Towards Early Breast Cancer Detection: A Deep Learning Approach

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ABSTRACT

Early detection of breast cancer is crucial for patients' recovery chances to be improved. Artificial intelligence techniques, and more particularly Deep Learning (DL), may contribute to enhancing the accuracy of this detection. The main objective of this paper is to propose a DL model in an attempt to detect and classify breast cancer, and thus help people suffering from this disease. The Breast Cancer Wisconsin dataset was implemented to train neural networks, and their performance was subsequently evaluated on certain test datasets. The findings revealed that this approach provides promising results in terms of detection accuracy, with high sensitivity and specificity. The study also compares the performance of this approach with other breast cancer detection works, demonstrating that DL can provide significantly better results.

Keywords-breast cancer; deep learning; classification; Wisconsin dataset; hyperparameters; evaluation

I. INTRODUCTION

Breast cancer is a disease characterized by the uncontrolled proliferation of cells within the breast. Various types of breast cancer exist, categorized based on the specific cells in the breast that become cancerous [1]. Breast cancer can originate in any part of the breast, which is composed of three major components: ducts, lobules, and connective tissue. Most breast cancers begin in the lobules or ducts. The disease can spread beyond the breast through the lymphatic and blood vessels. Breast cancers represent a major public health problem worldwide. Over the past 25 years, the incidence of these cancers has been doubled, reaching tens or even hundreds of thousands of new cases per year, while it is estimated that one out of eight or nine women will develop breast cancer during their lifetime.

Breast cancer is the most common cancer among women and a significant public health issue, with over 1.7 million new cases worldwide being annually diagnosed. However, there are significant variations between certain regions of the world. In 2012, the incidence rates (number of new cases per year reported to the population) were four times higher in Europe (96 cases per 100.000 women per year) or in North America than in Central Africa or Asia (27 cases per 100.000 women per year). In these regions, however, breast cancer rates are growing rapidly, so the gap when the former are compared to other regions is equivalently diminishing [2]. Only part of the recent increase in the incidence rates seems to be possible to be explained through the implementation of systematic screening programs [3].

Breast cancer represents the fifth leading cause of cancer death worldwide (522.000 deaths in 2012) [2]. Variations in

breast cancer mortality among regions of the world are less significant than the incidences of this disease, due to the better survival rates documented in developed countries after patients having experienced breast cancer (mortality from 6 to 20 per 100.000 women per year). The causes of breast cancer are multiple, while they are both genetic and environmental in origin. Nevertheless, despite the numerous studies carried out regarding this disease, its causes are not entirely known. The main established or the suspected risk factors for breast cancer are: age, reproductive factors (age at first period and menopause, parity and age at first pregnancy, breastfeeding) [4], exogenous hormones (oral contraception [5], hormonal treatments for menopause [6, 7]), physical activity and anthropometric factors [8], diet [9], night work and disruption of the circadian rhythm [10], genetic factors such as high-risk genes [11], and genes with low penetrance [12].

Today, there are general principles in the implementation of breast cancer treatments. Surgery and radiotherapy are local treatments, while chemotherapy, hormone therapy or targeted therapies treat the body as a whole, to prevent the formation of metastases. The future, though, is a tailor-made treatment adapted to each patient [13].

Artificial intelligence has the potential to significantly expedite the diagnosis and management of breast cancer. It can identify benign cancer cells up to ten times faster than a traditional microscopic examination. Currently, a pathologist takes around 40 minutes to analyze potentially cancerous cells placed between two glass slides under a microscope. With the aid of artificial intelligence, this diagnostic process could be reduced to just five minutes.

This work proposes a DL model to detect and classify breast cancer using the Wisconsin dataset.

