Diagnosing Breast Cancer Using AI: A Comparison of Deep Learning and Traditional Machine Learning Methods

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Abstract:- Breast cancer remains a significant health concern globally, with early detection being crucial for effective treatment. In this study, we explore the predictive power of various diagnostic features in breast cancer using machine learning techniques. We analyzed a dataset comprising clinical measurements of mammograms from 569 patients, including mean radius, texture, perimeter, area, and smoothness, alongside the diagnosis outcome. Our methodology involves preprocessing steps such as handling missing values and removing duplicates, followed by a correlation analysis to identify and eliminate highly correlated features. Subsequently, we train eight machine learning models, including Logistic Regression (LR), K-Nearest Neighbors (K-NN), Linear Support Vector Machine (SVM), Kernel SVM, Naïve Bayes, Decision Trees Classifier (DTC), Random Forest Classifier (RFC), and Artificial Neural Networks (ANN), to predict the diagnosis based on the selected features. Through comprehensive evaluation metrics such as accuracy and confusion matrices, we assess the performance of each model. Our findings reveal promising results, with 6 out of 8 models achieving high accuracy (>90%), with ANN having the highest accuracy in diagnosing breast cancer based on the selected features. These results underscore the potential of machine learning algorithms in aiding early breast cancer diagnosis and highlight the importance of feature selection in improving predictive performance.

Keywords:- *Cancer, Breast Cancer, Machine Learning, Artificial Intelligence.*

I. INTRODUCTION

Healthcare systems globally are grappling with the significant challenge of achieving the ‘quadruple aim’ in healthcare (Arnetz et al., 2020): enhancing population health, improving patient care experience, enriching caregiver experience, and reducing escalating healthcare costs. Factors such as aging populations, the increasing prevalence of chronic diseases, and the rising costs of healthcare are challenges which compel governments, taxpayers, regulators, and providers to innovate and transform healthcare delivery models. The COVID-19 pandemic has further intensified these challenges, highlighting the need for healthcare systems to both deliver effective, high-quality care and to transform care at scale by utilizing real-world data-driven insights directly into patient care. Additionally, the pandemic has underscored existing workforce shortages and inequities in healthcare access, issues previously noted by The King's Fund and the World Health Organization (Bajwa et al., 2021; Mudgal et al., 2022)

Artificial intelligence (AI) has been a concept of interest since it was first introduced by computer scientist, John McCarthy in 1956, aiming to develop machines that replicate human intelligence (Siegel et al., 2023). Over the decades, AI has evolved significantly, finding applications across various industries, particularly in healthcare. The journey of AI in medicine began in the 1970s with clinical decision support systems (CDSS) that depended heavily on human-provided rules and manual selection of attributes for decision-tree techniques. Despite the initial enthusiasm, the technology faced several challenges, leading to a period known as the "AI winter," characterized by a decline in AI adoption due to unmet expectations. However, recent events surrounding the COVID-19 pandemic suggest that telemedicine will be vital in health care delivery in the future and AI might be a large player in this move (Iyengar et al., 2020).

Cancer represents a broad spectrum of diseases marked by uncontrolled cellular growth and potential spread throughout the body. Tumors arise from this unregulated growth, exhibiting six cancer hallmarks: uncontrolled cell division, resistance to growth suppression, evasion of programmed cell death, limitless replication, promotion of blood vessel formation, and tissue invasion (Brown et al., 2023). Symptoms of cancer vary depending on the type and location and typically appear only in advanced stages, often mimicking other diseases. Cancer becomes more severe and advanced in the occurrence of metastasis. Metastasis being the spread of cancer cells from the primary site to other body parts via local spread, the lymphatic system, or the bloodstream (Leong et al., 2022). The symptoms of metastatic cancer depend on the location of the tumor, with potential indicators including enlarged lymph nodes, liver, or spleen, bone pain or fractures, and neurological issues.

Most cancers, approximately 90 to 95%, are attributed to environmental factors, with the remaining 5 to 10% due to genetic inheritance (Anand et al., 2008). Common environmental factors contributing to cancer include obesity, tobacco use, dietary habits, radiation exposure, physical inactivity, and pollutants. Determining a single cause for cancer is often challenging due to these multiple contributing factors.

Breast cancer, the most diagnosed cancer worldwide, recorded 2.3 million new cases in 2020 with a mortality rate of almost 30%. 90-95% of cases are recorded in women and the future burden of breast cancer is predicted to exceed three million new cases and hit a mortality rate of 33.33% by the 2040 (Ahmad, 2019; Arnold et al., 2022). Effective prognosis of breast cancer is linked to early detection and treatment. Even though much research is going into improving the health outcomes for people diagnosed with breast cancer at more advanced stages, there is still a great deal of emphasis on timely and improved screening strategies (Ahmad, 2019).

Today, AI is gradually getting adopted into clinical training, research, and practice (Varghese, 2020; van Kooten et al., 2024). In clinical practice, AI tools are used to seamlessly organize patient data and health records to optimize physician care and departmental workflows. With the prevalence of AI on the rise, physicians will have to become familiar with the use of AI; understanding its benefits and limitations to apply it in their healthcare delivery. Very recently, a team of researchers developed a framework to incorporate AI training into radiology residency programs. The framework demonstrated the feasibility and effectiveness of integrating AI education into radiology training, which is essential for preparing future radiologists to utilize AI in clinical practice (van Kooten et al., 2024).

AI has also been particularly useful in medical image analysis. By leveraging on machine learning models, screening processes can be automated reducing strain on the physician and become more precise by reducing noise in the medical images (Rajpurkar et al., 2022). Consequently, the potential for the use of AI in healthcare for breast cancer is unquestionable, as effective treatment for breast cancer relies heavily on early detection which is possible by precise breast image analysis and interpretation.

This paper aims to make a comparison of the most reported machine learning models as they are used in the prediction of breast cancer. First, we report methods currently used in clinical diagnosis and the increasing contribution of AI. Furthermore, we discuss successes of AI particularly in breast cancer diagnosis amongst others and some challenges still faced by AI technology. We then employ eight machine learning models to analyze dimension quantities, such as size and texture of tumors, pulled from real-world medical image data and predict if the tumors are cancerous or not. We report the performance of each model using metrices such as accuracy, specificity, sensitivity and error to provide an overview of the applicability of AI in clinical decision making and diagnosis particularly in breast cancer. Finally, the discussion addresses the AI model we propose to be most effective for binary classification of breast cancer diagnoses.

