



Exploratory classification of breast cancer status using anthropometric and physiological parameters: A logistic regression pilot study

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Abstract

Context: Breast cancer is a major global health problem, and early identification of individuals requiring further clinical assessment remains important. Anthropometric and physiological measurements are inexpensive and readily obtainable, but their ability to distinguish malignant from benign breast conditions is uncertain.

Objective: This pilot study evaluated the exploratory classification performance of anthropometric and physiological variables in distinguishing breast-cancer status using logistic regression.

Materials and Methods: A hospital-based observational pilot study was conducted at the University of Benin Teaching Hospital. Data from 20 participants were analysed. The recorded variables were age, weight, height, systolic blood pressure, diastolic blood pressure, and body-surface temperature. Missing values were replaced using column means, and the predictors were standardized before model fitting. The dataset was divided into training and testing subsets using an 80:20 split. Classification performance was assessed using accuracy, precision, recall, F1 score, confusion-matrix analysis, and the area under the receiver-operating-characteristic curve.

Results: The test set contained four participants. The logistic-regression model achieved an accuracy of 75.0%. For the benign class, precision was 1.00, recall was 0.50, and the F1 score was 0.67. For the malignant class, precision was 0.67, recall was 1.00, and the F1 score was 0.80. The ROC-AUC was 0.50, indicating no demonstrated discrimination beyond chance in this test set. Because the model was evaluated on only four participants, these performance estimates are highly unstable and should not be interpreted as definitive.

Conclusion: In this small pilot dataset, age, weight, height, blood pressure, and body-surface temperature alone did not demonstrate adequate discriminatory performance for breast-cancer classification. Larger, independently validated datasets incorporating clinical, imaging, pathological, and possibly molecular variables are required before such a model can be considered for clinical risk stratification.

Keywords: Breast cancer; exploratory classification; logistic regression; anthropometric parameters; physiological parameters; machine learning.

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Introduction

Cancer is a major global health burden, responsible for nearly one in six deaths worldwide^{1,2,3}. Early prediction and detection are crucial in improving survival rates, as they allow for timely interventions and targeted treatments.⁴ Breast cancer is a prevalent global health issue, causing high incidence and mortality rates, particularly among women. Breast

cancer accounts for 24.5% of newly diagnosed cancer cases worldwide.⁵ Early detection is crucial for reducing mortality. The focus has shifted from treatment-based methods to preventative and predictive methods, emphasising the need for reliable tools to identify individuals at higher risk of developing breast cancer^{7,8}.

Research is exploring the role of anthropometric parameters like Body Mass Index (BMI), Waist-to-Hip Ratio (WHR), and body fat percentage as risk indicators for breast cancer.⁹ Excess body weight has been linked to increased risk, especially among postmenopausal women.¹⁰ Anthropometric measurements, which are easy and cost-effective, could supplement traditional risk assessment tools and improve early detection efforts¹¹. Despite other predictive factors like genetics, environment, and lifestyle, the relationship between body composition metrics and cancer risk has gained more attention^{12,9}.

Researchers are exploring the use of machine learning algorithms to enhance cancer prediction accuracy. These models, which utilise large datasets and complex patterns, offer a promising approach in oncology^{13,14}. Python, a widely used programming language, has become important in health care research due to its extensive library ecosystem, including data processing tools like Pandas and Numpy^{15,16}. This study aimed to conduct an exploratory assessment of whether routinely obtainable anthropometric and physiological parameters—age, weight, height, systolic blood pressure, diastolic blood pressure, and body-surface temperature—could distinguish breast-cancer status in a small hospital-based dataset using logistic regression.

Literature review

Existing Models for Breast Cancer Prediction

Breast cancer prediction models have evolved significantly over the years, transitioning from traditional statistical methods to more advanced machine learning (ML) approaches. Early models predominantly utilised logistic regression and Cox proportional hazards models, focusing on clinical and genetic risk factors such as age, family history, and BRCA gene mutations.¹⁷ While these models provided valuable insights, they often lacked sensitivity for early-stage predictions and failed to account for non-linear relationships in data.