II. RELATED WORK

Various DL techniques have been developed for the diagnosis of breast cancer using different diagnostic tools. Authors in [14] proposed the improvement of a conventional CNN architecture with a Trapezoidal Long Short-Term Memory (TLSTM) layer, achieving a 98.33% accuracy in diagnosing breast cancer using HER2-stained pathological images as input. Authors in [15] used deep manifold preserving autoencoders to diagnose breast cancer with histopathological images of varying resolutions. Authors in [16] developed a five-layered ANN model with 99% accuracy for breast cancer diagnosis, leveraging a combination of features extracted from CT and MRI scans. Authors in [17] designed a 3D-CNN-based diagnostic aid for breast cancer using Contrast-Enhanced Ultrasound (CEUS) videos. The proposed CNN modules extracted both temporal and spatial information from these videos. Authors in [18] proposed a three-layered Convolutional Neural Network (CNN) for diagnosing invasive ductal carcinoma utilizing histological images. This network comprised max pooling, convolution, batch normalization, and dropout layers. Authors in [19] compared the performance of four algorithms – Support Vector Machine (SVM), Logistic Regression, Random Forest, and KNN – in predicting breast cancer outcomes using various datasets. Authors in [20] categorized breast cancer as malignant or benign, performing early diagnosis using various machine learning techniques, and investigated the best technology for curing breast cancer in terms of accuracy rate. The authors conducted tests on the following machine learning algorithms: KNN, RF, NB, and SVM. The results demonstrated that RF 98.11 and SVM 92.6 are the best with less error rates.

The Wisconsin Breast Cancer Dataset is a widely used and reliable resource for training machine learning models due to its large number of virtually noise-free instances. This dataset has been the subject of numerous research studies. Authors in [21] utilized the Wisconsin dataset to compare the performance of different machine learning techniques in terms of accuracy and precision for breast cancer detection. Their findings showed that all algorithms achieved an accuracy exceeding 94% in identifying malignant tumors, with KNN emerging as the most efficient method for detecting breast cancer. A Mamdani fuzzy inference system for breast cancer risk identification was proposed in [22]. This system aimed to reduce the number of features needed for diagnosis, thereby accelerating the identification process. The evaluation of the system demonstrated an accuracy of 93.6%. Authors in [23] developed a hybrid approach for breast cancer classification and detection that combines Decision Tree (DT) and SVM algorithms. Their method involves information treatment and option extraction, followed by predictions using a DT-SVM hybrid model. The authors compared their approach to other classifier algorithms using the WEKA tool. Authors in [24] presented a breast cancer diagnosis system that combines a Naive Bayes Classifier and a Relevance Vector Machine (RVM). Using the Wisconsin original dataset, their approach achieved an accuracy of 95%. Authors in [25] applied convolutional neural models to mammograms for the detection of abnormal images. Their experiments were conducted on the MIAS dataset. To enhance the model's precision, preprocessing techniques and adjustments to channel sizes were implemented to reduce noise. Authors in [26] investigated the characterization of breast cancer through gene mutations. Two different classifiers, Naive Bayes and K-Nearest Neighbor (KNN), were applied and compared. Evaluation using cross-validation demonstrated that KNN achieved a higher accuracy (97.5%) than that of the Naive Bayes classifier (96.19%). Authors in [27] developed an Artificial Neural Network (ANN) where parameters were optimized using Differential Evolution (DE). Previous studies have demonstrated the effectiveness of DE in improving ANN learning. The resulting neural network possesses several advantageous properties, including learning ability, generalization, and reminiscence.

Authors in [28] employed a weighted Naïve-Bayes classifier model for breast cancer detection. The Wisconsin Diagnosis Breast Cancer dataset was deployed to evaluate its performance in comparison to the non-weighted Naive Bayes classifier and other contemporary models, such as WAC, FWAC, and RBF. Authors in [29] conducted a comparative study of the RVM, highlighting its low computational cost. The study compared RVM with other machine learning techniques for breast cancer detection and classification. The results indicated that RVM outperforms other machine learning algorithms in diagnosing breast cancer, even when the number of variables is reduced.

