Artificial Neural Networks to Predict Breast Cancer Outcomes

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ABSTRACT

Breast cancer ranks as the second most common cancer among women in the United States. Mortality rates have steadily decreased, largely due to earlier detection through screening and a deeper understanding of the disease. Accurate prediction models for breast cancer are therefore essential to further improve survival outcomes. In this study, we utilized the Wisconsin Breast Cancer Original and Diagnostic datasets to classify cells as cancerous or non-cancerous. An artificial neural network (ANN) model was developed, demonstrating both rapid and accurate detection capabilities. The proposed ANN achieved a recall of 98% and precision of 97% for malignant tumors in the Wisconsin Breast Cancer Original dataset, and a recall of 98% with precision of 99% in the Wisconsin Breast Cancer Diagnostic dataset. The model introduced in this study holds potential as a clinical tool for identifying individuals at higher risk of breast cancer, ultimately promoting improved patient outcomes.

Introduction

Breast cancer is the most common malignancy among women and remains one of the leading causes of cancer related deaths worldwide (Ferlay et al., 2010). Accurate diagnosis relies on the integration of multiple clinical variables and mammographic features. An ideal diagnostic system must effectively distinguish between benign and malignant tumors (Ayer et al., 2010). According to the World Health Organization, breast cancer affects more than 1.5 million women globally each year and is the second leading cause of cancer-related mortality among women (Mohammed et al., 2018). The etiology of breast cancer is not fully understood, and the disease often develops without early symptoms. Early detection through regular screening is therefore essential, as it enables timely treatment and significantly improves survival rates predominantly for women at high or average risk. Cancer cells proliferate and spread through tumor growth.

Tumor analysis is central to breast cancer screening, where tumors are categorized as benign or malignant. Detecting malignant neoplasms requires active diagnostic strategies; however, even expert clinicians face challenges in accurately identifying cancers (Gayathri et al., 2013). Consequently, automated diagnostic methods are increasingly necessary to assist in cancer detection.

The application of machine learning (ML) in medicine has expanded rapidly due to its effectiveness in prediction and classification tasks. In breast cancer diagnosis, ML models are now widely used to enhance accuracy and reliability in biomedical research. The objective of this study is to evaluate the performance of various machine learning classifiers in diagnosing breast cancer, focusing on accuracy, precision, and recall.

Data mining involves discovering useful patterns and information from large datasets. In healthcare, these techniques facilitate disease identification and prediction. ML, a core component of data mining, typically involves three main stages: data preprocessing, feature selection or extraction, and classification. Among these, feature extraction plays a crucial role in the diagnosis and prognosis of cancer by distinguishing between benign and malignant tumors (Witten and Frank, 2005).

Artificial intelligence (AI) and machine learning have become vital tools in identifying breast cancer and extracting insights from complex medical data. AI techniques excel at uncovering hidden patterns within large datasets and are extensively applied in disease classification and modeling (Chong et al., 2025). These technologies offer significant potential in medical diagnostics, particularly for conditions such as cancer (Pacal, 2024; Aslan et al., 2024; Işık and Pacal, 2024).

Machine learning models, such as artificial neural networks (ANNs), can learn from large datasets to detect subtle variations that traditional diagnostic methods might overlook. This capability enables earlier diagnosis, reduces the likelihood of complications, and supports more personalized treatment strategies.

This study explores the use of an artificial neural network model to detect breast cancer. Specifically, it aims to determine whether an ANN trained on a large, retrospectively collected dataset of mammographic findings can accurately distinguish between benign and malignant cases and predict the probability of breast cancer in individual patients.

Background

Cancer is the second leading cause of death worldwide, accounting for approximately 9.6 million deaths in 2018 (Siegel et al., 2018). Among women, the most prevalent cancers are those of the breast, lung, and colon. Of these, breast cancer remains the most common and major cause of cancer-related mortality. Its incidence continues to rise globally, making it a critical public health concern. Early detection remains the most effective strategy for improving patient outcomes and survival rates.

