BREAST CANCER TYPE CLASSIFICATION USING MACHINE LEARNING

A RESEARCH PROJECT

ABSTRACT

Breast cancer is one of the most common and life-threatening diseases affecting women worldwide. Early detection and accurate diagnosis are essential for improving treatment outcomes and reducing mortality rates. Machine learning techniques have emerged as effective tools for assisting medical practitioners in the classification and diagnosis of breast cancer by identifying hidden patterns within clinical data. This study developed a breast cancer classification model using the Stochastic Gradient Descent (SGD) classifier to distinguish between benign and malignant breast tumors. The study utilized the Wisconsin Diagnostic Breast Cancer (WDBC) dataset obtained from the UCI Machine Learning Repository. The dataset contains 569 patient records with 30 diagnostic features extracted from digitized images of fine-needle aspirates of breast masses. Before model development, the dataset was preprocessed through data cleaning, label encoding, and feature standardization using the StandardScaler technique to improve data quality and ensure effective model training. The model was implemented using Python and Scikit-learn, while Pandas, NumPy, Matplotlib, and Seaborn were used for data manipulation, visualization, and performance evaluation. Three train-test partitioning strategies of 80:20, 75:25, and 70:30 were adopted to evaluate the influence of different data splits on classification performance. The classifier was trained for 20 epochs using the Stochastic Gradient Descent optimization approach. The performance of the proposed model was evaluated using Accuracy, Precision, Recall, F1-Score, Confusion Matrix, Classification Report, Receiver Operating Characteristic (ROC) Curve, Area Under the Curve (AUC), Precision-Recall Curve, Macro Average, and Weighted Average. The experimental results showed that the 80:20 and 70:30 partitioning strategies achieved an overall classification accuracy of 98%, while the 75:25 partition achieved 97% accuracy. These findings indicate that the proposed SGD classifier is capable of accurately distinguishing between benign and malignant breast tumors with high reliability and strong generalization performance. The study concludes that the Stochastic Gradient Descent classifier is an effective and computationally efficient approach for breast cancer classification..

Keywords: Breast Cancer, Machine Learning, Stochastic Gradient Descent (SGD), Wisconsin Diagnostic Breast Cancer Dataset, Classification.

CHAPTER ONE

INTRODUCTION

1.0 Background of the Study

Breast cancer is a major global health problem and remains one of the leading causes of cancer-related deaths among women. According to global health organizations, early detection significantly increases the chances of successful treatment and survival. Medical diagnosis of breast cancer often involves imaging techniques such as mammography, ultrasound, and biopsy analysis. However, interpreting these diagnostic results requires expertise and may sometimes lead to inconsistencies. Traditionally, breast cancer diagnosis involves clinical examination, imaging techniques such as mammography, ultrasound, and magnetic resonance imaging (MRI), as well as histopathological analysis of biopsy samples. While these methods are effective, they often depend heavily on the expertise and experience of medical professionals. This reliance can lead to variability in diagnosis, delays in decision-making, and potential human error. In addition, manual analysis of medical data can be time-consuming, especially when dealing with large datasets.

Brown & Miller (2019) stated that breast cancer is one of the most prevalent and deadly cancers affecting women globally. It occurs when abnormal cells in the breast grow uncontrollably and form tumors that may spread to other parts of the body if not detected early. The increasing global burden of breast cancer has made early detection and accurate classification a major focus in modern healthcare systems. Researchers explained that breast cancer is not a single uniform disease but consists of several types and subtypes such as ductal carcinoma, lobular carcinoma, and inflammatory breast cancer. Each type has different biological behavior, progression rate, and response to treatment. Therefore, accurate classification of breast cancer types is essential for effective treatment planning and improving patient survival rates (Singh & Patel 2021).

Davis & Clark (2020) Traditionally, breast cancer diagnosis involves clinical examination, imaging techniques such as mammography, ultrasound, and MRI, as well as biopsy analysis. It was noted that these conventional methods rely heavily on the experience of medical experts, which can lead to variability in diagnosis, delays in decision-making, and

possible human error. In addition, manual interpretation of large volumes of medical data is time-consuming and inefficient. Recent advancements in artificial intelligence and machine learning have introduced new opportunities for improving breast cancer diagnosis and classification. Machine learning algorithms can analyze large datasets, identify hidden patterns, and make accurate predictions with minimal human intervention. These systems enhance diagnostic efficiency and reduce the risk of errors associated with manual processes (Garcia et al., 2020).

Wang et al. (2020) further emphasized that deep learning models, especially Convolutional Neural Networks (CNNs), have revolutionized medical image analysis. These models automatically extract important features from images such as mammograms and histopathology slides, eliminating the need for manual feature engineering and improving classification accuracy. Despite these technological advancements noted that challenges still exist in breast cancer classification systems. These include data imbalance, noisy datasets, overfitting, and poor generalization of models when applied to real-world medical data. Such limitations reduce the reliability of some machine learning systems in clinical practice (Rahman et al. 2020).

Li et al. (2022) added that feature selection plays a very important role in improving model performance. Irrelevant or redundant features can reduce classification accuracy and increase computational complexity. Therefore, selecting the most relevant features is critical for building efficient and reliable prediction models. The availability of benchmark datasets, such as the Wisconsin Diagnostic Breast Cancer dataset, has significantly contributed to research in this field by providing standardized data or training and evaluating models. These datasets allow researchers to compare different algorithms and identify the most effective approaches for breast cancer classification (Street et al., 1993).

