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From Traditional ML to Advanced Neural Networks: A Multidimensional Analysis and Systematic Evaluation of Classification Models for Breast Cancer Detection

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Abstract

Breast cancer is among the most common cancers in women worldwide and has notable international implications. Although the number of survival have upgraded due to medical advances, it is still considered as one of the leading causes of death. Artificial intelligence (AI), especially deep learning, is playing a key role in medicine, particularly in oncology, where early detection helps lessening mortality rate by allowing quicker action and more effective treatment. A comprehensive comparative analysis of machine learning and deep learning approaches for breast cancer prediction using the Wisconsin Diagnostic Breast Cancer (WDBC) dataset is presented by this study. 29 traditional machine learning algorithms and neural network architectures, evaluating their performance through multiple metrics including accuracy, precision, recall, F1-score, and ROC curves, has been evaluated. Our study shows that traditional machine learning methods, especially Logistic Regression reaches a higher ranking performance with 98.2% accuracy, outperforming deep learning perspective. The study provides insights into feature correlations, dimensionality reduction techniques, and model interpretability for clinical decision support systems.

Keyword: Machine Learning; Deep Learning; Neural Networks; Artificial Intelligence; Breast Cancer; Wisconsin Dataset; Medical Diagnosis

Introduction

Breast cancer is the second most common cancers among women worldwide. According to projections from the World Health Organization (WHO), the number of diagnosed cases of breast cancer is expected to increase by 38% to 3.2 million new cases per year by 2050 [1]. Meanwhile, the death rates associated with the disease could increase by 68% to 1.1 million deaths per year. Breast cancer statistics differ crucially around the world, reflecting differences in health care systems, screening programs, and risk factors. In 2022, there were approximately 2.2million new cases of breast cancer and more than 666,000 deaths from the disease in sub-Saharan Africa. Although the incidence of breast cancer in Africa is lower compared to other regions, the continent has one of the highest mortality rates. This situation is mainly due to late diagnosis and limited access to medical care. If left unaddressed, some 135,000 women in sub-Saharan Africa could die from breast cancer by 2040 [2]. According to the 2020 World Health Organization data, Madagascar had 629 deaths from breast cancer, representing 0. 38% of all deaths. The age-adjusted mortality rate is 8.32 per 100,000 women, ranking the country 173rd in the world [3]. In 2020, breast cancer was responsible for 23,242 deaths, or 1.41% of all deaths, in Russia. The age-adjusted mortality rate is 16.34 per 100,000 population, ranking Russia 98th in the world [4]. Breast cancer caused 48,671 deaths in 2020, in the United States, accounting for 1.94% of all deaths. The age-adjusted death rate is 15.93 per 100,000 population, ranking the country 105th in the world [5]. In France, breast cancer rates are particularly high. A group of 1,055 French women diagnosed before the age of 50 recently called for more research resources, particularly to better identify and address environmental risk factors such as exposure to pollutants and chemicals [6]. Although breast cancer incidence rates are among the highest in the world, there has been a marked reduction in mortality, with an annual decline of 2.1%, in Australia and New Zealand. This positive trend is attributed to effective screening programs and improved access to treatment [7]. Universal inconsistency in breast cancer incidence, highlighting the necessity to enhance screening programs and ameliorate access to care, particularly in the most affected regions, is emphasized by these statistics. Early detection and accurate diagnosis are evaluative factors that notable influence treatment result and the number of survival rates. Traditional diagnostic methods, while effective, can be instinctive and laborious, resulting in probable delay in treatment initiation. The primary objectives of this study are to:

1. Demonstrate a comprehensive exploratory data analysis of the Wisconsin dataset,
2. Assess and contrast the performance of 29 traditional machine learning algorithms,
3. Evaluate the efficacy of different neural network architectures,
4. Study characteristic importance and correlations for clinical interpretability,
5. Supply recommendations for practical implementation in clinical settings.

