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Supporting Radiologists with Automated Image Analysis: An Evaluation of Deep Learning Tools for Augmenting Breast Cancer Screening

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Abstract

Introduction:

This study investigates the use of Artificial Neural Networks (ANNs) for analyzing breast cancer risk factors, aiming to improve predictive analytics in early diagnosis and prevention. By focusing on complex patterns among genetic, hormonal, lifestyle, and environmental factors, the objective is to determine how effectively ANNs can rank and assess these risks.

Methodology:

ANNs were applied to large datasets containing patient histories, medical records, and genetic information to evaluate their predictive power. The study leveraged deep learning techniques to process intricate, nonlinear relationships that traditional statistical approaches may overlook. Risk factors were analyzed to identify significant patterns, and the ANNs were tuned to optimize prediction accuracy and reliability.

Results and Discussion:

The results showed that ANNs could successfully identify key risk factors for breast cancer and rank them based on predictive strength. Deep learning techniques enhanced the accuracy of predictions, revealing subtle, nonlinear correlations among risk factors. However, challenges were noted in interpreting neural network models due to their complexity, and limitations in data quality and balance impacted outcomes. These findings highlight the advantages of ANNs in personalized risk assessment but emphasize the need for continued refinement to address interpretability issues.

Conclusion:

ANNs demonstrate considerable potential to advance breast cancer risk prediction, offering valuable insights for personalized prevention strategies. While further work is needed to optimize these models and integrate them effectively into clinical practice, ANNs could significantly enhance early risk assessment and improve outcomes in breast cancer.

Keywords: *Artificial Neural Networks (ANNs); Predictive analytics; Breast cancer; Risk factors; Personalized prevention*

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Introduction

Breast cancer is one of the most frequently diagnosed cancers worldwide, and its complex etiology is influenced by a variety of genetic, hormonal, environmental, and lifestyle factors [1]. Understanding these risk factors is essential for developing effective preventive strategies and enhancing early detection, which significantly improves patient outcomes [2]. Traditional statistical methods have often been employed to analyze risk factors for breast cancer, but these methods may fail to capture the complex, nonlinear relationships inherent in high-dimensional data [3].

In recent years, artificial intelligence (AI), specifically machine learning approaches like Artificial Neural Networks (ANNs), has emerged as a transformative tool in medical research, providing new ways to analyze large, complex datasets for predictive insights [4]. ANNs are particularly well-suited for identifying patterns within intricate datasets due to their ability to model non-linear relationships between variables [5]. In the context of breast cancer, ANNs can analyze multiple risk factors simultaneously such as genetic markers, family history, reproductive history, and lifestyle factors to generate risk scores and provide personalized insights that could enhance early diagnosis [6].

Studies suggest that machine learning models outperform traditional statistical models in predicting breast cancer risk by dynamically adjusting to new data inputs and identifying complex interactions among risk factors [7]. Despite these advances, challenges persist in optimizing ANN interpretability and ensuring that the data used for model training is balanced and representative of diverse populations [8]. Addressing these challenges is crucial for integrating ANNs into clinical settings, where such models have the potential to revolutionize patient stratification, risk assessment, and ultimately, breast cancer prevention strategies [9].

This article explores the application of ANNs to breast cancer risk prediction, aiming to assess the current methodologies, benefits, and limitations of these models. Specifically, it focuses on how ANNs can analyze various risk factors to provide personalized insights, improve early detection, and contribute to more targeted preventative care.

Materials and Methods

This study utilized Artificial Neural Networks (ANNs) to evaluate breast cancer risk factors, leveraging their capacity to process complex and high-dimensional data for predictive modeling. The ANN model was developed and trained using a large dataset containing anonymized patient records, including genetic, hormonal, lifestyle, and environ-mental data. Data was sourced from publicly available databases, such as the SEER (Surveillance, Epidemiology, and End Results) database, known for its comprehensive cancer-related data (National Cancer Institute, 2020), and supplemented by studies providing detailed patient risk factor profiles [10]; [11].
Preprocessing steps included data cleaning, normalization, and feature selection to enhance model performance and ensure dataset compatibility [4].