II. REVIEW OF LITERATURES

A. Medical Diagnosis

Medical diagnosis is a complex process of identifying a disease or condition that explains a patient's symptoms and signs, often starting with the patient's medical history and physical examination, supplemented by various diagnostic tests. The challenge lies in the fact that many symptoms can overlap between different diseases, making accurate diagnosis difficult. Essentially, diagnosis aims to classify an individual's condition to guide treatment and prognosis, although it does not necessarily involve determining the underlying cause of the condition (Bolboacă, 2019).

Various methods are employed individually or in combination in diagnostic procedures to formulate a hypothesis concerning the cause of a disease and evaluate evidence to accept the hypothesis or reject it and reformulate a better explanation for the patient’s condition. According to (Langlois, 2002) there are four approaches: exhaustive, algorithmic, pattern recognition, and hypothetico-deductive diagnosis. However, another approach called differential diagnosis is also used. Furthermore, with the aid of various technological advancements, there is a development in a field called medical or clinical decision support systems (CDSS).

Differential diagnosis is an organized process used to single out a correct diagnoses from a list of possible competing diagnoses (Cook & Décary, 2020). This involves systematically ruling out potential diseases that could explain the patient's symptoms from a list through further tests. The process often narrows down the diagnosis to one probable disease or a ranked list of possible conditions, which can sometimes exclude life-threatening diseases. The approach is iterative and may involve multiple rounds of testing and hypothesis revision (Cook & Décary, 2020).

CDSS are computer programs designed to assist health professionals in making clinical decisions. They typically function as interactive tools where the clinician uses both their expertise and the system's suggestions to arrive at a diagnosis. These systems combine patient data with medical knowledge to provide case-specific advice, improving the accuracy of diagnoses. They are designed to enable clinicians to harness the vast quantities of data available, by offering a digital framework that combines evidence-based knowledge with individual patient details. This integration results in an improved and economically efficient healthcare delivery by offering recommendations and highlighting potential diagnostic errors (Asgari et al., 2019; Sutton et al., 2020).

Effective medical diagnosis requires the ability to limit the number of hypotheses under consideration and focus computational resources on evaluating these possibilities. Expert systems in CDSS use strategies from human experts to streamline this process. These systems must have a comprehensive knowledge base of possible diseases and be able to match patient data against this knowledge. The diagnostic process involves evaluating the likelihood of various diseases based on the patient's symptoms and iteratively gathering more information to refine the diagnosis. Advanced systems incorporate pathophysiological knowledge and consider the severity of the illness to enhance diagnostic accuracy (Sutton et al., 2020).

Another diagnostic method, pattern recognition, relies heavily on the clinician's expertise and experience to match a set of symptoms with known disease patterns. This method is effective for "obvious" diseases where the symptoms strongly suggest a specific diagnosis but has limitations when diseases present with similar symptoms (Dias & Torkamani, 2019).

B. *Breast Cancer*

(Giaquinto et al., 2022) provides a comprehensive update on female breast cancer statistics in the United States, highlighting critical trends in incidence, mortality, survival, and mammography screening. The data reveals that breast cancer incidence rates have increased over the past four decades, with a notable annual rise of 0.5% from 2010 to 2019, primarily driven by localized-stage and hormone receptor-positive disease. Contrarily, breast cancer mortality rates have seen a consistent decline since their peak in 1989, with a total reduction of 43% by 2020, translating to 460,000 fewer deaths.

However, the pace of this decline has slowed in recent years. The study also underscores significant racial disparities, with Black women experiencing higher mortality rates compared to White women, despite lower incidence rates. This disparity is particularly pronounced in younger women and across various molecular subtypes and stages of disease (Giaquinto et al., 2022).

(Smolarz et al., 2022) delve into the epidemiology, classification, pathogenesis, and treatment of breast cancer, presenting it as the most diagnosed malignancy in women worldwide and a leading cause of cancer-related death. They note that despite advancements in detection and treatment, the incidence of breast cancer continues to rise globally. Treatment strategies are highly dependent on the molecular subtype of the cancer, with systemic therapies including hormone therapy, chemotherapy, anti-HER2 therapy, and immunotherapy for specific subtypes. The review highlights triple-negative breast cancer (TNBC) as a particular area of concern due to its aggressive nature and poor response to treatment. Future therapeutic approaches aim to personalize treatment plans based on cancer biology and early responses to therapy, potentially improving outcomes (Smolarz et al., 2022).

(Britt et al., 2020) emphasize the need for effective breast cancer prevention strategies amidst rising incidence rates. They advocate for a dual approach: population-based strategies to reduce exposure to modifiable risk factors and precision-prevention strategies targeting women at increased risk. The authors highlight the existing capacity to estimate individual breast cancer risk using validated models, which are expected to improve with the inclusion of newer risk factors. Despite the availability of risk-reducing medications, widespread implementation faces challenges that need addressing to enhance adherence and effectiveness.

(Waks & Winer, 2019) provide a detailed review of current and evolving breast cancer treatment strategies, noting that breast cancer affects 12% of women in the United States. They categorize breast cancer into three major subtypes: hormone receptor-positive/ERBB2-negative, ERBB2-positive, and triple-negative. Treatment approaches could be local (as in Surgery and Radiation therapy) or systemic. These approaches, however, vary significantly by breast cancer subtype, with systemic therapies tailored to the molecular characteristics of the tumor. The review discusses an increasing trend of administering systemic therapy before surgery. For metastatic breast cancer, the treatment focuses on prolonging life and symptom palliation, with median survival varying significantly by subtype. The authors underscore the importance of individualized treatment plans to optimize patient outcomes.

C. *Artificial Intelligence and Medicine*

AI has been implemented in various industries to enhance productivity, efficiency, and accuracy (Prevedello et al., 2019). In the healthcare sector, AI is utilized in patient monitoring, drug dispensing, and hospital management. AI has also significantly impacted complex image analysis, providing quantitative assessment data through automation and eliminating radiation risks associated with breast radiological examinations (Marinovich et al., 2022; Prevedello et al., 2019).

AI has emerged as a transformative tool in cancer diagnosis treatment. The integration of automated AI capabilities in cancer imaging offers numerous potential applications in diagnosis, tracking and precise monitoring of multiple lesions in parallel to precise volumetric delineation of tumor size and interpreting intratumoral nuances. While manual segmentation methods suffer from inherent biases and inconsistencies due to varying experience level of physicians and fatigue, AI-driven approaches promise greater objectivity and reproducibility. Tumor characterization benefits from AI-based segmentation techniques, offering more accurate tumor delineation and aiding in subsequent diagnostic work and treatment planning.

Malara et al., (2024) developed a multicancer screening test utilizing circulating non-hematological proliferating atypical cells combined with AI to predict cancer risk. This non-invasive test aimed to detect cell abnormalities at a subclinical stage, thus improving early cancer diagnosis. The study reported an accuracy of 98.8%, with 100% sensitivity and 95% specificity. These results suggest that integrating innovative non-invasive methods with predictive models can significantly enhance cancer prevention and management. The study highlights the potential of AI-driven screening tests in assessing individual health statuses and early cancer detection.