With the rapid advancement of technology, machine learning (ML), a subset of artificial intelligence, has emerged as a powerful tool for improving disease diagnosis and classification. Machine learning algorithms can automatically learn patterns from data and make predictions without being explicitly programmed. In the context of breast cancer, ML models can analyze clinical data, imaging data, and histopathological features to classify tumors more accurately and efficiently.

1.1 Statement of the Problem

Breast cancer diagnosis remains a challenging task due to the complexity and

variability of tumor characteristics. Traditional diagnostic approaches rely on manual examination of medical images and clinical data, which may lead to delays or errors in classification. Another challenge is the increasing amount of medical data generated from diagnostic tests, making manual analysis inefficient. Breast cancer diagnosis remains a major challenge in modern healthcare due to the complexity of the disease and limitations of conventional diagnostic methods. Although imaging techniques such as mammography, MRI, and biopsy analysis are widely used, they are often time-consuming, expensive, and heavily dependent on specialist interpretation. This dependency introduces variability in diagnosis and increases the risk of human error (Davis & Clark 2020).

Hassan & Ibrahim (2021) Another major challenge is feature selection in high-dimensional medical datasets. The presence of irrelevant or redundant features can negatively affect model performance and reduce classification accuracy. Effective preprocessing and feature selection are therefore essential for improving the reliability of machine learning models. predictions are made, limiting trust and adoption in clinical settings (Gupta and Patel 2021) . Although deep learning models achieve high accuracy in breast cancer detection, they often lack interpretability. This "black-box" nature makes it difficult for medical professionals to understand how predictions are made, limiting trust and adoption in clinical settings (Gupta and Patel 2021) .

Rahman et al. (2020) Several studies have applied machine learning techniques to breast cancer classification and achieved promising results. However, many of these models suffer from issues such as overfitting, poor generalization, and sensitivity to noisy or incomplete data, which reduces their effectiveness in clinical practice. A high-dimensional medical datasets present additional challenges in classification tasks. Many features in such datasets may be irrelevant or redundant, which can lead to reduced model performance and increased training time. Effective feature selection and dimensionality reduction techniques are therefore necessary for building efficient classification systems (Li et al. 2022) .

Rodriguez & Martinez (2021) also noted that while optimization techniques can improve model performance, many existing breast cancer classification systems do not fully explore parameter tuning and hybrid optimization strategies, resulting in suboptimal performance. Therefore, there is a clear need to develop a more robust, accurate, and efficient machine learning-based system for breast cancer type classification that addresses challenges such as feature selection, data imbalance, model interpretability, generalization ability, and computational efficiency.

1.2 Research Aim and Objectives

The aim of this project is to develop a breast cancer type classification system using machine learning techniques. The specific objectives are however, as follows:

i. To obtain and preprocess breast cancer datasets from publicly available sources.

ii. To extract and analyze relevant features associated with breast cancer diagnosis.

iii. To apply machine learning models for breast cancer type classification.

iv. To train machine learning models for accurate classification of breast cancer cases.

v. To evaluate the performance of the developed models using metrics such as accuracy, precision, recall, and F1-score.

1.3 Significance of the Study

This study on Breast Cancer Type Classification Using Machine Learning is significant in the following ways:

i. Enhancement of Early Detection Systems: This study contributes to improving early detection of breast cancer by developing a machine learning-based classification system.Early and accurate detection is essential for timely treatment and significantly increases the survival rate of patients.

ii. Improvement in Diagnostic Accuracy: The proposed system helps improve diagnostic accuracy by reducing human errors that often occur in manual interpretation of medical images and clinical data. Machine learning models can identify complex patterns that may not be easily detected by humans.

iii. Support for Clinical Decision-Making: This research provides an intelligent tool that supports doctors and radiologists in making more informed and data-driven decisions. It reduces dependence on subjective judgment and increases diagnostic consistency.

iv. Reduction of Workload for Medical Experts: By automating part of the diagnostic process, the system reduces the workload of healthcare professionals. This allows doctors to focus more on critical cases and treatment planning rather than repetitive analysis tasks.

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viii. Reduction of Workload for Medical Experts: By automating part of the diagnostic process, the system reduces the workload of healthcare professionals. This allows doctors to focus more on critical cases and treatment planning rather than repetitive analysis tasks.

ix. Time Efficiency in Diagnosis: The study improves the speed of breast cancer classification compared to traditional diagnostic methods. Automated systems can process large datasets quickly, leading to faster diagnosis and treatment initiation.

x. Improvement of Healthcare Accessibility: Machine learning-based diagnostic systems can be deployed in areas with limited access to specialist doctors. This can help improve healthcare services in rural or underserved regions.

xi. Reduction of Healthcare Costs: By improving early detection and reducing misdiagnosis, this system can help reduce unnecessary medical tests and treatment costs, making healthcare more affordable for patients and healthcare providers.

xii. Foundation for Development of Advanced Models: This study provides a foundation for future researchers to develop more advanced hybrid or deep learning models for breast cancer classification and other medical diagnosis tasks.

xiii. Contribution to Medical Research and Education: The findings of this study can serve as a learning resource for students, researchers, and professionals interested in medical data science, machine learning, and healthcare analytics.