Current detection and diagnosis methods

Breast cancer detection and diagnosis methods rely on diverse complementary modalities, including mammography, ultrasound, MRI and biopsy. Each of these methods plays a crucial role in patientcare and helps to clarify the diagnosis in order to prescribe appropriate treatment.

Mammography, which is the most widely used imaging method for breast cancer screening, uses Xrays to provide detailed images of breast tissue. This enables early abnormalities, including microcalcifications, to be detected before symptoms appear. Noneheless, this method has weakness: it is less effective in women with dense breast tissue, where some lesions may be masked, and exposes patients to a low dose of ionizing radiation [8].

Breast ultrasound, uses ultrasound to examine breast tissue and is frequently requested inclusive of mammography, especially for young women or women with dense breast tissue. Its advantages include the absence of Xrays, making it safe, and its ability to distinguish benign cysts from solid masses, avoiding unnecessary biopsies. Notetheless , it does not always detect microcalcinates, which can be early signs of breast cancer [9].

Breast MRI is an advanced imaging technique that uses magnetic fields and radio waves to provide detailed images of the breast. It is specifically suggested to patients with high genetic risk (BRCA1/BRCA2mutations) to assess tumor spread before surgery or to monitor response to neoadjuvant treatment. Its benefits involve excellent sensitivity in detecting invasive cancers, especially in dense tissues. Nonetheless, it can generate false-positive results, requiring additional examinations, and remains more expensive and less accessible than mammography or ultrasound [10].

Breast biopsy is a standard test to confirm or rule out breast cancer after an abnormality is detected on imaging. It involves taking a sample of breast tissue for pathologic analysis. There are several types of biopsy: fine-needle biopsy (especially for cysts), micro biopsy (taking a few fragments), and macro biopsy (or vacuum biopsy), performed under the supervision of mammography, ultrasound, or MRI to obtain a larger sample [11].

All of these methods form a complementary arsenal for the detection and diagnosis of breast cancer. Mammography remains the gold standard for screening, while ultrasound and MRI allow for more accurate diagnoses based on patient characteristics. Finally, only biopsy can make a definitive diagnosis by determining the benign or malignant nature of the detected neoplasms. But in addition to these classical methods, several other technologies such as *tomosynthesis* [12], *scintimammography* or *Molecular Breast Imaging* (*MBI*) [13], *elastography* [14], *thermography* [15] and *liquid biopsy* [16] are being developed or used to improve breast cancer screening and diagnosis.

Related work in ML Models for tumor detection

Machine learning has appeared as an impressive tool in medical diagnosis, offering the potential to enhance diagnostic accuracy, reduce human error, and provide consistent results. The Wisconsin Diagnostic Breast Cancer dataset, introduced by Wolberg et al., has become a benchmark dataset for evaluating machine learning algorithms in breast cancer diagnosis. This dataset contains features computed from digitized images of fine needle aspirates (FNA) of breast masses, providing quantitative measurements that can be used to distinguish between malignant and benign cases. Numerous researchers have utilized the Wisconsin Breast Cancer dataset to develop and validate predictive models.

Traditional Machine Learning Approaches: The efficacy of traditional machine learning algorithms for breast cancer diagnosis has been presented by this study. Asri et al. [17] contrasted four machine learning techniques (SVM, Decision Trees, Naive Bayes, and k-NN) on the Wisconsin dataset, reporting accuracies ranging from 93.07% to 97.13%. Chaurasia and Pal [18] achieved 96.84% accuracy using a hybrid approach combining SVM with feature selection techniques.

Ensemble Methods: Ensemble learning has shown promising results in medical diagnosis. Ahmad et al. [19] proposed a hybrid ensemble method combining multiple classifiers, achieving 99.51% accuracy on the Wisconsin dataset. Due to their capacity to handle features interactions reduction overfitting, Random Forest and Gradient Boosting methods have been particularly promising.