Authors in [30] investigated the informational indexes available for training machine learning models and provided a comprehensive comparison of various models applied to predict breast cancer. Authors in [31] implemented several classification models for identification, including KNN, SVM, Naive Bayes, decision trees, and other algorithms. The procedure involved raw datasets, data preparation, data statistics, classification techniques, and performance evaluation. The shortcoming of this research is the lack of an accuracy-enhancing algorithm, which could have been used to increase accuracy and improve cancer detection. Authors in [32] employed a classification model to detect cancer. Their methodology for handling raw data included a data dictionary, summary statistics of the dataset, an exploratory data analysis, and a model construction and evaluation. The shortcoming of this research is its focus on only three classifications; incorporating more classifications could improve the accuracy of cancer prediction. Authors in [33] established a random forest prototype for malignancy prediction, achieving 98% accuracy with this algorithm. Their methodology included exploratory data analysis and other techniques. The shortcoming of this research is the use of only one classifier; incorporating additional algorithms could potentially achieve higher accuracy in breast cancer detection. Authors in [34] developed a breast cancer segmentation system using an enhanced version of the U-Net 3+ neural network, incorporating various optimizations to boost localization and segmentation performance. The system was evaluated against other state-of-the-art networks utilizing the INbreast Full-Field Digital Mammographic dataset (INbreast FFDM). The proposed model achieved a dice score of 98.47%, setting a new benchmark in segmentation accuracy and demonstrating its potential for real-world breast cancer detection applications. Authors in [35] proposed an advanced breast cancer detection and classification system leveraging mammogram images. The method involves several steps: image preprocessing with Homo Morphic Adaptive Histogram Equalization (HMAHE) to enhance contrast and remove noise, identification of breast boundaries using the canny edge detector, removal of pectoral muscles with the Global Pixel Intensity-based Thresholding (GPIT) method, and tumor identification and segmentation implementing the Centroid-based Region Growing Segmentation (CRGS) algorithm. After clustering and feature extraction, the Chaotic Function-based Black Widow Optimization Algorithm (CBWOA) selects the relevant features. These features are then classified into six categories by the Convolutional Squared Deviation Neural Network Classifier (CSDNN). The proposed system shows improved efficiency and accuracy over the existing methods.

III. METHODOLOGY

To achieve the research objectives, the Breast Cancer Wisconsin (BCW) dataset, a widely recognized and publicly available dataset in the field of breast cancer detection, was deployed. Trough the BCW utilization, the present study sought to develop a robust and accurate DL model for breast cancer detection. Figure 1 depicts the DNN implementation.

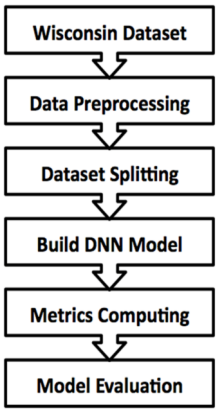

Fig. 1. DNN implementation

A. Dataset

The considered BCW dataset [36] contains measurements of cell characteristics scanned from breast tumor biopsies, such as cell size, shape, uniformity, and compactness, as well as information on tumor malignancy. The dataset includes 569 instances (biopsies) and 30 characteristics (features). Each instance is labeled as benign or malignant, with of 357 benign instances and 212 malignant instances. The dataset is widely used to train and evaluate binary classification models in the field of machine learning and data science, especially for the classification of breast tumors according to their malignancy.

B. Dataset Preprocessing

Pre-processing is a necessary step to transform raw data into data that can be used by a model. During this stage, the data undergo processing to be cleaned, normalized, and reduced in dimensions. The goal is to prepare the data in such a way that they are suitable for model training.

Data normalization can be useful for several reasons. First, it ensures that all variables have the same influence on learning, because they are all in the same range of values. Normalization can be done following different methods, but one of the most common ones is the Min-Max normalization. This method involves transforming each value of a variable into a new value that falls within a specific range, usually between 0 and 1. To enhance the performance of the introduced model, a data preprocessing technique was adopted. This involved calculating the minimum and maximum values of each variable and applying the following formula for normalization:

$$z_i = \frac{x_i - \min(x)}{\max(x) - \min(x)} \quad (1)$$

where z_i corresponds to the i_{th} normalized value and x represents all values.

The dataset may contain categorical variables that must be encoded into numeric variables to be utilized by machine learning algorithms. Encoding techniques can be labeled as encoding, one-hot encoding or binary encoding. Figure 2 illustrates the distribution of classes in this study's target as a bar graph. After encoding, B becomes 0 and M becomes 1.