Calderaro et al., (2024) explored the application of AI in liver cancer research and patient management. They highlighted that AI could analyze histopathology, radiology, and natural language to access hidden information in clinical data. Despite AI's rapid advancement and approval in some tumor types like colorectal cancer, its application in liver cancer has not yet been translated into large-scale clinical trials or approved products. The authors emphasized the need for integrating AI into all stages of liver cancer management, proposing a taxonomy of AI approaches with academic and commercial potential. They advocated for interdisciplinary training for researchers, clinicians, and patients to maximize AI's potential in liver cancer care.

The application of AI in cervical cancer diagnosis has seen substantial advancements, contributing to more accurate and efficient detection and classification of cervical cancer cells. (Sokouti et al., 2014) introduced a novel Levenberg-Marquardt feedforward MLP neural network (LMFFNN) model for classifying cervical cell images, achieving a 100% correct classification rate, thus aligning perfectly with medical experts' decisions. The model operates in two stages: initial noise reduction in images without compromising resolution, followed by the application of image processing algorithms to generate linear plots used as inputs for the LMFFNN. This semi-automated system displays the potential for AI in enhancing diagnostic accuracy.

Mat-Isa et al., (2008) developed an automated diagnostic system integrating automatic feature extraction and intelligent diagnosis, using a novel region-growing-based features extraction (RGBFE) algorithm to extract critical features from cervical cells. The system employs a hybrid multilayered perceptron (H2MLP) network to classify cells into normal, low-grade intra-epithelial squamous lesion (LSIL), and high-grade intra-epithelial squamous lesion (HSIL). With a strong linear relationship observed between the mean grey level and size as estimated by the system and expert cytotechnologists, the automated approach demonstrates a promising alternative to manual methods.

In radiotherapy, AI enables automated treatment planning and target delineation, improving treatment efficiency and accuracy. Deep learning algorithms integrated with radiomics facilitate predictive modeling of treatment response, guiding clinical decision-making. Furthermore, AI-driven algorithms in cervical and breast cancer screening reduce unnecessary treatments and improve biopsy targeting, enhancing patient outcomes.

D. Limitations of AI in Medical Diagnosis

Despite the advancements, the practical use of AI in medical imaging has been limited by the lack of large public databases. These databases will require massive volumes of properly labelled and annotated data such that machine learning models can be thereby trained. These activities are quite laborious and time consuming (Goyal & Shrivastava, 2021).

Another limitation of AI in medical diagnosis is in its ability to distinguish between correlation and causation, which can lead to sub-optimal and even dangerous diagnoses. Many existing machine learning approaches to diagnosis identify diseases that are strongly associated with the symptoms the patient presents making it purely associative (Richens et al., 2020). Thus, further research and activities such as competitions that improve machine learning models as well as medical algorithms are increasingly essential (Prevedello et al., 2019).

E. AI in Breast Cancer Diagnosis

Despite limitations, AI already has practical applications that are broadly beneficial in breast cancer diagnosis. Medical professionals and researchers have recognized this potential due to AI’s ability to handle complex and multi-dimensional data from various clinical experiments (Sun et al., 2022). The National Breast Cancer Foundation's 2020 report highlights the successful use of AI in diagnosing over 276,000 breast cancer cases (H. Liu et al., 2022). Convolutional neural networks (CNNs) have demonstrated the ability to match the detection capabilities of experienced radiologists, eliminating variability and accurately delineating lesion boundaries (Rodriguez-Ruiz et al., 2019; Goyal & Shrivastava, 2021; L. Liu et al., 2020).

Deep learning (DL) algorithms, in particular, have shown promising results in breast cancer image processing research (Burt et al., 2018; Sharma & Mehra, 2020). These algorithms can reduce false positives, enhance the detection of breast cancer's morphological characteristics, and if done preoperatively, can prevent unnecessary biopsies (Carriero et al., 2024; Sun et al., 2022). The data from mammograms and other breast imaging reports are used to train these algorithms. As a result, AI is also employed in classifying breast tumors as benign or malignant using ultrasonography.

Breast imaging is made possible by various technologies that are employed to provide a clearer picture of the breast’s anatomy. Chemical labeling of cancer cells with radioisotopes has also improved the accuracy and ease of getting mammograms as in scintimammography (Das et al., 2006). The imaging technologies associated with breast cancer diagnosis commonly employ X-ray technologies such as mammography (film-screen and digital), thermoacoustic computed tomography (CT) and positron emission tomography (PET). However, there are non-X-ray radiation technologies that do not use ionizing radiation such as Optical imaging, ultrasound, magnetic resonance imaging (MRI), thermography, electrical impedance imaging, optical imaging, electric potential measurement and microwave imaging, amongst others (Moore, 2001; Herranz & Ruibal, 2012). Compared to other imaging techniques, ultrasound offers advantages such as being non-ionizing, affordable, and providing detailed insights (Goyal & Shrivastava, 2021). These technologies can be used individually or in combination.

In examining breast cancer pathology and early detection, Zhang et al., (2021) review advancements in medical image processing as a vital tool for early breast cancer diagnosis. Their paper systematically explores methods for breast cancer detection through image segmentation, registration, and fusion, emphasizing the role of supervised, unsupervised, and deep learning, including Convolutional Neural Networks (CNN). These techniques have significantly enhanced the accuracy and efficiency of detecting potential breast cancer cases. Furthermore, the paper discusses the future prospects of unsupervised learning and transfer learning in breast cancer diagnosis, as well as the critical issue of privacy protection for patients undergoing these imaging processes (Zhang et al., 2021).

(Ng et al., 2023) conducted a study on the implementation of an AI system as an additional reader to enhance breast cancer screening. This research was carried out in three phases: a single-center pilot rollout, a multicenter pilot rollout, and a full live rollout. The AI system's performance was compared to standard double reading practices. The results indicated that the AI-assisted process could detect 0.7–1.6 additional cancer cases per 1,000 screenings, with minimal increases in recall rates and unnecessary recalls. Notably, most detected cancers were invasive and small-sized, suggesting the AI system's efficacy in early detection. The study concluded that the AI-assisted additional-reader workflow could improve early breast cancer detection while maintaining a high positive predictive value.

AI-based systems have shown tendency to have a superior diagnostic accuracy compared to conventional techniques, and this trend is expected to continue (Díaz et al., 2024). AI has been integrated into screening procedures to determine breast mass, density, and segmentation, and it has the potential to reduce the workload of radiologists (Parvathavarthini et al., 2019).