Recent advancements in ML have introduced more sophisticated algorithms for cancer prediction,

including support vector machines (SVM), random forests, and artificial neural networks. For instance, Murtaza et al. (2020)¹⁸ demonstrated the effectiveness of a deep learning model in predicting breast cancer from mammographic images, achieving higher accuracy compared to traditional methods. However, these models primarily rely on imaging and genetic data, which can be expensive and inaccessible in resource-limited settings.

Anthropometric Parameters and Breast Cancer Risk
Anthropometric parameters, including body mass index (BMI), waist-to-hip ratio (WHR), and body fat percentage, have been extensively researched for their possible association with breast cancer risk. Epidemiological studies indicate that obesity, especially in postmenopausal women, correlates with an elevated risk of breast cancer attributable to increased circulating oestrogen and inflammatory markers¹⁰. Waist-to-hip ratio (WHR), an indicator of central obesity, has been recognised as a substantial predictor of breast cancer risk¹¹. Notwithstanding these results, the majority of prediction models fail to include anthropometric data fully, underscoring a potential area for improvement.

Machine Learning and Python in Cancer Prediction
Machine learning (ML) has gained popularity in healthcare due to its ability to analyse large, complex datasets and uncover patterns. Python, with its robust library ecosystem, is a preferred tool for ML applications in cancer research. Libraries like Scikit-learn, TensorFlow, and Keras enable efficient development, training, and optimisation of predictive models¹⁹. Numerous machine learning algorithms, including Support Vector Machine (SVM), Random Forest, Logistic Regression, Decision Tree (C4.5), and K-Nearest Neighbours (KNN Network), are available for breast cancer prediction and diagnosis. Researchers have used various datasets, such as the SEER dataset, mammogram images, the Wisconsin dataset, and hospital datasets, to extract and select features for their research²⁰.

Nayak and Gobe (2017)²¹ showed the use of multiple supervised machine learning algorithms for breast cancer classification using 3D pictures and concluded that SVM exhibited the highest overall performance. Conversely, Gayathri and Sumathi (2016)²² conducted a comparative study on the Relevance Vector Machine (RVM), highlighting its low computational cost relative to other machine learning techniques employed in breast cancer detection. They elucidated how RVM surpasses other

algorithms in diagnosing breast cancer, even with a reduction in variables, achieving an accuracy of 97%. Asri et al. (2016)²³ found that the Support Vector Machine (SVM) is effective in breast cancer prediction and detection, achieving optimal performance characterised by precision and a low error rate, with an accuracy of 97.13%. Similarly, Naji et al. (2021)²⁰ employed a Python-based environment and the Scikit-learn module on five machine learning methods, including Support Vector Machine (SVM), Random Forest, Logistic Regression, Decision Tree (C4.5) and K-Nearest Neighbours (KNN), on the Breast Cancer Wisconsin Diagnostic dataset. It was noticed that the support vector machine beat all other classifiers and obtained the greatest accuracy of 97.2%.

Our study is focused on examining the logistic regression machine learning algorithm for breast cancer prediction and detection.

Materials and methods

Study Design and Setting: This was a hospital-based observational pilot study conducted at the Department of Radiotherapy, University of Benin Teaching Hospital (UBTH), Benin City, Nigeria. Ethical approval was obtained from the UBTH Ethics and Research Committee, and all participants provided written informed consent prior to participation.

Participants: A total of 20 subjects (2 males and 18 females) were recruited using convenience sampling from patients attending the radiotherapy clinic. Inclusion criteria were: (i) confirmed diagnosis of breast cancer or benign breast lesion based on clinical and histopathological findings and (ii) age ≥ 18 years. Exclusion criteria were: (i) presence of other malignancies, (ii) active infection or fever at the time of measurement, and (iii) inability to provide informed consent.

Anthropometric Parameters: To achieve the aim of this study, data was collected from breast cancer patients at the University of Benin Teaching Hospital (UBTH) using their anthropometric and physiological parameters, including weight, height, temperature, and blood pressure. These measurements were obtained using an infrared (IR) camera, a digital blood pressure monitor, and a stadiometer. A total of 20 subjects, consisting of two (2) males and eighteen (18) females, were randomly

selected from the Department of Radiotherapy at UBTH. Informed consent was obtained from all participants through a voluntary consent form. Each patient was examined by a clinician and diagnosed based on clinical findings. The study was approved by the University Teaching Hospital's Ethics and Research Committee. A summary of these parameters is presented in Table 1.