Breast cancer represents about 30% of all new cancer diagnoses in women (Siegel et al., 2018). Machine learning (ML) techniques have emerged as powerful tools for analyzing complex medical data and identifying key diagnostic features. Research indicates that ML algorithms can be effectively applied for the early detection, classification, and prognosis of cancer (Maity and Das, 2017).

Tumors can be classified as benign or malignant, and differentiation between the two is essential for appropriate treatment planning. However, even experienced clinicians may find this distinction challenging based on imaging and clinical features alone. Therefore, automated diagnostic systems are increasingly important to assist in the reliable identification of tumor

characteristics. Malignant tumors grow aggressively and invade surrounding tissues, emphasizing the importance of early and accurate detection.

Recent advances in machine learning have significantly enhanced medical diagnostics and patient monitoring (Pacal, 2024). Traditional diagnostic methods rely on manual feature extraction which can be time-consuming. In contrast, deep learning approaches automate feature extraction, enabling the system to learn directly from raw data and improving diagnostic efficiency (Gardezi et al., 2019).

Gupta et al. (2025) proposed a hybrid deep transfer learning framework combining Xception with Support Vector Classifier (XSV) and Random Forest (XRF) models to improve breast cancer classification. The hybrid model was evaluated on the BreakHis dataset (Spanhol et al., 2015) and outperformed traditional classifiers such as Random Forest, Logistic Regression, Support Vector Classifier, K-Nearest Neighbors, and AdaBoost. Similarly, Alshayeji et al. (2022) developed a simplified artificial neural network with a single hidden layer for breast cancer diagnosis and prediction using the Wisconsin Breast Cancer Dataset (WDBC) and the Wisconsin Diagnostic Breast Cancer (WDBC) dataset. Their approach demonstrated effective performance without applying feature selection or optimization techniques.

Artificial neural networks have been widely utilized in clinical applications for pattern recognition and survival prediction (Baxt et al., 1996). One of their major strengths lies in their ability to capture nonlinear relationships and complex interactions between prognostic factors. Neural network models have shown improved accuracy in predicting survival for patients with lung and colorectal cancers (Burke et al., 1997) and have produced promising results in breast cancer prognosis. De Laurentiis and Ravdin (1994) further enhanced survival prediction models by incorporating a time variable into prognostic inputs to estimate the probability of cancer recurrence.

The use of intelligent classification systems in medical diagnosis, including breast cancer detection, continues to expand. While expert medical evaluation remains essential, intelligent algorithms can support clinicians, particularly less experienced practitioners by minimizing diagnostic errors and improving decision accuracy (Akay, 2009).

Several studies have demonstrated the successful application of ANNs in breast cancer diagnosis and prognosis as shown in Table 1. For example, Utomo et al. (2014) employed an Extreme Learning Machine Neural Network (ELM ANN) model, achieving significant improvements in diagnostic accuracy. Boeri et al. (2020) utilized both ANN and Support Vector Machine (SVM) models to estimate post-surgical prognosis in breast cancer patients, reporting that both approaches accurately predicted individualized risks of recurrence. Likewise, Dihge et al. (2019) used ANN ensemble technique to predict the likelihood of breast cancer and suggested its potential as a clinical decision-support tool to enhance the predictive value of biopsy recommendations.

Table 1. Review of Artificial Neural Network Techniques

Year / Reference	Tool / Technique	Dataset / Description
Utomo et al., 2014	ELN (Extreme Learning Technique)	WBC Original
Ravdin et al., 1992	Nworks Professional II software (Neuralware, Pittsburgh, PA)	Nichols Institute on tumor specimens: training set of 1008 patients and a validation set of 960 patients
Bourdès et al., 2010	Statistical Neural Networks software	Data collection at Centre Léon Bérard (CLB), Lyon: primary or secondary following neoadjuvant chemotherapy
Boeri et al., 2020	IBM SPSS Modeler 18.1 software	Retrospective analysis of 1021 consecutive patients (both genders) who underwent surgery for breast cancer from April 2008 to December 2016
Nasien et al., 2022	Graphical User Interface in MATLAB R2016a software	WBC Diagnostic dataset
Dihge et al., 2019	Ensemble technique	Swedish National Quality Registry for Breast Cancer and public mammography screening program records
Jouni et al., 2016	Two programs in MATLAB simulating different activation functions for hidden and output layers	MathWorks (cancer_dataset.MAT)
Ayer et al., 2010	MATLAB 7.4	Froedtert and Medical College of Wisconsin Breast Care Center (April 5, 1999 – February 9, 2004)