F. AI Techniques

Various AI techniques use machine learning (ML) models and deep learning (DL) models for breast cancer classification. ML models such as SVM, K-NN, genetic algorithms, Naïve Bayes have been employed, with SVM showing the highest accuracy (Ozcan et al., 2022; Rajaguru & S R, 2019). DL models are a more recent subtype of ML and they use neural network (NN) architectures (Díaz et al., 2024). Researchers have also explored the use of multiple imaging modalities, such as mammograms, ultrasound, MRI, and histopathological images, to improve diagnostic accuracy (Dileep et al., 2022; Shah et al., 2022).

III. RESEARCH DESIGN

A. Dataset Source

Our study dataset was sourced from the University of Wisconsin Hospitals in Madison, courtesy of Dr. William H. Wolberg. It encompasses diagnostic information compiled when 569 patients presented with abnormal growths detected through self-examination or mammography, or when minuscule calcium deposits were identified in x-rays. Upon discovery of these irregularities, medical professionals would proceed with a comprehensive diagnostic evaluation to ascertain the presence of cancer and assess if metastasis has occurred. It consists of clinical measurements collected from breast cancer patients, including features such as mean radius, texture, perimeter, area, and smoothness, along with the corresponding diagnosis outcomes (malignant or benign). This data is publicly available and was accessed as a comma separated values (.csv) file at https://www.kaggle.com/datasets/merishnasuwal/breast-cancer-prediction-dataset.

B. Data Processing

- **Handling Missing Values**: Any missing values in the dataset were handled using appropriate techniques such as imputation or removal based on the extent of missingness and the nature of the data.
- **Removing Duplicates**: Duplicate records, if any, were identified and removed to ensure data cleanliness and prevent bias in the analysis.
- **Feature Selection**: A correlation analysis was conducted to identify highly correlated features. Redundant or highly correlated features were either removed or selected based on their importance in predicting the diagnosis outcome.

C. Machine Learning Models

We employed seven traditional ML models (Logistic regression, K-Nearest Neighbors, Linear SVM, Kernel SVM, Naïve Bayes, Decision Trees Classifier, Random Forest Classifier) and one DL model (Artificial Neural Network) in our study. They are described below:

➢ *Logistic Regression (LR):*

LR is a binary classification algorithm that models the probability $P(y=1|x)$ of a binary outcome (e.g., malignant, or benign) based on one or more independent variables (diagnostic features). It uses the logistic function to estimate the probability of the outcome.

- Mathematically, the probability of the outcome is given by the logistic function:

$$P(y = 1 \mid \mathrm{x}) \frac{1}{1+e^{-(w^T+b)}} \tag{1}$$

Where:

- w is the weight vector,
- x is the vector of input features,
- b is the bias term.

➢ *K-Nearest Neighbors' Classifier (K-NN):*

K-NN is a non-parametric and instance-based learning algorithm that classifies data points based on the majority class of their neighboring data points. The class of a data point is determined by a majority vote among its k nearest neighbors, where k is a user-defined parameter.

- Mathematically, the class of a data point x is determined by:

$$y = mode\{y_i | x_i \in N_k(x)\} \tag{2}$$

Where:

- $N_k(x)$ represents the set of k nearest neighbors of x,
- y_i is the class label of the i-th nearest neighbor.

➢ *Linear Support Vector Machines (SVM):*

Linear SVM or SVM is a supervised learning algorithm that performs classification by finding the hyperplane that best separates the classes in the feature space. It aims to maximize the margin between the classes while minimizing the classification error.

- The decision boundary is represented by the hyperplane:

$$w^T x + b = 0 \tag{3}$$

Where:

- w is the weight vector
- b is the bias term

- The optimization problem of SVM is to maximize the margin $\frac{2}{\|w\|}$ subject to the constraints:

$$y_i(w^T x + b = 0) \geq 1, \forall i \tag{4}$$

➢ *Kernel SVM:*

Kernel SVM is an extension of linear SVM that allows for non-linear decision boundaries by transforming the input features into a higher-dimensional space using kernel function ϕ (e.g., polynomial, radial basis function) to make them separable. This allows for non-linear decision boundaries.

- The decision function becomes:

$$f(x) = \sum_{i=1}^{n} \propto_i y_i K(X_i, X) + b \tag{5}$$

Where:

- $\propto_i$ are the Lagrange Multipliers,
- $K(X_i, X) = \phi(X_i)^T$ ϕ(X) is the kernel function.

➢ *Naïve Bayes:*

Naïve Bayes is a probabilistic classifier based on Bayes' theorem with an assumption of independence among features. It calculates the posterior probability of each class given the input features and selects the class with the highest probability.

The posterior probability of each class given the input features is calculated as:

$$P(y|x_1, x_2, \ldots\ldots, x_n) = \frac{P(y)\prod_{i=1}^{n} P}{P(x_1, x_{2,\ldots\ldots,} x_n)} \tag{6}$$

Where:

- $P(y)$ is the prior probability of class y,
- $P(x_i|y)$ is the likelihood of feature $x_{1,}$ given class y
- $P(x_1, x_{2,\ldots\ldots,} x_n)$ is the marginal likelihood.

➢ *Decision Trees Classifier (DTC):*

DTC are hierarchical tree-like structures where each node represents a feature, each branch represents a decision based on that feature, and each leaf node represents a class label. They are constructed recursively by selecting the best feature to split the data at each node.

The decision at each node is based on selecting the feature that maximizes the information gain or minimizes the impurity (e.g., Gini impurity, entropy):

$$Information\ Gain = Entropy\ (S) - \sum_{i=1}^{k} \frac{|S_i|}{|S|} Entropy\ (S_i) \tag{7}$$

➢ *Random Forest Classifier (RFC):*

RFC is an ensemble learning method that constructs multiple decision trees during training and outputs the mode of the classes (classification) or the mean prediction (regression) of the individual trees.

$$\hat{y} = mode(\{T_1(x), T_2(x), \ldots, T_B(x)\}) \tag{8}$$

Where:

- $T_i\ is\ the\ i - th\ decision\ tree\ in\ the\ forest.$

➢ *Artificial Neural Networks (ANN):*

ANN is a computational model inspired by the structure and function of biological neural networks. It consists of interconnected nodes (neurons) organized in layers, including input, hidden, and output layers. The input layers receive the data, and the output layer returns the output data to the user, while the hidden layer conducts the computation and other hidden tasks. An ANN learns to map input features to output labels through an iterative optimization process using backpropagation and gradient descent.