Table 1: Anthropometric and Physiological Parameters for Breast Cancer Patients at UBTH

Type of cancer	Freq. (%)	Tsk (°C)	Sex	Age (yrs)	Weight (kg)	Height ($\times 10^{-2}$) m	Systolic/Diastolic blood pressure (mmHg)
Breast	20(100)	35.20	M(2)	49	62.0	1.84	119/76
		35.00	F(18)	51	80.0	1.66	121/67
		33.10		54	71.0	1.67	141/97
		35.30		48	57.0	1.68	120/79
		34.90		52	65.0	1.73	125/79
		33.50		60	86.0	1.41	110/75
		34.50		50	85.0	1.66	139/93
		34.70		67	62.0	1.56	116/76
		34.30		70	72.0	1.64	122/81
		35.50		48	71.0	1.72	111/81
		34.50		51	73.0	1.64	135/89
		31.40		66	60.0	1.70	130/90
		32.10		51	70.0	1.64	136/91
		34.10		50	74.0	1.64	120/71
		34.70		55	100.0	1.66	100/71
		34.90		55	52.0	1.55	123/75
		35.00		34	78.0	1.68	112/70
		36.60		38	86.0	1.60	86/68
		34.40		82	76.0	1.62	126/74
		35.40		51	70.0	1.58	123/83

Machine Learning Algorithm: This study utilised the logistic regression model, a powerful modelling tool that assesses the likelihood of a disease or health condition based on risk factors and covariates²⁴. It assesses the association between an independent variable (X_i) and a dichotomous dependent variable (Y), primarily used for predicting binary or multiclass dependent variables²⁰. It computes the probability of the positive class (i.e., presence of breast cancer) given the input features. The equation for logistic regression is given by:

$$P(y=1|X)=1/e^{-(w_0+w_1x_1+w_2x_2+\dots)}$$

where

$P(y=1 | X)$ is the probability of having breast cancer.

$w_0, w_1, \dots$, are the learned coefficients.

$x_1, x_2, \dots$, are the input anthropometric parameters (e.g., age, weight, blood pressure).

e is the base of the natural logarithm.

Experiment Environment: The Scikit-learn python

packages were used to perform the experiment on the classifier presented in this article. Scikit-learn is a set of data mining, machine learning and deep learning algorithms used for classification, regression, data pre-processing and clustering^{19,25}. The sklearn libraries were used to construct machine learning algorithms for numerous real-world problems. Developers and practitioners may design and assess acceptable models using this framework. The experiment undertaken in this environment is conducted in ANACONDA. It has many apps, and we have selected Spyder, which is a development environment that supports python^{25,16}. It is a strong IDE for python compared to others. It also offers introspection characteristics. Since our issue could demand such functionalities, and also debugging is simpler in this platform, it is chosen.

Results

Data Preparation and Model Implementation

A dataset was collected from 20 patients at the University of Benin Teaching Hospital, of which 18 were females and 2 were males. Variables collected were the patients' age, weight, height, systolic and diastolic blood pressure, and body surface temperature, as shown in Table 1. Missing data were replaced by the column mean, and all the data was normalised by StandardScaler. For the testing and training split, 80% was for testing, and 20% was for the test set. For classification, the logistic regression algorithm was implemented for breast cancer classification, which was 0 for benign and 1 for malignant.

Since the sample size is limited, model evaluation aims to be exploratory, demonstrating its feasibility rather than its ultimate predictive capabilities.

Exploratory Data Analysis:

Figure 1 illustrates the relationships between the various linear measurements that come in pairs. From the kernel density plots, it can be observed that there is considerable overlap between the benign and the malignant ones. This suggests that not any one feature can distinguish between the two distinct groups. The bivariate scatter plots reflect this, as well, showing the typical physiological correlations for weight versus height, systolic versus diastolic blood pressure, etc. The implications of these findings are that, although no individual characteristic is particularly indicative, the interplay of several characteristics may contain predictive clues not

necessarily evident when viewed one characteristic at a time.