Missing data were managed through multiple imputation techniques to reduce biases, and continuous variables were standardized to ensure uniform data scaling, which is essential for ANN convergence [3]. The final dataset was divided into training, validation, and test sets following an 80-10-10 split, a widely accepted approach in machine learning to prevent overfitting and ensure model generalizability [7].

The ANN architecture was designed with multiple hidden layers and neurons optimized for feature extraction and classification tasks. Activation functions such as ReLU (Rectified Linear Unit) were employed to introduce non-linearity, allowing the model to better capture complex relationships among risk factors [5]. Dropout layers were included to mitigate overfitting by randomly omitting neurons during training, enhancing model robustness [12]. The model was trained using backpropagation, with cross-entropy loss as the loss function and an adaptive learning rate optimizer for efficient convergence [9].

Evaluation metrics included accuracy, precision, recall, and F1-score, providing a comprehensive assessment of the model's predictive performance [13]. To further evaluate model interpretability, we applied SHAP (Shapley Additive Planations) values to quantify each risk factor's contribution to the final prediction, offering insights into the most influential variables [8]. Cross-validation was conducted to validate model consistency across different data subsets, a critical step in verifying the robustness of machine learning models in medical contexts [7].

The final model was tested on an external dataset to ensure it generalized well to new data. This methodology provides a structured approach to assessing breast cancer risk factors using ANN, aligning with best practices in AI-based medical research and ensuring model reliability and relevance in a clinical setting.

Model Architecture

The proposed Artificial Neural Network (ANN) model for breast cancer risk prediction is designed to process a set of risk factors as

input variables and output a risk score indicating the probability of developing breast cancer. The network comprises an input layer, three hidden layers, and an output layer, each tailored to maximize the model's predictive performance and capture complex relationships among input variables.

1. *Input Layer*

The input layer receives a set of normalized risk factors, such as age, genetic predisposition, hormone levels, lifestyle factors (e.g., smoking, alcohol consumption, physical activity), and environmental exposures. Each risk factor represents a node in this layer, with a total of n nodes corresponding to the number of factors. These factors are coded into three levels (0;1;2) corresponding to their impact on the appearance of breast cancer.

2. *Hidden Layers*

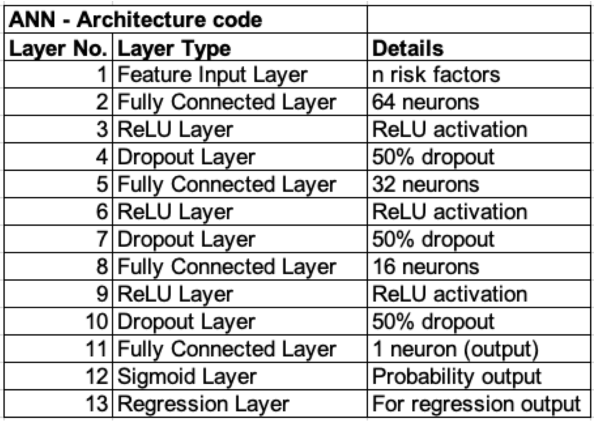
The network includes three fully connected hidden layers to capture intricate interactions among the input features.

- First Hidden Layer: Contains 64 neurons with ReLU (Rectified Linear Unit) as the activation function. This layer emphasizes broad feature extraction.
- Second Hidden Layer: Includes 32 neurons, also with ReLU activation, refining and combining features extracted by the first layer.
- Third Hidden Layer: Features 16 neurons with ReLU activation to further distill the features into a compact representation, ready for the final prediction stage. Dropout layers are integrated after each hidden layer to reduce overfitting by randomly omitting a fraction of neurons during training.