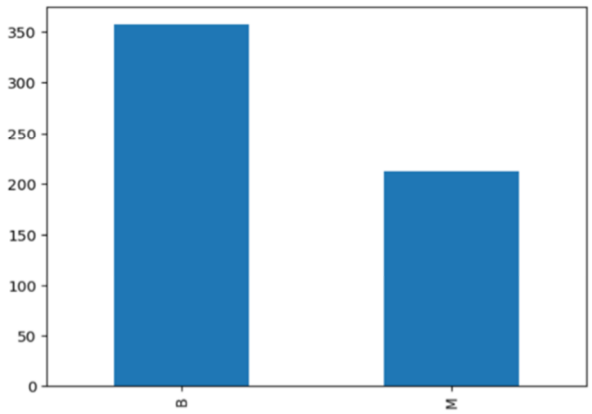

Fig. 2. Categorical standard class distribution.

The dataset was split into two parts, a training set and a test set, representing 80% and 20% of the total dataset, respectively. The categories were randomly distributed into the training and testing sets.

C. Evaluation Metrics

The following metrics were utilized to validate the proposed model's performance: [37]

Accuracy is a metric that assesses the correctness of a model's positive predictions. It is calculated by dividing the number of true positive predictions by the total number of predictions made by the model.

$$Accuracy = \frac{TP+TN}{TP+TN+FP+FN} \quad (2)$$

where TP True Positive predictions, TN represents True Negative, FP represents False Positive, and FN represents False Negative.

Recall, also known as sensitivity, measures the proportion of the actual positive cases that are correctly identified as positive by the model. It is calculated as the ratio of true positive predictions to the total number of actual positive cases.

$$Recall = \frac{TP}{TP+FN} \quad (3)$$

Precision, also known as Positive Predictive Value (PPV), represents the proportion of correct predictions among all positive predictions made by the model. In other words, it measures the accuracy of the model's positive predictions.

$$Precision = \frac{TP}{TP+FP} \quad (4)$$

Specificity measures the proportion of actual negative cases that are correctly identified as negative by the model. In other words, it reflects the model's ability to correctly identify TNs.

$$Specificity = \frac{TN}{TN+FP} \quad (5)$$

The F- or F1-score, is a harmonic mean that combines precision and recall into a single metric. It provides a balanced measure of the model's performance, considering both its ability to correctly identify positive cases (recall) and the accuracy of its positive predictions (precision).

$$F - score = \frac{2TP}{2TP+FP+FN} \quad (6)$$

D. The Proposed Model

The complexity of breast cancer diagnosis is a challenge for pathologists. However, with the advancement of artificial intelligence, machines can potentially reduce errors and help improve diagnostic accuracy. In this work, a DL model will be proposed to assist in breast cancer diagnosis.

The proposed model is a deep neural network composed of an input layer, whose number of units is equal to the number of features in the dataset, three hidden layers having, respectively, 64, 32, and 8 nodes with an activation function of type ReLU, and a single unit output layer with a "sigmoid" activation function since it is a binary classification problem. The model has been trained for 80 epochs and a validation_split equal to 0.2. Several tests were performed to find the best hyper-parameters for the introduced model. This study's attention was particularly focused on the L2 regularization parameter, which makes it possible to limit overfitting by penalizing coefficients that are too large. After carrying out several tests, the L2 regularization parameter was set to 0.001, which allowed the acquisition of very satisfactory results. It was discovered that this regularization parameter enabled the acquisition of a better generalization of this study's model. That is, the model was able to better generalize its predictions on data it had not seen before.

E. Results and Discussion

The model's performance was assessed by monitoring its loss and accuracy during the training process. The model achieved a high accuracy of 99.12%. The accuracy graph shows a significant increase in the accuracy of the proposed model over time as it was trained on the introduced dataset. It can be observed that accuracy started to increase rapidly at the beginning of the training, and then continued to increase more slowly as the model fit the dataset. Accuracy reached a stability level at a certain point in training, indicating that the proposed model cannot improve further with the addition of training data. However, it can be noted that the level of accuracy achieved by the presented model is high (see Figure 3).