Methodology

Data sets

In this study, we analyzed the Wisconsin Breast Cancer dataset (Wolberg, Mangasarian, and Street, 1993) obtained from the University of California Irvine (UCI) Machine Learning Repository. These datasets (Frank et al., 2010) are widely used to classify breast tissue samples as either malignant (cancerous) or benign (non-cancerous). Breast cancer is generally categorized into two main types based on risk: benign and malignant. Benign breast cancer consists of non-cancerous growths in the breast tissue. While these tumors may cause discomfort or concern, they are typically not life-threatening. In contrast, malignant breast cancer involves cancerous growths that can spread to other parts of the body, necessitating prompt treatment to prevent progression and reduce the risk of mortality.

A brief description of these datasets is presented in Table 2. The original Wisconsin Breast Cancer (WBC) dataset has 699 rows, while the more recent and commonly used Wisconsin

Diagnostic Breast Cancer (WDBC) dataset has 569 rows, because the two datasets are derived from different image analysis methods.

Table 3 describes the dataset features (Street et al., 1993). Each dataset consists of some classification patterns or instances with a set of numerical features or attributes. The WDBC data was extracted from preprocessed Fine Needle Aspiration biopsy image of cell slides. The WBC dataset contains the extracted features of the acquired images after the image pre-processing, image segmentation, and feature extraction steps have been conducted.

Table 2. Description of the Datasets

Dataset	No. of attributes	No. of instances
Wisconsin Breast Cancer (Original)	11	699
Wisconsin Diagnosis Breast Cancer (WDBC)	32	569

Table 3. Dataset features of Cell Nucleus

Feature	Description
Radius	The radius of each cell nucleus.
Perimeter	The total distance between the points on the boundary of the cell nucleus constitutes the nuclear perimeter.
Area	The nuclear area measured by counting the number of pixels on the interior of the nucleus boundary and adding one-half of the pixels in the perimeter.
Compactness	Perimeter and area are combined to give a measure of the compactness of the cell nuclei.
Smoothness	The smoothness of a nuclear contour is quantified by measuring the difference between the length of a radial line and the mean length of the lines surrounding it.
Concavity	Severity of concave portions of the contour.
Concave Points	Similar to *Concavity*, but measures only the number rather than the magnitude, of contour concavities.
Symmetry	Measures symmetry by calculating the length difference between lines perpendicular to the major axis to the cell boundary in both directions.
Fractal Dimension	Approximated using the “coastline approximation”; corresponds to a less regular contour and thus a higher probability of malignancy.
Texture	Measured by computing the variance of the gray-scale intensities in the component pixels.

Figure 1 shows the steps applied in building the breast cancer prediction model and to evaluate the model. We built the Artificial Neural Network model in Python using the keras package. Keras is an open-source library offering a Python interface for building and working with artificial neural networks. First, we cleaned the data by checking for null values. Next, we identified and removed highly correlated variables to improve the model. Finally, we evaluated the model's performance using recall and precision with the ANN algorithm.

The dataset was split into training and testing sets, with 80% of the data used for training the system and the remaining 20% reserved for testing. Using this dataset, we developed and analyzed an artificial neural network model to predict whether a given set of symptoms indicates breast cancer. No instances of overfitting were observed with the breast cancer dataset employed in this study. Once the ML model is built, it is evaluated using recall and precision.