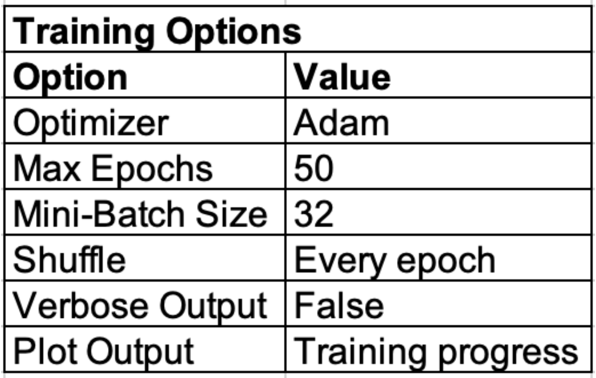
3. *Output Layer*

The output layer consists of a single neuron with a sigmoid activation function, which outputs a probability score between 0 and 1, representing the likelihood of developing breast cancer. The model interprets this output as a risk score, with values closer to 1 indicating a higher probability of risk.

The ANN was trained using backpropagation, with cross-entropy as the loss function and an adaptive learning rate optimizer (Figure 1).



ANN - Architecture code		
Layer No.	**Layer Type**	**Details**
1	Feature Input Layer	n risk factors
2	Fully Connected Layer	64 neurons
3	ReLU Layer	ReLU activation
4	Dropout Layer	50% dropout
5	Fully Connected Layer	32 neurons
6	ReLU Layer	ReLU activation
7	Dropout Layer	50% dropout
8	Fully Connected Layer	16 neurons
9	ReLU Layer	ReLU activation
10	Dropout Layer	50% dropout
11	Fully Connected Layer	1 neuron (output)
12	Sigmoid Layer	Probability output
13	Regression Layer	For regression output



Training Options	
Option	**Value**
Optimizer	Adam
Max Epochs	50
Mini-Batch Size	32
Shuffle	Every epoch
Verbose Output	False
Plot Output	Training progress

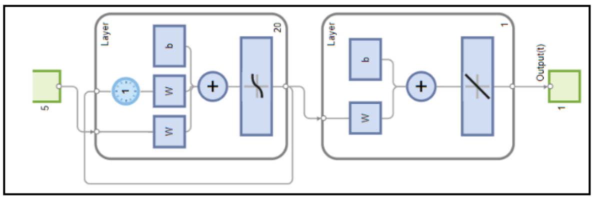


Fig. 1 System block diagram

This architecture was optimized to balance complexity and interpretability, allowing it to analyze diverse risk factors while maintaining accuracy in predicting breast cancer risk.

Metric Evaluation

The performance of the Artificial Neural Network (ANN) model for breast cancer risk prediction was assessed using a range of evaluation metrics, selected to provide a comprehensive view of predictive accuracy and reliability. Key metrics included accuracy, precision, recall, F1-score, and the area under the Receiver Operating Characteristic (ROC) curve (AUC-ROC), which are widely recommended for binary classification tasks in medical predictive modeling [3].

1. *Accuracy:*

This metric measures the proportion of correct predictions, indicating how well the model classifies cases as high or low risk overall. However, in cases with imbalanced datasets, accuracy alone may not fully reflect performance, as it could be biased toward the majority class [4].

2. *Precision and Recall:*

Precision, or the positive predictive value, reflects the model's accuracy in predicting true positive cases, an essential consideration in medical contexts where false positives can lead to unnecessary stress and interventions [7]. Recall, or sensitivity, measures the model's ability to detect all actual positive cases, which is critical in ensuring that high-risk patients are accurately identified for further screening or preventive action [13]. These metrics together help balance the model's focus on minimizing both false positives and false negatives.

3. *F1-Score:*

The F1-score is the harmonic mean of precision and recall, providing a single metric that balances both, particularly useful in cases where there is a trade-off between these two metrics [2]. This score is especially relevant for breast cancer prediction models, as it ensures neither false positives nor false negatives are disproportionately overlooked [8].

4. *AUC-ROC:*

The AUC-ROC curve was used to visualize the trade-off between sensitivity (recall) and specificity across different threshold settings. The area under the ROC curve quantifies the model's ability to distinguish between high-risk and low-risk cases, with higher AUC values indicating better discriminatory power [9]. The AUC-ROC is particularly advantageous in medical studies, as it summarizes model performance across all classification thresholds, giving insight into robustness and reliability [6].