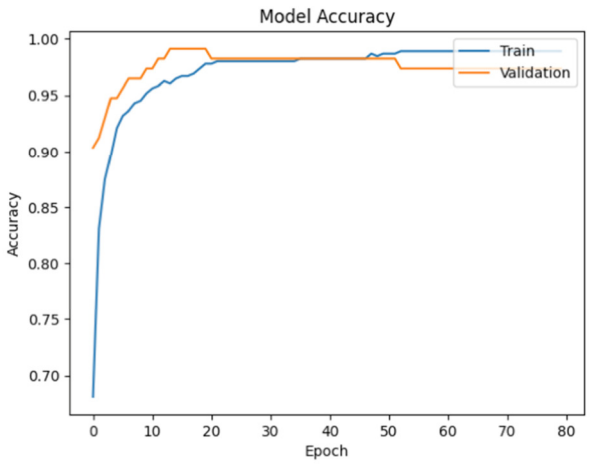

Fig. 3. Model's accuracy during the training process.

The loss plot exhibits a significant decrease in the model's loss function over time as it is trained on the proposed dataset (see Figure 4). It can be observed that the loss decreases rapidly at the start of training and then continues to decrease more slowly as the model fits the data set. A low loss value is encouraging, as it indicates that the model is able to minimize prediction error and best fit the proposed data set.

The confusion matrix given in Figure 5 displays a large number of TPs and TNs and a small number of FPs and FNs. This indicated that the proposed model is able to detect breast cancer with high accuracy and has a low probability of FPs or FNs. The ROC curve is a useful tool for evaluating model performance, as the area under the curve directly reflects its effectiveness. In this study, the ROC curve is positioned close to the upper left corner, indicating that the model is adept at detecting breast cancer, as shown in Figure 6.

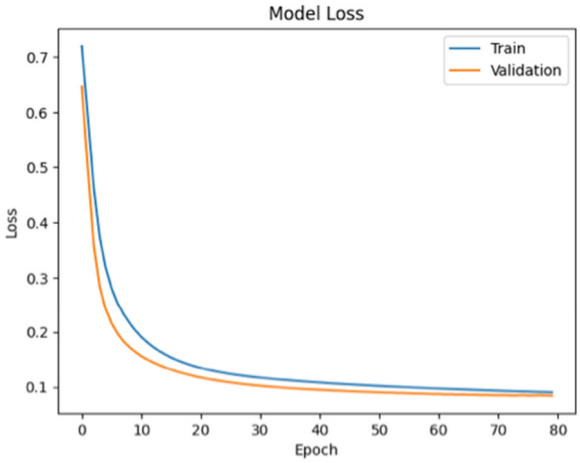

Fig. 4. Model's loss during the training process.

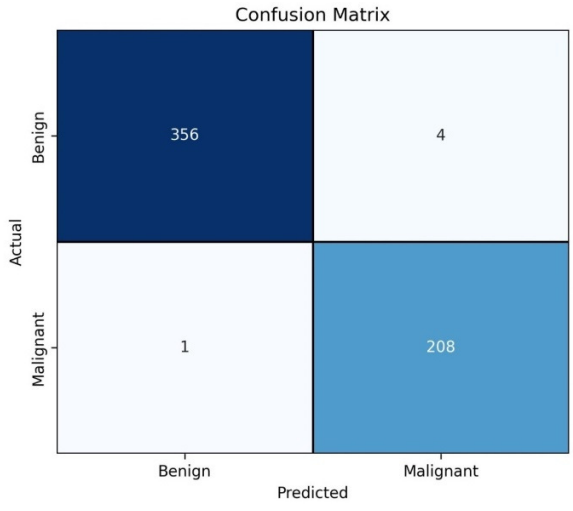

Fig. 5. Confusion matrix.

Regarding the results of precision, recall, and F1-score, it can be observed that the proposed model obtains high scores for each of these metrics. High precision indicates that the model accurately predicts malignancies, while high recall indicates that it is able to effectively detect malignancies. The F1 score combines these two metrics to give an overall measure of the model's performance, which is also high.