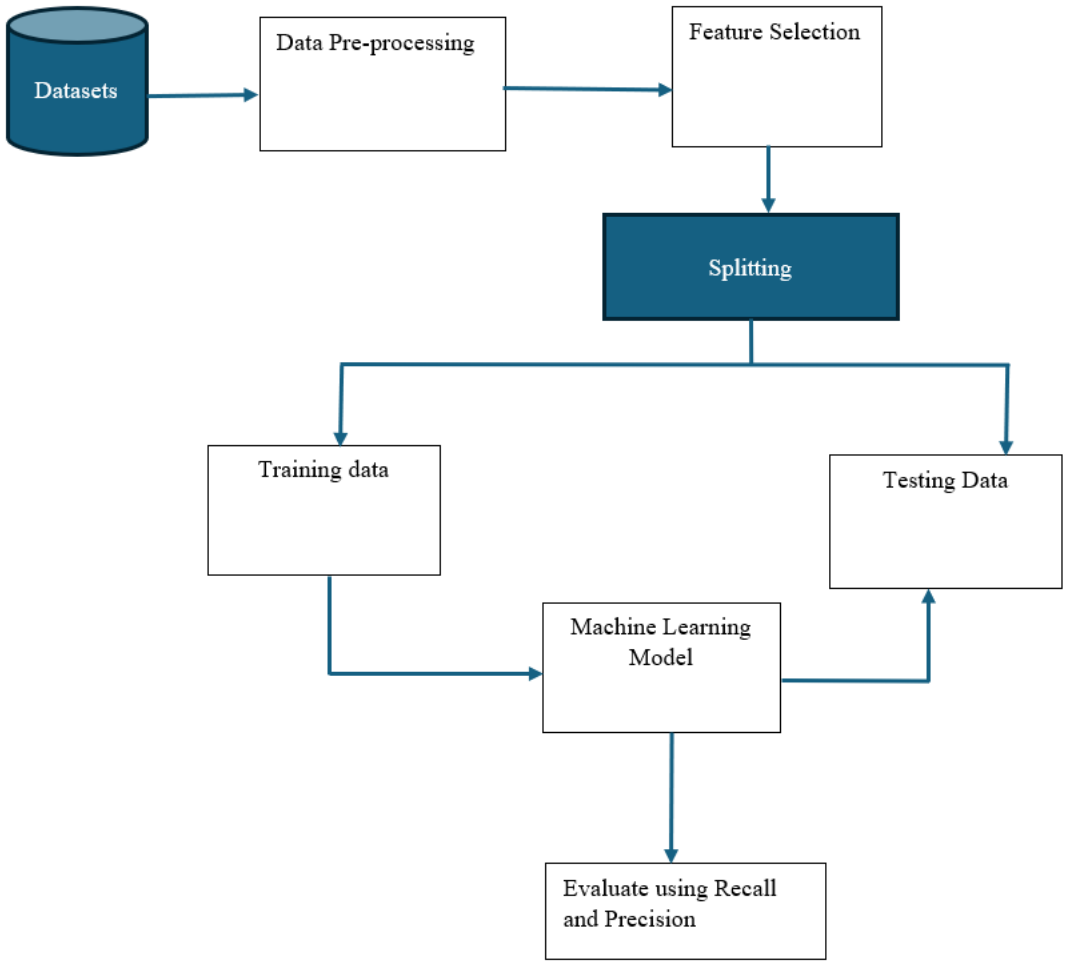

Figure 1. Methodology

What is ANN

Artificial Neural Networks are computational models inspired by the structure and learning behavior of biological neural networks (Floyd et al., 1994). They are commonly used to classify input patterns into predefined categories and have been applied to a wide range of problems in pattern recognition and decision-making. ANNs consist of interconnected processing units organized in layers, where each connection has an associated strength or "weight" that is adjusted through learning.

In this study, the ANN used for malignancy prediction employed a three-layer backpropagation architecture with a single hidden layer. The input features were mammographic findings identified by radiologists. The network's "trained knowledge" was embedded in its internal numerical weights, which were learned during training. When new input feature values were provided, the trained network produced an output corresponding to a classification, either malignant or benign based on the knowledge it had acquired. Figure 2 presents an example of an ANN model for predicting diagnostic outcomes.