1.4 Scope and Limitations of the Study

The scopes of this study is limited to the development and implementation of a machine learning-based system for breast cancer type classification using structured medical and diagnostic datasets which are:

i. Dataset Scope: This study focuses on publicly available breast cancer datasets such as the Wisconsin Diagnostic Breast Cancer dataset and similar structured clinical datasets.

ii. Focus on Breast Cancer Type Classification: The research is specifically focused on classifying breast cancer into different categories such as benign and malignant, and where possible, further subtype classification depending on available dataset features.

iii. Machine Learning Techniques: The study involves the application of traditional machine learning algorithms such as Decision Trees, K-Nearest Neighbors, Naïve Bayes, and Support Vector Machines. It may also include hybrid or optimized models for improved

accuracy.

iv. Feature-Based Prediction: The system is based on structured clinical and diagnostic features such as tumor size, cell texture, radius, perimeter, and other numerical attributes extracted from medical datasets.

v. Performance Evaluation: The study evaluates model performance using standard evaluation metrics such as accuracy, precision, recall, F1-score, amd confusion matrix analysis to determine classification effectiveness.

vi. Implementation Environment: The system is designed to be implemented using programming tools such as Python, with machine learning libraries like Scikit-learn and Pandas for data processing and model development.

The limitations of the study include the following:

i. Data Quality Constraints: Some datasets may contain missing values, noise, or imbalance between classes, which can affect model performance and reduce prediction accuracy.

ii. Limited Generalization: The trained models may perform well on the selected dataset but may not generalize perfectly to all real-world medical environments due to variations in patient data and imaging techniques.

iii. Lack of Real-Time Clinical Testing: The system is developed and tested using historical datasets only. It is not deployed in real-time hospital environments, which limits its clinical validation.

iv. Computational Constraints: Some machine learning models may require high computational resources for training and optimization, which could limit scalability on low-resource systems.

v. Focus on Structured Data Only: This study primarily focuses on structured/tabular data and does not deeply explore unstructured data such as raw medical imaging or genomic data in full detail.

1.5 Definition Of Terms

i. Breast Cancer: Breast cancer is a malignant disease that occurs when cells in the breast tissue begin to grow abnormally and uncontrollably. These cells form a mass known as a tumor, which may invade surrounding tissues and spread to other parts of the body through the blood or lymphatic system.

ii. Cancer Type Classification: Cancer type classification refers to the process of identifying and categorizing breast cancer into specific types based on patterns found in clinical,

biological, or diagnostic data. In machine learning systems, this usually involves classifying cases as benign or malignant, or further into subtypes depending on dataset availability

iii. Machine Learning: Machine learning is a branch of artificial intelligence that enables computer systems to automatically learn patterns from data without being explicitly programmed..

iv. Artificial Intelligence (AI): Artificial intelligence is the simulation of human intelligence in machines designed to perform tasks such as learning, reasoning, and problem-solving. AI systems can analyze large amounts of data, recognize patterns, and make decisions.

v. Dataset: A dataset is an organized collection of related data used for training and evaluating machine learning models. In breast cancer classification, a dataset typically consists of patient records containing diagnostic measurements such as tumor size, shape, texture, and other medical attributes.Feature: A feature is an individual measurable property or characteristic of data used as input for machine learning models. In breast cancer datasets, features may include tumor radius, perimeter, smoothness, compactness, and texture.

vi. Feature Selection: Feature selection is the process of identifying and selecting the most relevant variables from a dataset while removing irrelevant or redundant ones. This process improves model performance by reducing noise, enhancing accuracy, and decreasing computational complexity.

vii. Classification: Classification is a supervised machine learning technique that involves assigning input data into predefined categories based on learned patterns. In breast cancer diagnosis, classification models are used to determine whether a tumor is benign or malignant.

viii. Supervised Learning: Supervised learning is a type of machine learning where the model is trained using labeled data. This means that both input features and correct output labels are provided during training. The model learns the relationship between inputs and outputs so it can accurately predict results for new data.

ix. Unsupervised Learning: Unsupervised learning is a machine learning approach where the model learns patterns from data without labeled outputs. Instead of predefined categories, the system identifies hidden structures or groupings within the data. It is often used for clustering and exploratory data analysis.

x. Model Training: Model training is the process of feeding data into a machine learning algorithm so that it can learn patterns and relationships within the dataset. During training, the model adjusts its internal parameters to reduce errors and improve prediction accuracy. This process is essential for building a reliable classification system.

xi. Prediction: Prediction refers to the output generated by a trained machine learning model when it analyzes new or unseen data. In breast cancer classification, prediction involves determining whether a new patient case is likely to be benign or malignant based on learned patterns.

xii. Benign Tumor: A benign tumor is a non-cancerous growth that does not spread to other parts of the body. It usually grows slowly and is less dangerous compared to malignant umors. Although benign tumors are not cancerous, they may still require medical attention depending on their size and location.

xiii. Malignant Tumor: A malignant tumor is a cancerous growth that can invade surrounding tissues and spread to other parts of the body through metastasis. Malignant tumors are more aggressive and pose a serious health risk if not treated early.

xiv. Medical Diagnosis: Medical diagnosis is the process of identifying a disease or condition based on patient symptoms, clinical examination, and diagnostic test results. It involves analyzing medical data to determine the nature and severity of a disease.

xv. Diagnostic Data: Diagnostic data refers to medical information collected from patients during examinations and tests. In breast cancer studies, this may include imaging results, biopsy reports, and numerical measurements of tumor characteristics used for analysis and classification.

xvi. Pattern Recognition: Pattern recognition is the ability of machine learning systems to identify meaningful structures, trends, or relationships within data. In breast cancer classification, it helps the model distinguish between different types of tumors based on learned patterns.

xvii. Algorithm: An algorithm is a step-by-step set of rules or instructions used by a machine learning model to process data and generate results. Algorithms define how input data is analyzed and how predictions are produced.

xviii. Support Vector Machine (SVM): Support Vector Machine is a supervised machine learning algorithm used for classification tasks. It works by finding the optimal boundary (hyperplane) that separates different classes in the dataset with maximum margin.

xix. Decision Tree: A Decision Tree is a machine learning model that makes decisions by splitting data into branches based on feature conditions. It resembles a tree-like structure where each node represents a decision rule leading to a final classification outcome.

xx. K-Nearest Neighbors (KNN): K-Nearest Neighbors is a machine learning algorithm that classifies a data point based on the majority class of its closest neighboring data points. It is simple but effective for classification tasks, especially in structured datasets.