- The output of a neuron j in layer l is given by:

$$a_j^{(l)} = f\left(\sum_{i=1}^{n} w_i^{(l-1)} a_i^{(l-1)} + b_j^{(l)}\right) \tag{9}$$

Where:

- f is the activation function (e.g., sigmoid, tanh),
- $w_i^{(l-1)}$ is the weight from the neuron I in the layer l-1 to neuron j in layer l,

- $a_i^{(l-1)}$ is the activation of neuron I in layer l-1,
- $b_j^{(l)}$ is the bias term for the neuron j in layer l.

D. Evaluation Metrics

The prior assessment of data employed a confusion matrix that displayed the predicted diagnoses compared to the real diagnoses. The matrix thus provided four values for each ML model which are True positive (TP), True Negative (TN), False Positive (FP), False Negative (FN). TP is a predicted malignant diagnosis that is actually malignant. TN is a predicted benign that is actually benign. FP is a predicted malignant that is actually benign, and FN is a predicted benign that is actually malignant.

Using the confusion matrix values, performance metrices - Accuracy, Sensitivity, Precision, Specificity and Matthew's Correlation Coefficient (MCC) were calculated by methods described previously by (Islam et al., 2020).

Other performance metrices used were the Root-Mean-Square Error (RMSE), the Mean Square Error (MSE) and Training Loss. Training loss is a measure of how well a machine model fits with the training data. The lower the training loss, the better the fit and vice versa.

Furthermore, we compared our results against previously reported ML Performance assessment of physicians from the study by Lehman et al., (2015). The metrices we compared from that study were Specificity and Sensitivity. The Human (Physician's) specificity was 91.4% ± 0.6 (95% CI) and sensitivity was 87.3% ± 0.6 (95% CI). We set these values as the benchmark for the performance of the AI models we employed in our study.

E. Dataset Description

➢ *The Data Description is as Follows:*

- diagnosis: The diagnosis of breast tissues (1 = malignant, 0 = benign) where malignant denotes that the disease is harmful.
- mean_radius: mean of distances from center to points on the perimeter.
- mean_texture: standard deviation of gray-scale values.
- mean_perimeter: mean size of the core tumor.
- mean_area: mean area of the core tumor.
- mean_smoothness: mean of local variation in radius lengths.

F. Experimental Set-up

This experiment was designed using a Python script that performs the following tasks:

➢ *Data Import:*

- Imports the Breast Cancer Wisconsin (Diagnostic) Data Set from a Kaggle data source.
- Unzips the downloaded data and stores it in the appropriate directory.

➢ *Data Exploration and Preprocessing:*

- Checks for null and duplicate entries in the dataset and removes them if found.
- Drops highly correlated features to avoid multicollinearity (Figure 1).
- Splits the data into training and testing sets.
- Scales the features using Standard Scaler.

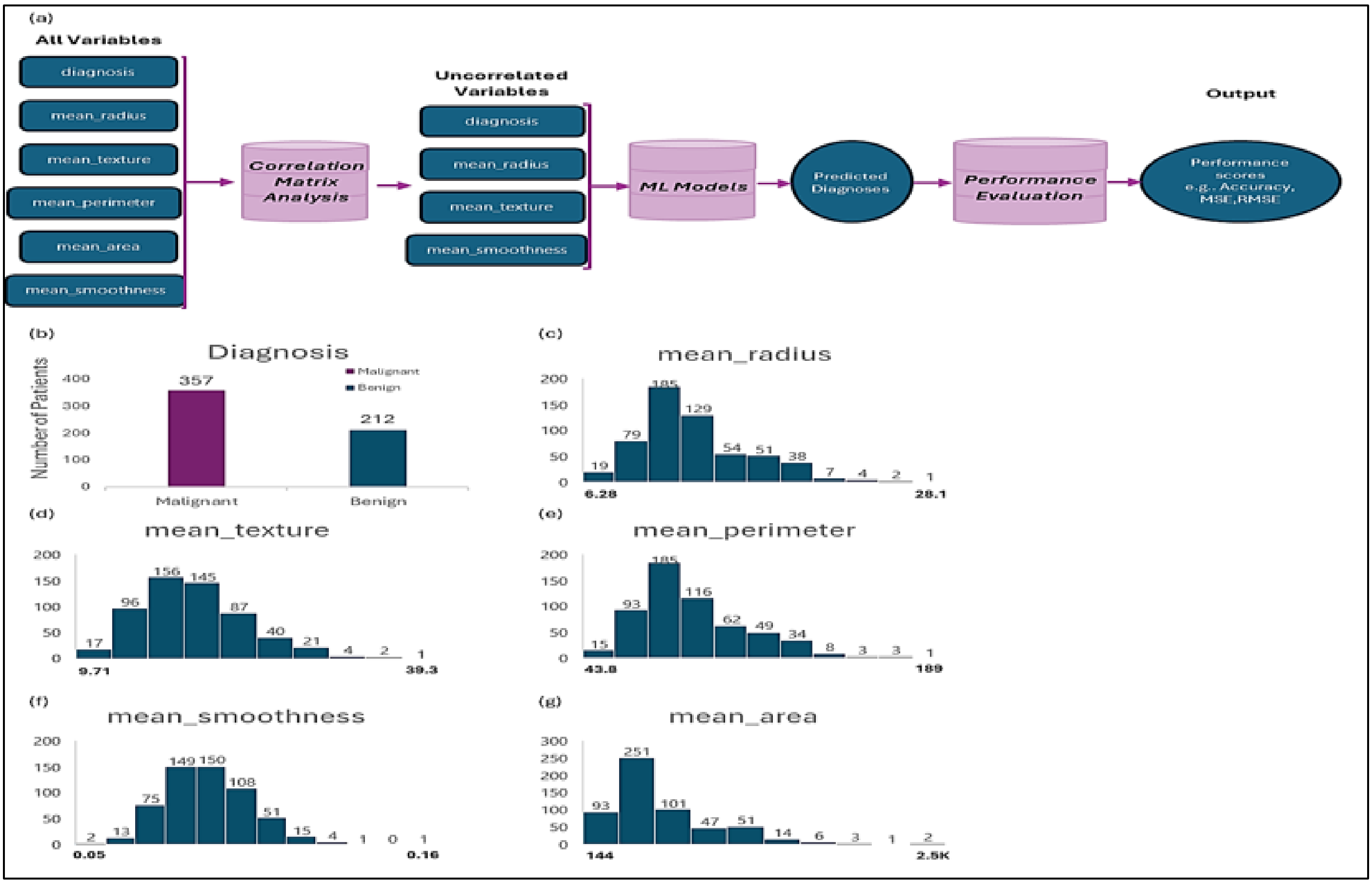
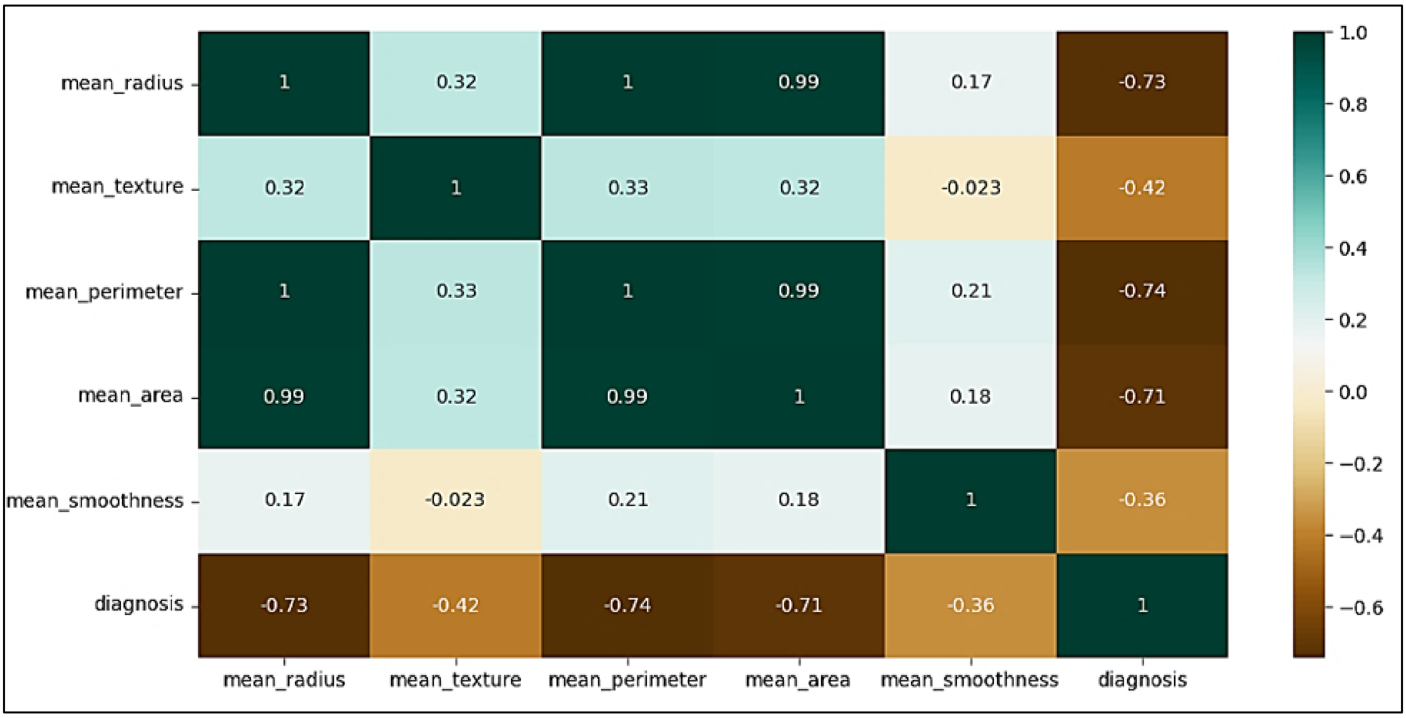