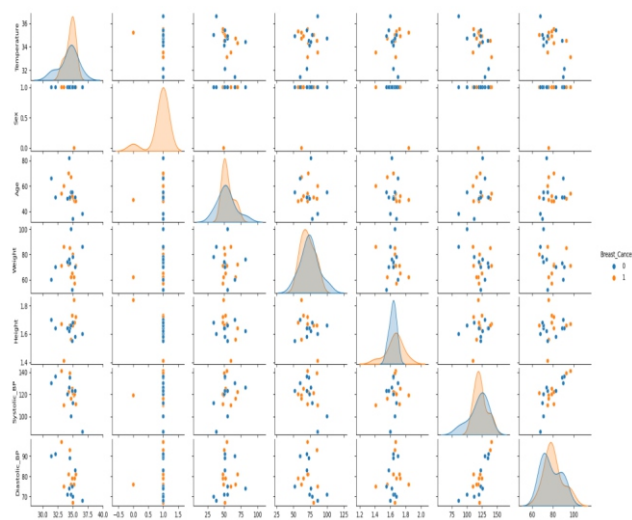


Figure 1: Pairwise distributions of anthropometric (age, weight, height) and physiological (systolic BP, diastolic BP, body temperature) parameters for benign (blue) and malignant (red) breast cancer cases.

Model Accuracy and Confusion Matrix Analysis

The logistic regression model attained a test accuracy of 75% (95% CI: 19.4–99.4%). However, the ROC AUC value was 0.50 (95% CI: 0.00–1.00), indicating no discriminative ability beyond chance. The confusion matrix presented in Table 2 and Figure 2 shows that for benign cases (n=2), precision was 1.00 and recall was 0.50, while for malignant cases (n=2), precision was 0.67 and recall was 1.00. The F1 scores were 0.67 and 0.80 for benign and malignant classes, respectively. Due to the very small test set size (n=4), these metrics should be interpreted with caution and are presented primarily to demonstrate feasibility.

Table 2: Classification Metric for the Logistic Regression Model

	Precision	Recall	F1 Score	Support
0	1.00	0.50	0.67	2
1	0.67	1.00	0.80	2
Accuracy			0.75	4
Macro average	0.83	0.75	0.73	4
Weighted Average	0.83	0.75	0.73	4

The confusion matrix indicates an imbalanced performance. The precision in the case of benign instances was 1.0, but the benign instances were recalled only to the extent of 0.5, implying that only half the instances were correctly picked, and the

remaining were indicated to be malignant by mistake, as shown in Figure 3. Malignant instances attained a recall value of 1.0, and precision fell to 0.67, which indicates a tendency to predict more instances as malignant.

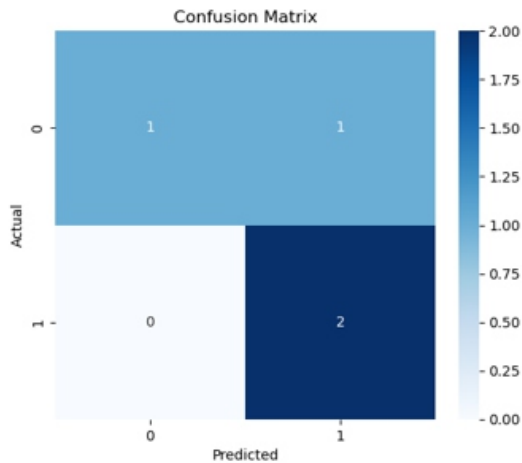


Figure 2: Confusion matrix for logistic regression model on pilot dataset (4 test samples). True positives and negatives, as well as false classifications, are shown