CHAPTER TWO

LITERATURE REVIEW

2.0 Introduction

Breast cancer is one of the most common and deadly diseases affecting women worldwide. It develops when abnormal cells in the breast tissue begin to grow uncontrollably, forming tumors that may spread to other parts of the body if not detected early. The increasing prevalence of breast cancer has become a major public health concern, leading researchers and healthcare professionals to focus on improving early detection, diagnosis, and treatment methods. Early diagnosis plays an important role in increasing survival rates and reducing the severity of the disease.

Traditional breast cancer diagnostic methods such as mammography, ultrasound imaging, magnetic resonance imaging (MRI), and biopsy analysis have been widely used in hospitals and medical centers. Although these methods are effective, they are often associated with challenges such as high cost, time consumption, dependence on expert interpretation, and the possibility of human error. Brown and Miller (2019) explained that inconsistencies in manual diagnosis may affect the accuracy and reliability of breast cancer detection and classification.

The advancement of artificial intelligence, machine learning, and deep learning technologies has introduced new opportunities for improving breast cancer diagnosis and classification systems. Machine learning models are capable of analyzing large medical datasets, identifying important patterns, and predicting cancer types with high accuracy. Algorithms such as Support Vector Machines (SVM), Decision Trees, Naïve Bayes, and K-Nearest Neighbors (KNN) have been successfully applied in breast cancer classification tasks. Deep learning approaches such as Convolutional Neural Networks (CNNs) have also demonstrated excellent performance in medical image analysis and automated diagnosis (Wang et al., 2020).

Despite the significant progress achieved through machine learning and deep learning techniques, several limitations still exist in current breast cancer classification systems. Challenges such as overfitting, poor generalization, limited dataset availability, and lack of interpretability continue to affect model performance in real-world healthcare applications. Therefore, there is a need for continuous research toward developing more accurate, reliable, and

efficient breast cancer classification models. This chapter reviews existing studies related to breast cancer classification, types of breast cancer, methods of diagnosis, machine learning and deep learning models, related works, and identified research gaps.

2.1 Related Works

Chen et al. (2019) developed a breast cancer diagnosis and classification framework using machine learning algorithms such as Support Vector Machines (SVM), Decision Trees, and Logistic Regression. Their research focused on improving the accuracy of breast cancer prediction using structured clinical datasets. The study revealed that machine learning algorithms can effectively distinguish between benign and malignant tumors with high reliability. The authors further explained that proper feature extraction and preprocessing techniques significantly improve the efficiency of classification models. Their work demonstrated the growing importance of machine learning in healthcare and highlighted the need for intelligent systems capable of supporting clinical diagnosis.

Garcia et al. (2020) investigated different machine learning approaches for breast cancer detection and diagnosis using multiple classification techniques. Their study compared algorithms such as Naïve Bayes, Decision Trees, K-Nearest Neighbors, and Support Vector Machines to determine the most effective model for breast cancer prediction. The researchers concluded that model performance depends greatly on dataset quality, feature relevance, and preprocessing techniques. They also emphasized that machine learning systems improve diagnostic consistency and reduce dependence on manual interpretation by medical experts.

Singh et al. (2019) proposed an intelligent supervised learning system for breast cancer classification using medical datasets containing tumor-related features. Their system achieved improved classification performance by applying supervised learning algorithms capable of identifying hidden relationships within clinical data. The study demonstrated that intelligent systems can reduce diagnostic errors and provide faster prediction results compared to traditional diagnostic methods. The authors also emphasized the importance of feature engineering in enhancing model performance.

Rahman et al. (2020) conducted a detailed performance analysis of different machine learning algorithms used for breast cancer prediction. Their study evaluated algorithms such as Random Forest, Support Vector Machines, Naïve Bayes, and Artificial Neural Networks. The findings showed that ensemble and hybrid models generally achieve better classification accuracy and generalization performance than single classifiers. However, the researchers identified

challenges such as overfitting, data imbalance, and computational complexity as major limitations affecting model effectiveness.

Ahmed et al. (2018) focused on breast cancer type classification using clinical and diagnostic datasets obtained from medical institutions. Their study demonstrated that combining multiple diagnostic parameters improves classification performance and predictive accuracy. The researchers emphasized that integrated systems using multiple sources of patient data provide better diagnostic reliability compared to systems based on single-source information. Their work also highlighted the importance of proper dataset preparation in medical diagnosis systems.

Kumar and Sharma (2019) applied the K-Nearest Neighbors (KNN) algorithm for breast cancer classification and evaluated its effectiveness using structured medical datasets. Their results showed that KNN performs effectively in identifying benign and malignant tumors when appropriate feature selection methods are applied. However, the study also noted that the computational cost of KNN increases significantly as dataset size becomes larger, making scalability a challenge in large medical applications.