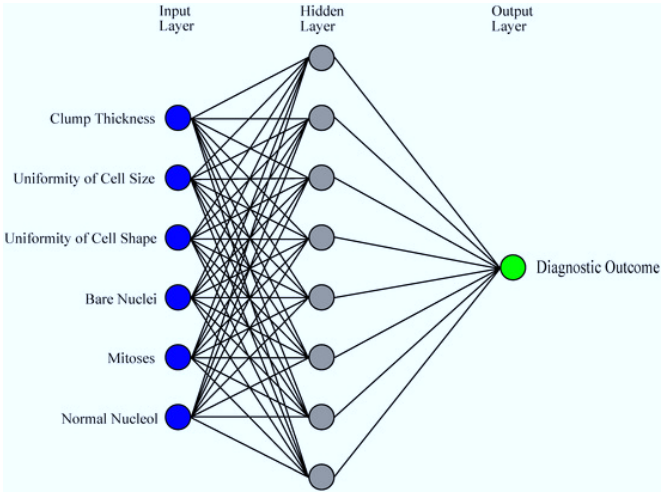

Figure 2. ANN Example to predict the diagnostic outcome
Figure Source: Yue et al., 2018

Results and Discussion

To detect breast cancer, we employed an Artificial Neural Network model to develop a predictive machine learning system for classifying cells as benign or malignant. Selecting the most relevant features from the dataset was crucial for effective prediction using the classification model. We utilized data from the Wisconsin Diagnostic Breast Cancer database. Figure 3 illustrates the different types of tumor classifications. As depicted, the dataset includes a greater number of benign cases. The ANN model's performance was evaluated using recall and precision metrics, demonstrating high accuracy as illustrated in Figure 5 and Figure 6.

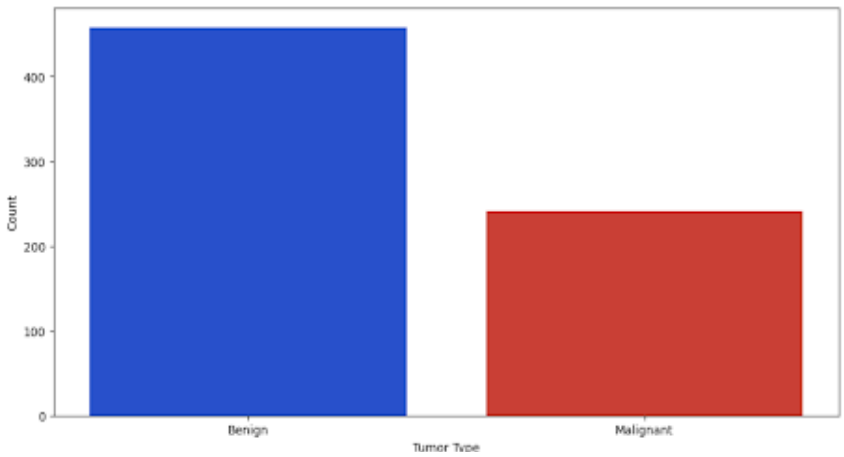

Figure 3. Classification of Tumor Types

Figure 4 presents the calculated correlations of the breast cancer features of diagnosis. Features with high correlation are eliminated from the prediction model. For example, the two features *Uniformity of Cell Size* and *Cell Shape* are highly correlated and were thus not useful in the prediction for breast cancer diagnosis.