Fig 1: (a) After Initial Cleanup, All Variables were put through a Correlation Matrix Analysis to Yield Four Uncorrelated Variables that were Included in the Final Analysis using our Selected Eight ML Models. The Output was Generated as Tables, Confusion Matrices, and Figures Displaying Various Performance Metrices. (b) Bar Graph Showing a Binary Summary of Diagnosis as Either Malignant or Benign from the Source Data. (c-g) Charts Showing a Summary of all the Variables. Figures 2b-g were Generated using Microsoft Excel



	mean_radius	mean_texture	mean_perimeter	mean_area	mean_smoothness	diagnosis
mean_radius	1	0.32	1	0.99	0.17	-0.73
mean_texture	0.32	1	0.33	0.32	-0.023	-0.42
mean_perimeter	1	0.33	1	0.99	0.21	-0.74
mean_area	0.99	0.32	0.99	1	0.18	-0.71
mean_smoothness	0.17	-0.023	0.21	0.18	1	-0.36
diagnosis	-0.73	-0.42	-0.74	-0.71	-0.36	1

Fig 2: Correlation Matrix Displaying the Pearson’s Correlation Coefficient Values for Each Pair of the Variables in the Study. CI was 95%; p >=0.05).

Figure 2 shows the correlation matrix showing the Pearson's correlation values between each of the data heads. Scores of 1 (green) signify a strong relationship, score of 0 (light yellow) signifies a neutral relationship, and score of -1 (brown) signifies a weak relationship. From the correlation matrix, we clearly observe the correlation coefficients of each pair of the indicators used.

We find that mean_perimeter and mean_radius are perfectly correlated (1), while observe high correlation between mean_area and mean_radius (0.99), and mean_area and mean_perimeter (0.99). Following this, we excluded the mean_perimeter and mean_area columns from our final analysis with the machine learning models because they are highly correlated with mean_radius. Additionally, both area and perimeter are dependent on two common factors, the radius and pi (π). By doing this, we further increased the effectiveness and speed of our various machine learning models (Rajaguru & S R, 2019). By reducing the overall number of variables in our study we improved the relevance of our output and cut out redundant factors.

➢ *Model Training and Evaluation*

- Trains and evaluates eight different classification models on the breast cancer dataset namely. LR, K-NN, Linear SVM, Kernel SVM, Naïve Bayes, DTC, RFC, and ANN.
- Plots the Confusion Matrix for each model
- For each model, it calculates the accuracy score, mean squared error (MSE), root mean squared error (RMSE), and Training Loss. Training loss is a measure of how well a machine model fits with the training data. The lower the training loss, the better the fit and vice versa.
- Plots the MSE, RMSE and Training Loss values for each model.

➢ *Results and Visualization*

- Creates a table summarizing the accuracy and other performance assessment scores of each model.
- Compares the MSE and RMSE values for each model and visualizes the results in a line chart.

By employing these methodologies, we identified the most effective approach for predicting breast cancer diagnosis based on the selected diagnostic features, thereby contributing to the advancement of early detection and treatment strategies. Additionally, we elucidate how machine learning models for predicting breast cancer compare to physicians' decisions which will inform our confidence in the adaptability of machine learning to real-life diagnoses. This will also suggest how beneficial current investments in computer aided detection can be.

IV. RESULTS

Table 1 is the summary of confusion matrices for each of the AI models employed in our study. ANN has the least number of FP and FN results combined (a total of 8), while K-NN has the highest number of combined FP and FN (a total of 13).