Patel et al. (2020) proposed a Naïve Bayes classifier for breast cancer detection and demonstrated that probabilistic machine learning methods can achieve satisfactory results in cancer prediction tasks. Their study emphasized that Naïve Bayes is computationally efficient and easy to implement, especially when working with structured datasets. The researchers also highlighted the importance of preprocessing techniques such as normalization and noise removal in improving classification accuracy.

Johnson & Lee (2018) implemented a Decision Tree model for breast cancer diagnosis and classification. Their findings showed that Decision Trees provide interpretable and understandable classification results, making them suitable for healthcare applications where transparency is important. The study demonstrated that the hierarchical structure of Decision Trees helps medical professionals understand how classification decisions are made, thereby increasing trust in intelligent diagnostic systems.

Hassan & Ibrahim (2021) investigated the impact of data preprocessing techniques on breast cancer classification accuracy. Their research demonstrated that preprocessing operations such as normalization, missing value handling, and data balancing significantly improve machine learning model performance. The authors explained that poor-quality datasets negatively affect predictive systems and may lead to unreliable diagnosis. Their study highlighted preprocessing as one of the most important stages in developing effective machine learning systems.

Li et al. (2022) proposed a hybrid feature selection and classification framework for breast cancer diagnosis. Their system combined feature selection methods with machine learning classifiers to eliminate redundant and irrelevant attributes from the dataset. The study achieved improved classification accuracy while reducing computational complexity. The researchers concluded that hybrid approaches provide better performance than traditional standalone classification methods.

Rodriguez & Martinez (2021) explored optimization techniques for improving machine learning models used in breast cancer prediction. Their study focused on hyperparameter tuning, optimization strategies, and model evaluation techniques. The findings revealed that optimized models achieve better prediction accuracy, robustness, and generalization capability compared to non-optimized models. They further emphasized the importance of parameter tuning in machine learning applications.

Wang et al. (2020) applied Convolutional Neural Networks (CNNs) for breast cancer histopathology image classification. Their study demonstrated that CNN models can automatically learn complex image features without requiring manual feature extraction. The researchers achieved high classification accuracy and showed that deep learning techniques outperform many traditional machine learning methods in image-based diagnosis. Their findings highlighted the effectiveness of CNNs in medical image analysis.

Gupta and Patel (2021) developed an automated breast cancer detection system using deep neural networks. Their study showed that deep learning models improve diagnostic accuracy by learning complex representations directly from medical images. The authors concluded that deep neural networks provide superior feature extraction capability and significantly reduce manual intervention during diagnosis.

Khan & Rahman (2022) investigated the application of transfer learning techniques in breast cancer image classification. Their study utilized pre-trained deep learning models and demonstrated that transfer learning improves classification performance even when limited medical image datasets are available. The researchers explained that transfer learning reduces training time and improves model generalization.

Nguyen & Hoang (2021) conducted a comparative study of deep learning architectures for breast cancer diagnosis. Their research compared different CNN-based models and found that deep learning architectures consistently outperform traditional machine learning algorithms in image classification tasks. The study also highlighted the importance of dataset quality and architecture selection in deep learning performance.

Brown & Miller (2019) reviewed the application of artificial intelligence techniques in breast cancer detection and diagnosis. Their study concluded that AI-based systems improve healthcare delivery by increasing diagnostic speed, accuracy, and efficiency. The authors emphasized that intelligent systems can support medical professionals by reducing workload and improving decision-making processes.

Davis & Clark (2020) reviewed machine learning and deep learning methods for breast cancer diagnosis and classification. Their study discussed the strengths and limitations of intelligent diagnostic systems and highlighted issues such as interpretability, dataset dependency, and computational requirements. The authors concluded that despite current challenges, artificial intelligence remains highly promising in healthcare applications.

Singh and Patel (2021) examined recent advancements in artificial intelligence for breast cancer classification. Their study emphasized that integrating multiple AI techniques significantly improves classification accuracy and system reliability. The researchers further explained that hybrid intelligent systems have strong potential for future medical diagnosis applications.

Street et al. (1993) introduced the Wisconsin Diagnostic Breast Cancer dataset, which remains one of the most widely used benchmark datasets in breast cancer machine learning research. The dataset contains important tumor-related features such as radius, texture, perimeter, smoothness, and compactness used for training and evaluating machine learning models. Many researchers continue to rely on this dataset for performance comparison and experimental analysis.

Kaur & Singh (2020) conducted a comparative analysis of machine learning algorithms for breast cancer diagnosis and classification. Their study compared multiple algorithms and found that no single model consistently performs best across all datasets. The researchers recommended the development of hybrid and optimized models capable of improving prediction accuracy and handling diverse medical datasets more effectively.