Deep Learning Approaches: Recent studies have explored deep learning architectures for breast cancer prediction. Antropova et al. [20] used deep convolutional neural networks for mammographic mass classification, while Dhungel et al. [21] applied CNN architectures for automated massdetection. Nonetheless, the efficacy of deep learning on tabular medical data remains a subject to ongoing research.

Feature Analysis and Dimensionality Reduction: Some studies have concentrated on feature importance and dimensionality reduction techniques. PCA and t-SNE have been widely used for visualization and feature reduction in medical datasets. Osman and Bakar [22] demonstrated that proper feature selection could improve classification accuracy while reducing computational complexity.

Methodology

We have used the data from the Wisconsin Breast Cancer (WDBC) diagnostic dataset, which consist of 569 samples and 30 numerical features computed from digitized images of breast mass FNA samples. Each instance is labeled as either malignant (212 cases) or benign (357 cases).These features correspond to 10 properties of cell nucleus:

a) radius	f) texture
b) area	g) perimeter
c) smoothness	h) compactness
d) concavity	i) concave points
e) symmetry	j) fractal dimension

For each property, three types of indicators were selected: *mean, standard error* and *worst value (maximum value)*, hence a total of 30 features (fig.1). The main objective of this experiment is to identify the most effective machine learning model for classifying breast tumors (*benign* or *malignant*) from features obtained from fine needle aspiration (FNA) images. The performance criteria are mainly *accuracy*, *precision*, *recall*, and *F1 score*. In the preliminary analysis, the distribution of some features shows a clear separation between benign (green) and malignant (red) samples. This visual difference, shown in fig.2, indicates that the perimeter feature, with well-separated distributions, have a high discriminatory ability to distinguish benign tumors from malignant ones. Conversely, features like smoothness, whose distributions overlap to a greater extent, as seen in fig.3, are less informative for classification and cannot accurately confirm if the tumor is benign or malignant.

Out[6]:

	id	diagnosis	radius_mean	texture_mean	perimeter_mean	area_mean	smoothness_mean	compactness_mean	conc
0	842302	M	17.99	10.38	122.80	1001.0	0.11840	0.27760	
1	842517	M	20.57	17.77	132.90	1326.0	0.08474	0.07864	
2	84300903	M	19.69	21.25	130.00	1203.0	0.10960	0.15990	
3	84348301	M	11.42	20.38	77.58	386.1	0.14250	0.28390	
4	84358402	M	20.29	14.34	135.10	1297.0	0.10030	0.13280	
...	...	...	...	...	...	...	...	...	
564	926424	M	21.56	22.39	142.00	1479.0	0.11100	0.11590	
565	926682	M	20.13	28.25	131.20	1261.0	0.09780	0.10340	
566	926954	M	16.60	28.08	108.30	858.1	0.08455	0.10230	
567	927241	M	20.60	29.33	140.10	1265.0	0.11780	0.27700	
568	92751	B	7.76	24.54	47.92	181.0	0.05263	0.04362	

569 rows × 33 columns

Figure 1: Comparaison of features.

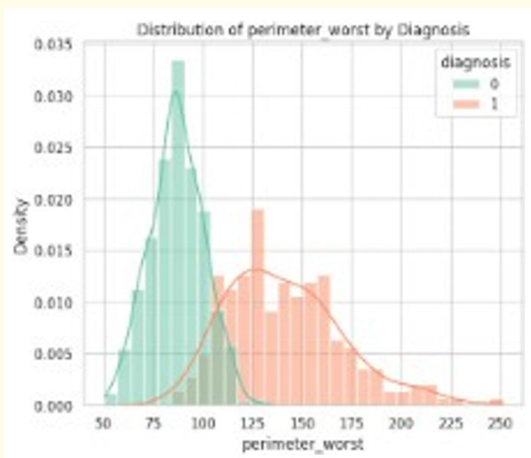

Figure 2: Distinct distribution.