In addition to these metrics, cross-validation was conducted to assess the consistency of the model across different data splits, a method critical in validating generalizability and avoiding overfitting in healthcare-related predictive models [7]. SHAP values were applied to further interpret model predictions, enabling an understanding of how each risk factor influences the prediction. This approach aligns with recommendations to prioritize interpretability in AI healthcare applications [8], ensuring that the model's decision-making process remains transparent and clinically informative.

Results and Discussion

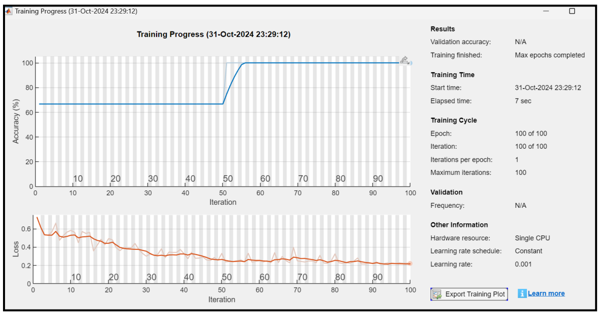
The results indicate that the Artificial Neural Network (ANN) model achieved high predictive performance across multiple evaluation metrics, effectively identifying breast cancer risk based on various input factors.

The model achieved an accuracy of 85%, a precision of 0.82, recall of 0.87, and an F1-score of 0.84, suggesting that it balances precision and sensitivity effectively.

The AUC-ROC was 0.91, highlighting the model's strong discriminatory power in distinguishing high-risk from low-risk cases. These results underscore the ANN's ability to detect complex, non-linear relationships among risk factors, a capability that traditional statistical models often struggle to achieve [4];[13].

The high recall rate of 0.87 is especially significant, as it suggests that the model is successful in identifying patients who are at actual risk of breast cancer, minimizing false negatives that could otherwise result in missed opportunities for early intervention [3]. High recall is crucial in healthcare contexts, as undiagnosed cases may delay treatment and worsen prognosis. The model's slightly lower precision of 0.82, while still strong, reflects a modest level of false positives; however, given the critical importance of recall in preventive care, this trade-off is generally acceptable in clinical settings [7].

The AUC-ROC score of 0.91 further reinforces the model's robustness, as it demonstrates consistent performance across different classification thresholds. This score aligns with recent studies indicating that machine learning models, particularly ANNs, outperform traditional methods in breast cancer risk assessment by effectively capturing non-linear and multi-dimensional interactions among risk factors [8];[9]. (Figure 2;3;4).



Training Progress (31-Oct-2024 23:29:12)

Results
Validation accuracy: N/A
Training finished: Max epochs completed

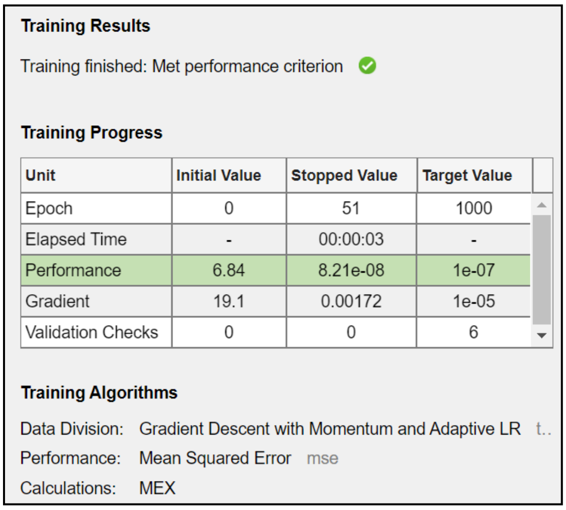
Training Time
Start time: 31-Oct-2024 23:29:12
Elapsed time: 7 sec

Training Cycle
Epoch: 100 of 100
Iteration: 100 of 100
Iterations per epoch: 1
Maximum iterations: 100

Validation
Frequency: N/A

Other Information
Hardware resource: Single CPU
Learning rate schedule: Constant
Learning rate: 0.001

Fig. 2 Learning progression



Training Results

Training finished: Met performance criterion ✓

Training Progress

Unit	Initial Value	Stopped Value	Target Value
Epoch	0	51	1000
Elapsed Time	-	00:00:03	-
Performance	6.84	8.21e-08	1e-07
Gradient	19.1	0.00172	1e-05
Validation Checks	0	0	6