Table 1: Results of Confusion Matrix Analysis

Model	**Confusion Matrix Results**			
	TP	TN	FP	FN
LR	62	42	5	5
K-NN	63	38	9	4
Linear SVM	62	42	5	5
Kernel SVM	61	41	6	6
Naïve Bayes	65	39	8	2
DTC	60	43	4	7
RFC	63	42	5	4
ANN	64	42	5	3

The comparative analysis of machine learning models' performances revealed varying performances in predicting breast cancer diagnosis based on selected diagnostic features (Table 2). Among the models evaluated, LR, Linear SVM, Naïve Bayes, DTC, RFC, and ANN demonstrated notable accuracies ranging from approximately 90% to 93%. Naïve Bayes model had the highest sensitivity, while DTC had the highest precision and specificity (93.75% and 91.49% respectively). K-NN has the least accuracy while LR, Linear SVM and Naïve Bayes tie at an accuracy of 91.23%. Interestingly, Kernel SVM has only 89.47% accuracy compared to Linear SVM at an accuracy of 91.23%.

Furthermore, the MCC produces an overall performance assessment of each model and showed that ANN had the best performance. Although Naïve Bayes has the highest sensitivity (97.01%), it comes up as fifth by accuracy and MCC metrices indicating that sensitivity is not as important as precision and specificity in providing accurate diagnoses.

Table 2: Comparative Analysis of Machine Learning Models by Rank

Rank	**Model**	**ML Model Performance Assessment**				
		Accuracy (%)	**Sensitivity (%)**	**Precision (%)**	**Specificity (%)**	**MCC**
1	ANN	92.98	95.52	92.75	89.36	0.85
2	RFC	92.11	94.03	92.65	89.36	0.84
3	LR	91.23	92.54	92.54	89.36	0.82
4	Linear SVM	91.23	92.54	92.54	89.36	0.82
5	Naïve Bayes	91.23	97.01	89.04	82.98	0.82
6	DTC	90.35	89.55	93.75	91.49	0.80
7	Kernel SVM	89.47	91.04	91.04	87.23	0.78
8	K-NN	88.60	94.03	87.50	80.85	0.76

A graph of the Root Mean Square Error (RMSE) and Mean Square Error (MSE) is presented in Figure 3a. A comparison of the training loss of all the models used in this study revealed that the DL model fit best with the data (Figure 3b). However, Kernel SVM has the greatest training loss. Interestingly, the MSE and RMSE do not overlap perfectly with the training loss. For instance, although K-NN has the highest MSE and RMSE (Figure 3a), it is Kernel SVM that has the most training loss (Figure 3b).

Although ANN shows the least error in prediction, all the models still show reasonably low error in performance. These results suggest the potential of machine learning approaches in aiding early breast cancer diagnosis, emphasizing the importance of feature selection and model selection for optimal predictive performance. Furthermore, the high accuracy achieved by certain models underscores their utility as potential tools for assisting healthcare professionals in clinical decision-making processes related to breast cancer diagnosis.

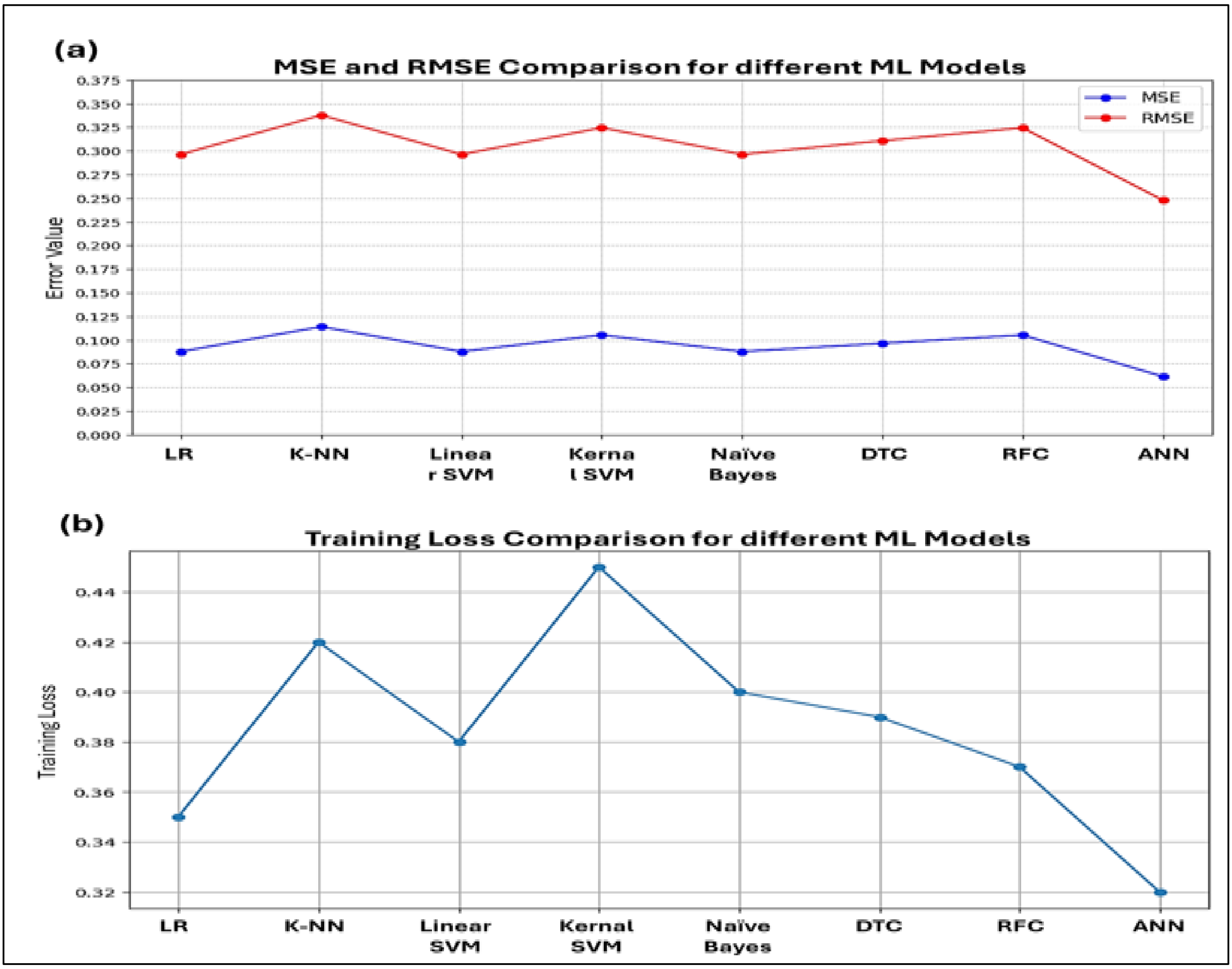


Fig 3: Machine Learning Output Metrices. (a) Comparison of MSE and RMSE for Each ML Model. (b) Training Loss for Each of the ML Models

Additionally, we compare our specificity and sensitivity scores with Lehman et al., (2015) (Figure 4). Using the Physician's (Human) metrices as our threshold we observe that all our ML models have relatively higher sensitivity. However, only DTC had higher specificity than the Human diagnosis. The computer aided diagnosis in the (Lehman et al., 2015) study was performed using a LR, which yielded an specificity score of 91.6% and sensitivity of 85.3% as compared to our own study, which came out to be 89.36% and 92.54% for specificity and sensitivity respectively.