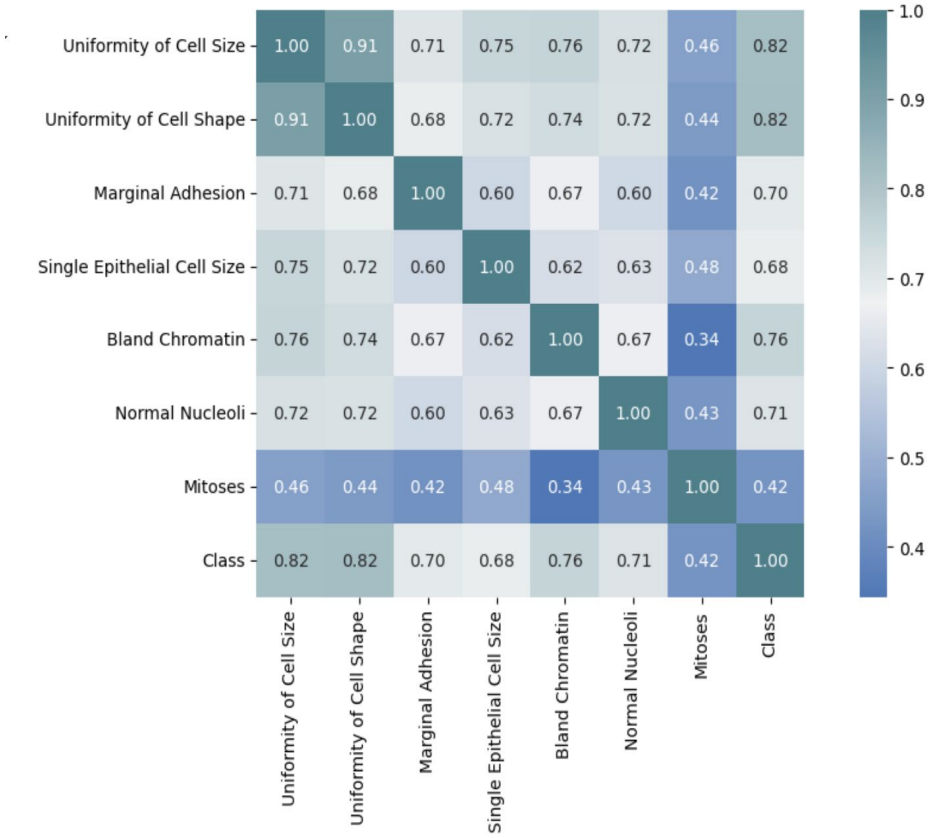

Figure 4. Correlation Matrix

80% of the data is used to train the system and the remaining 20% is used for testing. From the dataset, we analyzed and built a model to predict if a given set of symptoms lead to breast cancer. Figure 5 illustrates the model accuracy. Using ANN model, the model accuracy was 98%.