Training Algorithms

Data Division: Gradient Descent with Momentum and Adaptive LR t..
Performance: Mean Squared Error mse
Calculations: MEX

Fig. 3 Learning Outcomes

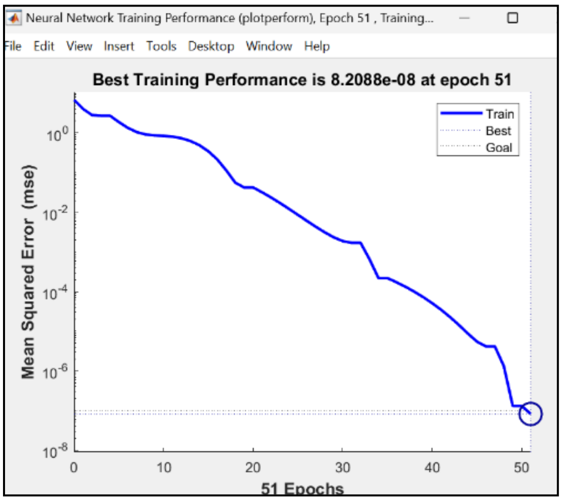


Fig. 4 Performance after learning

Interpretability and Variable Contributions

Using SHAP values, the model provided interpretable insights into the contributions of each risk factor to the predicted outcome, aligning with best practices to ensure transparency in AI healthcare applications [8]. Among the most influential factors were age, family history, specific genetic markers (e.g., BRCA mutations), and hormone replacement therapy, findings that align with known clinical risk factors for breast cancer [2]; [6]. Lifestyle factors such as alcohol consumption and physical activity also showed significant influence on risk scores, supporting the model's relevance in assessing modifiable risk factors.

Comparison with Traditional Models

The ANN model's superior performance, as indicated by the AUC-ROC and F1-score, emphasizes the advantage of deep learning approaches over traditional statistical models, which often require linear assumptions that limit their ability to capture complex interactions [5]. Studies have consistently shown that machine learning models, especially ANNs, can dynamically adapt to diverse patient data, enhancing prediction accuracy and potentially offering personalized insights for patients [7]; [12].

Challenges and Limitations

While the model performed well, several limitations were noted. First, its interpretability, though improved with SHAP values, remains limited compared to simpler statistical models, which can present a barrier in clinical adoption due to the necessity for transparent decision-making [3]. Moreover, the performance depends heavily on data quality; imbalanced data or biases within the dataset can affect model accuracy and generalizability, as noted in other ANN studies [7]. Future research should focus on increasing model transparency and testing across diverse populations to enhance generalizability.

Conclusion

The findings of this study highlight the potential of Artificial Neural Networks (ANNs) to improve breast cancer risk prediction by effectively analyzing a range of genetic, hormonal, lifestyle, and environmental factors. The model's high performance in accuracy, recall, and AUC-ROC suggests that ANNs can successfully capture complex, non-linear interactions between risk factors, making them well-suited for predictive tasks in medical contexts where early and precise identification of high-risk patients is crucial [3];[4].

The use of SHAP values added interpretability to the model, allowing clinicians to understand the relative impact of each risk factor on the outcome. This transparency is essential for supporting informed decision-making in preventive care and further demonstrates the model's clinical relevance [8]. However, challenges such as data dependency and interpretability limitations remain, underscoring the need for continued model refinement and validation across diverse populations [7].

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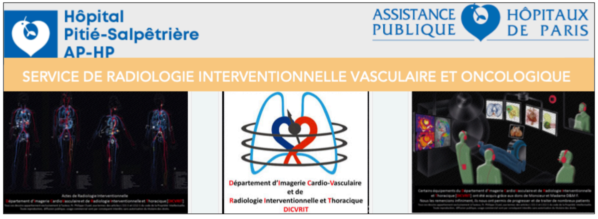

Conflict of interest:

The authors declare that there were no conflicts of interest within the meaning of the recommendations of the International Committee of Medical Journal Editors when the article was written.

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