2.1.1 Summary of Related Works

Authors/Year	Results and Findings	Limitations
Chen et al. (2019)	Developed a breast cancer diagnosis and classification framework using machine learning algorithms such as Support Vector Machines (SVM), Decision Trees, and Logistic Regression. The study achieved high classification accuracy in distinguishing between benign and malignant breast cancer cases. Their findings showed that machine learning models improve diagnostic reliability and reduce human error in medical diagnosis.	The research mainly focused on structured datasets and did not extensively evaluate image-based diagnosis or deep learning approaches. The model performance may also vary when applied to real-world hospital datasets.
Garcia et al. (2020)	Investigated multiple machine learning approaches for breast cancer detection and diagnosis. Their study compared algorithms such as Naïve Bayes, Decision Trees, KNN, and SVM, concluding that proper preprocessing and feature engineering significantly improve model accuracy.	The study depended heavily on dataset quality and lacked real-time clinical validation. The authors also did not address interpretability challenges in complex classification systems.
Singh et al. (2019)	Proposed an intelligent supervised learning system for breast cancer classification	The model required large amounts of labeled data for effective training and

	using structured clinical datasets. The system improved diagnostic accuracy and demonstrated that supervised learning techniques can assist healthcare professionals in decision-making processes.	may not perform efficiently on highly imbalanced datasets commonly found in healthcare environments.
Rahman et al. (2020)	Conducted a comparative analysis of different machine learning algorithms for breast cancer prediction. Their findings revealed that ensemble and hybrid models outperform single classifiers in terms of accuracy, robustness, and generalization capability.	The study identified overfitting, computational complexity, and class imbalance as major limitations affecting model reliability and real-world implementation.
Ahmed et al. (2018)	Focused on breast cancer type classification using clinical and diagnostic data. The study showed that integrating multiple sources of patient information improves prediction accuracy and classification efficiency.	The research used limited datasets and lacked practical deployment in clinical environments. The study also did not deeply explore optimization techniques.
Kumar & Sharma (2019)	Applied the K-Nearest Neighbors (KNN) algorithm for breast cancer classification and achieved satisfactory results in identifying benign and malignant tumors. The study demonstrated that KNN performs well on structured datasets with appropriate	KNN required high computational resources for large datasets and was sensitive to irrelevant or noisy features, reducing scalability in large healthcare systems.

	feature selection.	
Patel et al. (2020)	Developed a Naïve Bayes classifier for breast cancer detection and demonstrated that probabilistic machine learning methods can achieve reliable prediction performance with properly preprocessed datasets.	The Naïve Bayes model assumed independence among features, which may not accurately represent real-world medical relationships between clinical attributes.
Johnson & Lee (2018)	Implemented a Decision Tree model for breast cancer diagnosis and classification. Their findings showed that Decision Trees provide interpretable and transparent classification results that are easy for healthcare professionals to understand.	Decision Tree models are prone to overfitting and may experience reduced performance when handling highly complex medical datasets.
Hassan & Ibrahim (2021)	Investigated the effect of data preprocessing techniques on breast cancer classification accuracy. Their study demonstrated that normalization, feature scaling, and missing value handling significantly improve machine learning performance.	The research focused primarily on preprocessing and did not comprehensively analyze advanced classification algorithms or hybrid intelligent systems.
Li et al. (2022)	Proposed a hybrid feature selection and classification framework for breast cancer	The hybrid framework required careful parameter tuning and

	diagnosis. The framework improved prediction accuracy while reducing computational complexity by removing irrelevant features.	increased implementation complexity, making deployment more challenging.
Rodriguez & Martinez (2021)	Explored optimization techniques for improving machine learning models used in breast cancer prediction. Their findings showed that hyperparameter tuning improves classification accuracy, robustness, and model generalization.	Optimization methods increased computational cost and required significant technical expertise for implementation and maintenance.
Wang et al. (2020)	Applied Convolutional Neural Networks (CNNs) for breast cancer histopathology image classification. Their study achieved high classification accuracy and demonstrated that CNNs automatically extract important image features without manual intervention.	CNN models required large image datasets and high computational resources for effective training and deployment.
Gupta & Patel (2021)	Developed automated breast cancer detection systems using deep neural networks. Their research demonstrated that deep learning approaches outperform many traditional machine learning methods in image-based diagnosis tasks.	Deep learning systems lacked interpretability and transparency, making clinical adoption more difficult in some healthcare settings.

Khan & Rahman (2022)	Investigated transfer learning techniques for breast cancer image classification. Their study showed that transfer learning improves classification accuracy and reduces training time, especially when working with limited datasets.	The performance of transfer learning models depended heavily on the quality of pre-trained architectures and dataset similarity.
Nguyen & Hoang (2021)	Conducted a comparative study of deep learning architectures for breast cancer diagnosis. Their findings showed that CNN-based models consistently outperform traditional machine learning algorithms in image analysis tasks.	Deep learning architectures required extensive computational power and large-scale labeled datasets for effective performance.
Brown & Miller (2019)	Reviewed artificial intelligence applications in breast cancer detection and diagnosis. The study concluded that AI systems improve diagnostic speed, efficiency, and prediction accuracy while supporting healthcare professionals.	The review identified issues related to lack of interpretability, ethical concerns, and challenges in integrating AI systems into clinical practice.
Davis & Clark (2020)	Reviewed machine learning and deep learning methods for breast cancer diagnosis and highlighted their advantages in healthcare applications. The	The review identified limitations such as dataset dependency, computational requirements, and poor

	study emphasized the effectiveness of intelligent systems in improving diagnostic accuracy.	interpretability in many deep learning systems.
Singh & Patel (2021)	Examined recent advancements in artificial intelligence for breast cancer classification and emphasized the effectiveness of hybrid intelligent systems in improving classification reliability and performance.	The study focused mainly on theoretical advancements and did not provide extensive practical implementation analysis.
Street et al. (1993)	Introduced the Wisconsin Diagnostic Breast Cancer dataset, which became one of the most widely used benchmark datasets in breast cancer machine learning research. The dataset has been extensively used for model evaluation and comparison.	The dataset may not fully represent modern real-world clinical diversity, large imaging datasets, or advanced genomic information.
Kaur & Singh (2020)	Conducted a comparative study of machine learning algorithms for breast cancer diagnosis and found that no single model consistently performs best across all datasets and classification tasks.	The study recommended hybrid systems but did not propose a unified framework capable of addressing all identified limitations.