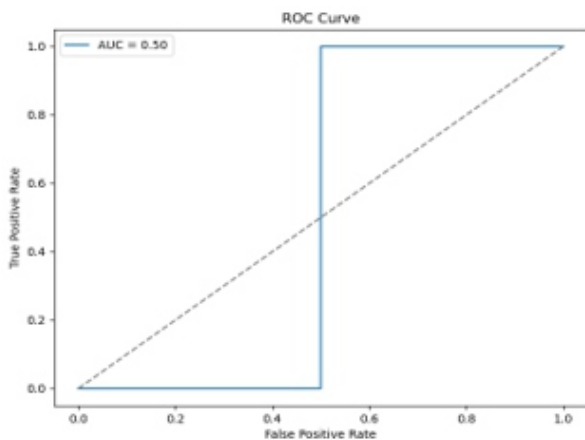


Figure 3: Receiver Operating Characteristic (ROC) curve for logistic regression model. The area under the curve (AUC = 0.5) indicates limited discriminative power.

Discussion

The finding that the logistic regression model achieved an accuracy of 75% but an AUC of 0.50 highlights an important distinction between accuracy and discriminative ability. While the model correctly classified 75% of cases in this small test set, the AUC of 0.50 indicates that the model's ability to distinguish between benign and malignant cases was no better than random chance. This is likely

attributable to the substantial overlap in the distributions of individual anthropometric and physiological variables between the two groups, as shown in Figure 1. These results are consistent with the findings of McCowan et al. (2011)²⁶, who reported that while individual clinical variables may have overlapping distributions, combinations of variables can provide useful predictive information. However, our study extends this observation by demonstrating that even combined anthropometric and physiological variables may lack sufficient discriminative power when used in isolation, particularly in a small sample. Further evidence on the effectiveness of multivariate correlations can be seen in Ding et al. (2023)²⁸, who found the combination of physiological variables such as heart rate variability and biomarkers in the serum to be beneficial in improving the discriminative power of models. Along similar lines, the importance of using models based on Gaussian processes with multiple variables related to human physiology, such as anthropometrics, was stressed in the study conducted by Tonmoy et al. (2021)²⁹. Though the model reached a moderate level of accuracy at 75%, the logistic regression model that was used in this pilot study had an imbalanced level of classification, especially among benign samples. This was reflected in the level of overclassification among the malignant samples, and this is an indicator that the model is limited due to the use of a small number of samples. The model used only 20 samples and had only 4 samples in the test data, and this affects the measures of accuracy.

In general, the results indicate that although anthropometric and physiological measures are feasible and relatively inexpensive variables potentially useful in initial breast cancer risk stratification, they are not very informative alone for predictive purposes. Future studies should aim at expanding the set of data to include more subjects and incorporating more variables, such as histopathological, imaging, or molecular information. More advanced machine learning algorithms such as Random Forest Classifiers, Support Vector Machines, and Neural Networks should also be investigated to more accurately model complex relationships, as these types of models would greatly benefit initial breast cancer screening in resource-limited settings.

Conclusion

In this study, the viability of using a logistic

regression model with anthropometric/physiological variables for the prediction of breast cancer was examined. Although the model had a fair accuracy of 75% in its predictions, its discriminatory power was not strong, with an ROC-AUC score of 0.5, reflecting no better than random predictions. There was much overlap in variables such as age, weight, blood pressure, and temperature, emphasising the poor discriminatory power of individual variables. The interaction variables indicated some potential in improving the predictions but not enough for the pilot study. The confusion matrix, classification metrics, and the trade-off between sensitivity and specificity showed the superiority of the model in predicting malignant samples over benign samples. These results emphasise the limitations of linear models with small sample sizes in accurately predicting the outcome of breast cancer. In general, the findings show that more complex models involving more factors and interactions are required to increase the discriminative ability. Future work should focus on using more comprehensive parameters, including clinical and imaging factors, and more complex machine learning models to improve the accuracy and reliability of models used in predicting breast cancer.

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Statements and declarations

Consent for publication: Participants consented to the publication of anonymised data, with all information presented in aggregate to ensure privacy.

Availability of data and material: The data obtained and analysed are included within this work.

Competing Interest: The authors declare that they have no known competing financial interests or personal relationships that could appear to influence the work.

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investigation. Jude Oghenekome Omoriwhovo: Data curation, validation, software. Eki Crownbirth Ebipade: writing review and editing.

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