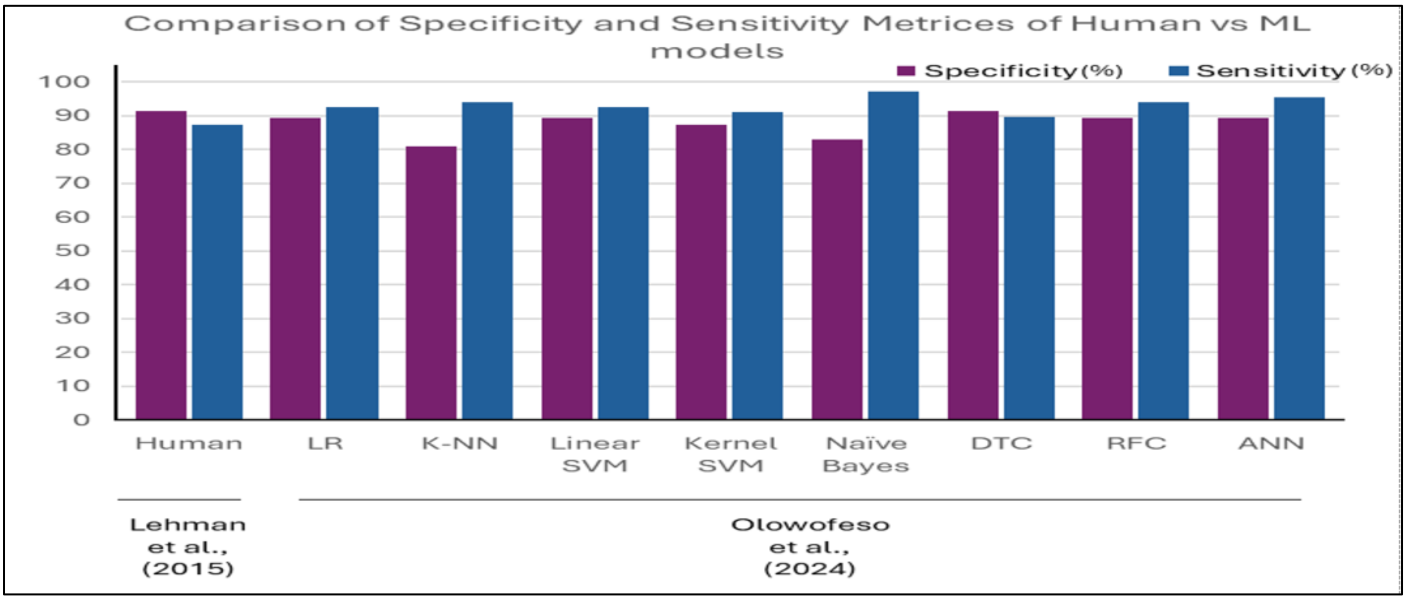


Fig 4: Comparison of Specificity and Sensitivity Scores of 8 ML Models from our Study with Specificity and Sensitivity Scores of Physician Diagnoses (Lehman et al., 2015).

V. DISCUSSION

ANN had the least amount of MSE, RMSE, and training loss, with relatively high precision and specificity. ANNs have been reported in other studies to be less prone to errors. Consistent with this, the accuracy of ANN is the highest amongst the 8 models we tested. (Díaz et al., 2024) reported that ANNs are more precise than traditional ML models like SVM, LR, K-NN and DTC. Additionally, in a comparison of five ML models, a recent research reported that ANNs had the highest precision, specificity and accuracy (Islam et al., 2020). The reason for this high accuracy in the DL model may be because of the high degree of fit due to the low training loss.

Traditional ML models have shown varying accuracy scores in different studies. Islam et al., (2020) showed that Linear SVM and K-NN came up next as most accurate behind ANN. Interestingly, we find in our study that RFC and LR came as a runner up in accuracy, with K-NN being the least accurate (88.60%). We also recorded that Linear SVM (91.23%) was more accurate than Kernel SVM (89.47%). This, we reason, is because Kernel SVM is more suited to non-linear decision boundaries, unlike what we have in a study which is a binary classification of a tumor as either malignant or benign. Another study by, (Rajaguru & S R, 2019) showed that K-NN was a more accurate predictor of breast cancer than DTC. Our results on the other hand showed the opposite. DTC ranked sixth out of eight models, while K-NN ranked eighth.

Discrepancies in our results indicates that while DL models like ANN consistently rank higher than traditional ML models in breast cancer diagnosis accuracy, different ML models are suited variably to data sets, and their accuracy is tied to the uniqueness of the data being analyzed or the output desired from the analysis.

Taken together, we propose that DL models are more accurate than traditional ML models for breast cancer diagnosis prediction and have a better fit with the breast cancer diagnoses when a binary output is desired. We also reason that use of ML models for breast cancer diagnoses cannot be a one-size fits all but should be applied on a case-by-case basis. Furthermore, we propose that investment in developing DL models may be a worthwhile effort for improving Computer-aided detection (CAD) systems.

Despite these promising advancements, challenges remain in AI application in oncology. Issues such as data heterogeneity, overfitting, and privacy concerns pose significant hurdles to AI-driven solutions. Standardization of training datasets and ethical considerations are essential to ensure the reliability and safety of AI technologies in clinical practice. There have also been concerns over the overall benefit of investing in AI for CAD for breast cancer. Some studies have suggested that CAD does not improve diagnostic accuracy of mammography and thus, women are paying more for CAD with no established advantage (Lehman et al., 2015). As such, although AI has enormous potential in the field of diagnosis, much more research and improvement is required to increase clinical and public.

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In conclusion, AI holds immense potential to revolutionize cancer diagnosis and treatment, offering faster, more accurate, and personalized solutions. Collaboration between researchers, medical professionals, and technologists is crucial to overcome existing challenges and harness the full benefits of AI in oncology. As with all innovations, we suggest that AI be adopted in physician practice as this will expose its shortcomings and create measurable objectives for improvement in ML and DL models for breast cancer prediction. With continued innovation and interdisciplinary cooperation, AI-driven approaches will play a pivotal role in improving patient care and advancing cancer research in the future.

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