2.2 Concept of Breast Cancer and Breast Cancer Classification

2.2.1 Concept of Breast Cancer

Breast cancer is a malignant disease that originates from the uncontrolled growth and abnormal division of cells within the breast tissue. Under normal physiological conditions, body cells grow, divide, and die in a regulated manner. However, in breast cancer, this regulatory process breaks down, leading to continuous cell multiplication that forms a tumor. Chen et al. (2019) described breast cancer as one of the most prevalent and clinically significant cancers globally, contributing substantially to cancer-related morbidity and mortality, particularly among women. The disease can develop in one or both breasts and may remain localized for a period or become invasive and spread to other parts of the body.

Anatomically, the breast is composed of lobules (which produce milk), ducts (which transport milk to the nipple), fatty tissue, connective tissue, blood vessels, and lymphatic vessels. Breast cancer most commonly begins in the epithelial lining of the ducts, referred to as ductal carcinoma, or in the lobules, known as lobular carcinoma. Once cancer cells break through the duct or lobular walls, they can invade surrounding breast tissue and gradually enter the lymphatic system or bloodstream, enabling metastasis to distant organs such as the lungs, liver, brain, and bones. Garcia et al. (2020) emphasized that metastasis is one of the most dangerous aspects of breast cancer, as it significantly reduces survival chances and complicates treatment.

The etiology of breast cancer is multifactorial, involving genetic, hormonal, environmental, and lifestyle-related factors. Genetic mutations, particularly in the BRCA1 and BRCA2 genes, play a significant role in increasing susceptibility to breast cancer. Individuals with a family history of breast cancer are at a higher risk due to inherited genetic predisposition. Hormonal factors such as prolonged exposure to estrogen, early menstruation, late menopause, and hormone replacement therapy have also been associated with increased risk. Lifestyle factors including obesity, lack of physical activity, alcohol consumption, smoking, and unhealthy diets further contribute to disease development.

In addition, age remains one of the strongest risk factors, with most breast cancer cases occurring in individuals above 40 years. Environmental exposure to radiation and carcinogenic substances may also contribute to abnormal cellular changes in breast tissues. However, it is important to note that the presence of risk factors does not necessarily mean an individual will develop breast cancer; rather, they increase susceptibility.

One of the major challenges in breast cancer management is that the disease often remains asymptomatic in its early stages. When symptoms eventually appear, they may include the presence of a lump in the breast or underarm, changes in breast size or shape, nipple inversion or discharge, skin dimpling, redness, swelling, and persistent pain. Due to the subtle nature of early

symptoms, many cases are diagnosed at advanced stages, which reduces treatment effectiveness and survival rates.

Early detection is therefore critical in improving prognosis and reducing mortality. Common diagnostic methods include mammography, ultrasound imaging, magnetic resonance imaging (MRI), and biopsy. Mammography is widely used for screening due to its ability to detect early-stage tumors, while biopsy remains the gold standard for confirming malignancy. However, these methods are not without limitations. Brown and Miller (2019) noted that traditional diagnostic processes can be time-consuming, expensive, and highly dependent on the expertise of radiologists, which may introduce variability in diagnosis.

The limitations of traditional diagnostic approaches have led to increased interest in computational and automated systems. These systems aim to support clinicians by improving detection speed, reducing human error, and enhancing diagnostic accuracy through data-driven analysis.

2.2.2 Concept of Breast Cancer Classification

Breast cancer classification refers to the process of categorizing breast tumors into distinct groups based on their biological, structural, and clinical characteristics. The primary objective of classification is to determine whether a tumor is benign (non-cancerous) or malignant (cancerous). In more advanced clinical and computational systems, classification may also extend to identifying subtypes of breast cancer based on molecular, histopathological, or imaging features. Singh et al. (2019) emphasized that accurate classification is fundamental to effective diagnosis, treatment planning, and prognosis estimation in breast cancer management.

From a clinical perspective, classification plays a critical role in guiding treatment decisions. Benign tumors are generally non-invasive and do not spread to other parts of the body, although they may still require monitoring or surgical removal depending on their size and location. Malignant tumors, on the other hand, are invasive, aggressive, and capable of metastasizing to distant organs. Therefore, distinguishing between these two categories is essential for determining the urgency and type of treatment required.

Traditionally, breast cancer classification has been carried out through manual interpretation of medical images, histopathological examination, and biopsy results. Radiologists and pathologists analyze tissue samples under a microscope or examine imaging results to identify abnormal growth patterns. While these methods are widely accepted in clinical practice, they are associated with several limitations. Rahman et al. (2020) highlighted that manual classification is

often subjective, time-consuming, and prone to inter-observer variability, where different specialists may interpret the same case differently.

To address these challenges, artificial intelligence techniques such as machine learning and deep learning have been introduced into breast cancer classification systems. Machine learning algorithms are trained using structured datasets containing tumor-related features such as radius, perimeter, area, texture, smoothness, concavity, and symmetry. These algorithms learn patterns from historical data and use them to classify new, unseen cases. Chen et al. (2019) demonstrated that models such as Support Vector Machines (SVM), Decision Trees, K-Nearest Neighbors (KNN), and Naïve Bayes classifiers can achieve high accuracy in distinguishing benign from malignant tumors.