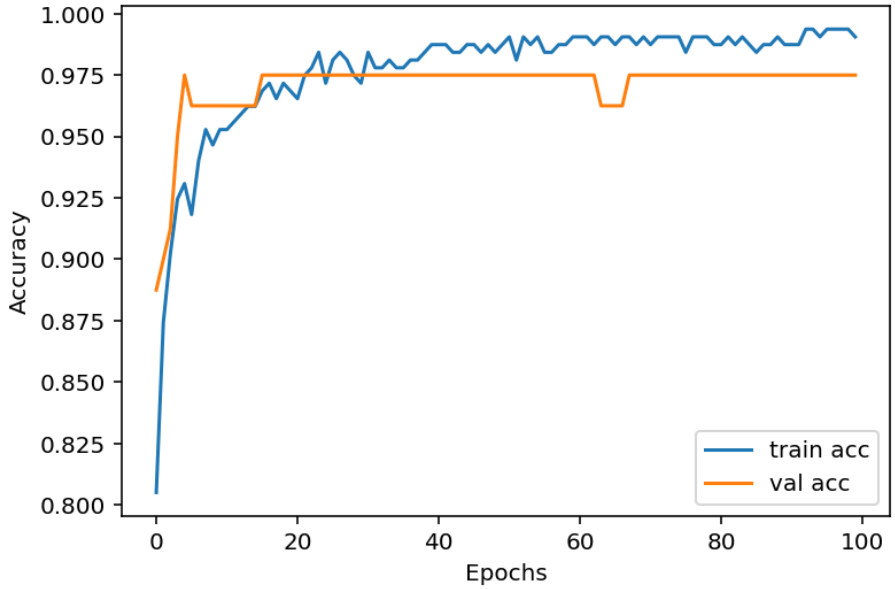

Figure 5. Model Accuracy

Recall measures a model's capability to identify all relevant data points within a dataset (Conciatori et al., 2024) while precision reflects a model's ability to correctly classify only the pertinent data points (Conciatori et al., 2024). In the equations below, TP_m represents *true positives* which occur when both the model's predicted value and the actual value are positive meaning the model correctly identified a positive case (Sharma et al., 2022). TN_m represents *true negatives* which occur when both the model's predicted value and the actual value are negative meaning the model correctly identified a negative case. FP_m represents *false positives* which occur when the model predicts a positive value while the actual value is negative. FN_m represents *false negatives* which occur when the model predicts a negative value while the actual value is positive (Sharma et al., 2022).

$$\text{Recall: } \frac{1}{n}\sum_{m=1}^{n}\frac{TP_m+TN_m}{TP_m+FN_m}$$

$$\text{Precision: } \frac{1}{n}\sum_{m=1}^{n}\frac{TP_m+TN_m}{TP_m+FP_m}$$

n = number of classes, $m \in \{1, 2, ...n\}$ = class index.

In this study, the ANN model demonstrated both high recall and high precision, highlighting its effectiveness in accurately extracting relevant malignant and benign cases, as illustrated in Figure 6. The elevated recall and precision values highlight the model's overall efficiency.

	Benign-Recall	**Benign-Precision**	**Malignant-Recall**	**Malignant-Precision**
Dataset 1 (Wisconsin Original Breast Cancer Dataset)	97%	99%	98%	97%
Dataset 2 (Wisconsin Diagnostic Breast Cancer Dataset)	98%	97%	98%	99%

Figure 6. Comparison of Recall and Precision for the ANN model built on the two breast cancer datasets in this study

Conclusion and Future Research

The survival rate, or survivability, of a particular disease can be determined by analyzing relevant data. This study explores the challenges and methodologies involved in predicting breast cancer survivability using Machine Learning techniques. Specifically, an Artificial Neural Network model was employed to predict whether a cell in a breast tumor is malignant.

Artificial Neural Networks have been widely applied to pattern recognition and classification tasks in medical imaging (Mehdy et al., 2017). They offer several advantages for information classification, including minimal requirement for formal statistical training and the ability to model complex interactions among predictor variables. ANNs can be developed relatively quickly and can handle both categorical and quantitative data.

Our study shows that the results are promising for the application of ANN models into the survivability prediction problem in cancer. Specifically, our model achieved high precision and recall when applied to the Wisconsin breast cancer datasets. Nevertheless, we recognize that the role of machine learning in breast cancer prediction warrants further exploration through broader applications of Artificial Intelligence (AI). Future research could involve evaluating additional breast cancer datasets using the model developed in this study.

AI-based diagnostic systems are revolutionizing cancer care by enabling early detection, improving treatment outcomes, and reducing the need for invasive procedures. For example, AI can assist physicians by predicting whether breast tissue is benign or malignant, potentially preventing unnecessary biopsies (Conner, 2024). With its ability to detect patterns and support decision-making, AI is particularly valuable for analyzing medical images such as mammograms. By learning from previous images, AI can identify anomalies and outliers that may indicate the presence of breast cancer. Due to its versatility and ability to detect patterns in both images and data, AI is a great tool to use. Additionally, AI can be used to create intelligent healthcare systems to improve patient outcomes (Saharan et al., 2025).

Future research should explore leveraging AI to integrate individual genetic information with cancer data to develop personalized treatment strategies. AI can also facilitate continuous monitoring of breast cancer progression in patients (AlSamhori et al., 2024). Longitudinal studies may further enhance the accuracy and precision of machine learning models for cancer prediction. Moreover, the application of advanced AI techniques and diverse AI models holds promises for improving breast cancer detection in the future.

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