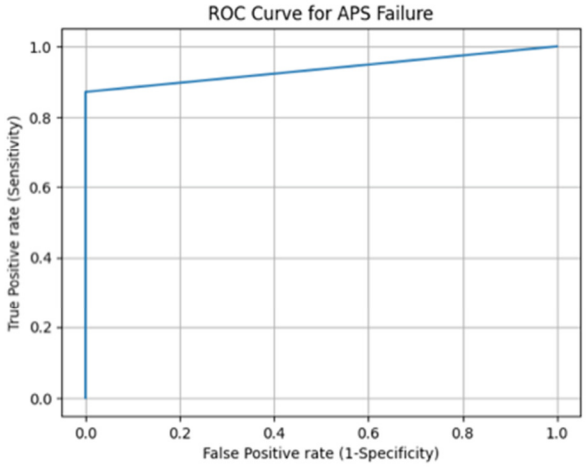

Fig. 6. ROC curve.

These results are encouraging and disclose that the introduced model is able to effectively detect malignancies in the test dataset. However, it is important to note that these results should be interpreted based on the characteristics of the proposed dataset and model, and do not necessarily guarantee similar performance in other datasets. Table I portrays the precision, recall, and F1-score for predicting the absence or presence of breast cancer in the Wisconsin dataset. Table II provides global performance metrics, such as accuracy, AUC, and F1-score, for the proposed DL model.

TABLE I. RESULTS OF THE EVALUATION METRICS FOR EACH CLASS

	Precision	**Recall**	**F1-score**
0	0.9971	0.9888	0.9929
1	0.9811	0.9952	0.9880

TABLE II. RESULTS OF THE EVALUATION METRICS

	Precision	**Recall**	**F1-score**
Macro Avg	0.9891	0.9920	0.9904
Weighted Avg	0.9911	0.9911	0.9910

IV. COMPARATIVE STUDY

As part of the performed comparative study, seven works involved in the analysis of the Wisconsin breast cancer dataset were also identified [21, 30-35]. This section aims to compare the obtained results with theirs, in order to evaluate the performance of the presented breast cancer detection model based on DL (see Table III).

Moreover, the comparative study entailing selected existing results confirmed the competitiveness of the proposed approach. These results open promising perspectives for the DL application in the field of early breast cancer detection.

TABLE III. COMPARISON OF THE RESULTS WITH PREVIOUS STUDIES USING THE 'WISCONSIN' DATASET

Pipeline	Technique	Accuracy
[30](2021)	Random Forest	94.74%
[21](2018)	KNN	95%
[31](2019)	Random Forest	95.95%
[38](2019)	SVM	96%
[32](2021)	Random Forest	96%
[39](2009)	Naive Bayes	97.36%
[33](2022)	Random Forest	98.24%
Proposed	Deep Neural Network	99.12%

V. CONCLUSION

Early detection of breast cancer is a major public health concern. Traditional detection methods have limitations in accuracy and reliability, emphasizing the need for more advanced and effective approaches to improve diagnosis. In this context, the use of artificial intelligence, particularly Deep Learning (DL), presents a promising opportunity. This study explores the utilization of these methods for breast cancer detection, focusing on the Wisconsin dataset. The DL model demonstrates exceptional performance across various evaluation metrics. With an impressive accuracy of 99.12%, it correctly classifies the vast majority of instances. The model exhibits very good recall and precision at 99.2% and 98.91%, respectively, indicating its ability to avoid False Positives (FPs) and make highly accurate positive predictions. The F1-score of 99.04% reflects a strong balance between precision and recall, further confirming the model's robust overall performance. These results suggest that the model is highly reliable, particularly in scenarios where minimizing false positives is crucial, though there may be room for improvement in detecting all positive instances. The results of this work can contribute to enhancing early detection of the disease, positively impacting patient survival and quality of life. Additionally, these findings may open new avenues for the application of artificial intelligence in healthcare. Future research on predicting breast cancer deploying DL on the Wisconsin dataset can focus on: Model Optimization, Data Augmentation, Transfer Learning, Multi-Modal Integration, Robustness, Personalized Medicine, Clinical Application, and so on.

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