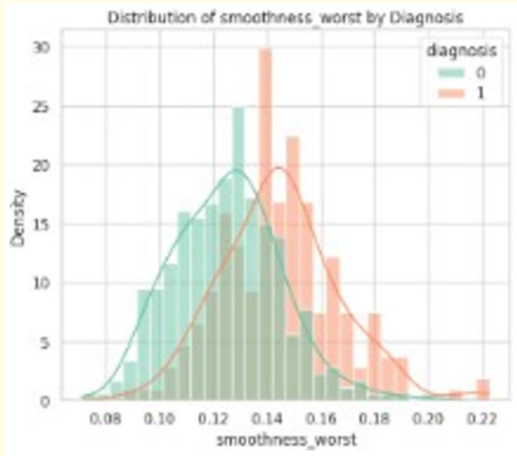

Figure 3: Convergent distribution.

In this experiment, a wide range of machine learning models were evaluated to compare their performance on tabular data. (fig.4) The selected models cover diverse families of algorithms involving linear, ensemble, Bayesian, principal, and semi-supervised to capture both linear and nonlinear relationships between cell morphological characteristics. This methodological diversity enable us to explore the strengths of each approach depending on the structure of the data, which is continuous, well-standardized, and relatively sparse. A total of 32 classification models were tested, covering a wide range of approaches:

Figure 4: Dimensionality Reduction.

Linear models: Logistic Regression, LinearSVC, Ridge classifier, SGD classifier, passive-aggressive classifier, perceptron.

Sets: Random Forest Classifier, Gradient Classifier, AdaBoost Classifier, Packing Classifier, ExtraResClassifier, Voting Classifier, Stacking Classifier

Bayesian methods: GaussianNB, BernoulliNB.

Distance methods: KNeighborsClassifier, NearestCentroid.

Basic methods: SVC, NuSVC.

Probabilistic methods: Gaussian Process classifier.

Discriminant methods: Linear Discriminant Analysis, Quadratic Discriminant Analysis.

Semi-supervised methods: LabelPropagation, LabelSpreading, SelfTrainingClassifier.

Others: DecisionTreeClassifier, MLPClassifier, Mock Classifier, OneVsRestClassifier, Onevsonclassifier.

The inclusion of base templates (such as DummyClassifier) and meta classifiers (such as Voting-Classifier) also helps to validate the relevance of the observed performance. This methodological choice ensures a complete and balanced comparison of models in a realistic biomedical analysis framework. It should be noted that 80% of the data used to train the models were already labeled indicating whether the tumors were benign or malignant. The remaining 20% was used for performance evaluation, where predictions were made by AI models. The results are presented below (fig. 5).

After training models on 80% of the annotated data and evaluating on the remaining 20%, the results show remarkable performance from several classifiers. The top five models, all with an F1 score of 0.987996, are: logistic regression, OneVsRestClassifier, OneVsOne-Classifier, LinearSVC, and the passive-aggressive classifier. This convergence of performance suggests that the WDBC data is particularly well suited to linear or maximum-margin models that can capture clear separations between classes.

Conversely, models with lower performance include GaussianNB, BernoulliNB, LabelPropagation, LabelSpreading, and DummyClassifier with F1 scores ranging from 0.928 to 0.540. These lower results can be explained by strong assumptions (such as independence of features for Bayesian models) or lack of directly supervised learning (in the case of semi-supervised and naive classifier models).

