extensive experiments, the performance of the model can be claimed to be remarkably good. Since our experiments have been conducted on a large dataset gathered from real hospitals, it can be argued that the proposed pipeline can be utilized efficiently in clinical contexts with ease.

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