Out[97]:

	Model	Accuracy	Precision	Recall	F1 Score
0	LogisticRegression	0.988235	0.989796	0.986486	0.987996
26	SelfTrainingClassifier	0.988235	0.989796	0.986486	0.987996
18	LinearSVC	0.976471	0.976070	0.976070	0.976070
16	PassiveAggressiveClassifier	0.976471	0.980000	0.972973	0.975907
25	VotingClassifier	0.976471	0.980000	0.972973	0.975907
7	AdaBoostClassifier	0.964706	0.963046	0.965653	0.964211
23	Perceptron	0.964706	0.963046	0.965653	0.964211
22	OneVsRestClassifier	0.964706	0.965703	0.962556	0.963988
21	OneVsOneClassifier	0.964706	0.965703	0.962556	0.963988
24	StackingClassifier	0.964706	0.965703	0.962556	0.963988
1	RandomForestClassifier	0.964706	0.965703	0.962556	0.963988
4	GradientBoostingClassifier	0.964706	0.965703	0.962556	0.963988
10	HistGradientBoostingClassifier	0.964706	0.965703	0.962556	0.963988
9	ExtraTreesClassifier	0.964706	0.965703	0.962556	0.963988
2	SVC	0.964706	0.965703	0.962556	0.963988
15	SGDClassifier	0.952941	0.950669	0.955236	0.952408
13	QuadraticDiscriminantAnalysis	0.952941	0.950669	0.955236	0.952408
8	BaggingClassifier	0.952941	0.952140	0.952140	0.952140

Figure 5: Result.

Future Work

In the near future, this work will continue with multimodal analysis accepting tabular data and images as input. Indeed, in the field of breast cancer diagnostics, a large and diverse volume of medical imaging is generated by various methods such as digital mammography, breast tomosynthesis (3D mammography), scintimammography (MBI), Magnetic Resonance Imaging (MRI) and conventional X-ray. These images contain extensive clinical and morphological information about tumors (shape, density, margins, calcifications, etc.), which can be exploited by artificial intelligence approaches.

In this second step, convolutional neural network (CNN) models, which are specifically adequate for image analysis due to their ability to automatically extract complex spatial features at different levels of abstraction, will be used. Unlike traditional models applied to tabular data, CNNs enable us to preserve the two dimensional structure of an image and effectively exploit local relationships between pixels.

By using medical images directly, we hope to improve diagnostic sensitivity and accuracy while reducing bias associated with manual feature selection. Not only this perspective simplify early detection of breast cancer ,but also allow for the prediction of high risk cases, thereby facilitating more personalized treatment and better patient care. In the long term, this method could play a key role in accelerating clinical research and developing decision support tools for healthcare professionals.

Conclusion

Breast cancer is acknowledged as one of the leading causes of death in women worldwide, with a huge impact on health care systems and patients' quality of life. Although traditional screening methods such as mammography, ultrasound or MRI play a crucial role in detection, they still have limitations in terms of sensitivity, subjectivity and early detection. It is in this light that our study is conducted, exploring the contribution of artificial intelligence in addition to classical approaches to improve the accuracy and efficiency of diagnosis.

In this first phase of our study, we used the Wisconsin Breast Cancer Diagnostic Dataset to test and compare the performance of 32 supervised classification algorithms. These models were assessed according to their ability to distinguish benign from malignant tumors based on numerical features extracted from cytology images. The results demonstrated that several linear or maximum margin classifiers, such as logistic regression, LinearSVC, or even PassiveAggressiveClassifier, provide exceptional performance, achieving F1 scores close to 0.99. These results highlight the potential usefulness of these approaches for well structured and annotated data.

Preliminary feature distribution analysis also revealed highly discriminatory variables, confirming the value of certain morphological features for cancer detection. However, the tabular nature of this data remains an abstraction from the actual imaging data. That is why the second phase of this work will focus on the direct analysis of medical images mammograms, tomosynthesis, scintimammography, MRI or Xray, using convolutional neural network (CNN)type models. This move to raw data is intended to provide a more accurate representation of tumor characteristics and facilitate even earlier and automated detection, with the potential for deployment in clinical settings.

Hence, this research marks the first step towards the gradual integration of AI into breast cancer diagnostic chains, providing clinicians with additional tools to refine medical decisions, optimize response times and ultimately save lives.

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