In addition, feature selection techniques are often applied to improve classification performance by removing irrelevant or redundant attributes from the dataset. Li et al. (2022) explained that hybrid models combining feature selection with classification algorithms enhance accuracy, reduce computational cost, and improve generalization performance.

Deep learning approaches have further advanced breast cancer classification, particularly in image-based diagnosis. Wang et al. (2020) showed that Convolutional Neural Networks (CNNs) are capable of automatically extracting complex hierarchical features from medical images such as histopathology slides and mammograms. This eliminates the need for manual feature extraction and allows the model to learn directly from raw image data. Nguyen and Hoang (2021) further confirmed that CNN-based architectures consistently outperform traditional machine learning models in image classification tasks due to their deep feature learning capability.

Transfer learning techniques have also become popular in breast cancer classification, especially when dealing with limited medical datasets. Khan and Rahman (2022) noted that pre-trained deep learning models can be adapted to medical datasets to improve performance and reduce training time. Despite these advantages, challenges such as lack of interpretability, high computational cost, and dependence on large datasets still limit widespread clinical adoption.

Overall, breast cancer classification has evolved from manual clinical assessment to advanced intelligent systems that integrate machine learning and deep learning techniques. These modern approaches have significantly improved diagnostic accuracy, efficiency, and reliability, although further research is still required to address existing limitations and improve real-world applicability.

2.3 Types of Breast Cancer

Breast cancer is not a single uniform disease; rather, it exists in different forms that vary based on the origin of the cancer cells, their biological behavior, rate of growth, and ability to spread. Understanding the different types of breast cancer is very important in medical diagnosis and classification because each type responds differently to treatment and has different survival outcomes. Ahmed et al. (2018) explained that identifying the specific type of breast cancer helps clinicians make accurate treatment decisions and improve patient prognosis.

1. **Ductal Carcinoma In Situ (DCIS):** Ductal Carcinoma In Situ is considered a non-invasive or early-stage breast cancer that begins in the milk ducts of the breast. In this condition, abnormal cells are confined within the ducts and have not spread to surrounding breast tissues. Although DCIS is not life-threatening at the moment of diagnosis, it is considered a precursor to invasive breast cancer if left untreated. Early detection of DCIS is very important because it can be completely treated before it progresses into a more dangerous stage.
2. **Invasive Ductal Carcinoma (IDC):** Invasive Ductal Carcinoma is the most common type of breast cancer, accounting for a large percentage of diagnosed cases worldwide. It begins in the milk ducts but breaks through the duct wall and spreads into surrounding breast tissues. From there, it may further spread to lymph nodes and other parts of the body. Garcia et al. (2020) noted that IDC is highly significant in breast cancer studies because of its high occurrence rate and invasive nature.
3. **Lobular Carcinoma In Situ (LCIS):** Lobular Carcinoma In Situ develops in the milk-producing lobules of the breast. Unlike invasive cancer, LCIS does not spread into surrounding tissues, but it serves as an indicator of increased risk for developing invasive breast cancer in the future. It is often discovered incidentally during biopsy procedures for other breast conditions.
4. **Invasive Lobular Carcinoma (ILC**): Invasive Lobular Carcinoma begins in the lobules and spreads into nearby breast tissues. It is the second most common type of invasive breast cancer after IDC. ILC is often difficult to detect through imaging techniques because it tends to spread in a single-file pattern rather than forming a distinct lump. This makes early diagnosis more challenging.
5. **Inflammatory Breast Cancer**: Inflammatory breast cancer is a rare but very aggressive form of breast cancer. It causes rapid swelling, redness, warmth, and thickening of the breast skin, often without forming a noticeable lump. Davis and Clark (2020) emphasized that this type of cancer progresses quickly and requires immediate medical attention due to its aggressive nature.

6. **Triple-Negative Breast Cancer:** Triple-negative breast cancer is a type of breast cancer that does not contain estrogen receptors, progesterone receptors, or excess HER2 protein. Because of this, it does not respond to hormonal therapy or HER2-targeted treatments. This makes it more difficult to treat compared to other types and is often associated with faster growth and higher recurrence rates.
7. **HER2-Positive Breast Cancer:** HER2-positive breast cancer is characterized by an overexpression of the HER2 protein, which promotes rapid growth of cancer cells. Although this type of cancer is aggressive, it can be effectively treated using targeted therapies that block HER2 activity. Nguyen and Hoang (2021) noted that targeted treatment has significantly improved survival outcomes for patients with this type.
8. **Metastatic Breast Cancer:** Metastatic breast cancer, also known as stage IV breast cancer, occurs when cancer spreads from the breast to distant organs such as the lungs, liver, brain, or bones. This is the most advanced stage of breast cancer and is considered difficult to cure, although it can be managed with ongoing treatment to control its spread and improve quality of life.
9. **Male Breast Cancer:** Although breast cancer is more common in women, it can also occur in men. Male breast cancer usually develops in older men and is often diagnosed at a later stage due to lack of awareness. Symptoms include lumps in the chest area, nipple discharge, and changes in skin texture.
10. **Recurrent Breast Cancer:** Recurrent breast cancer occurs when cancer returns after treatment. It may reappear in the same breast, the opposite breast, or other parts of the body. Recurrence can happen months or years after initial treatment, making continuous monitoring and follow-up very important for early detection.

2.4 Methods of Breast Cancer Classification

Breast cancer classification can be carried out using different approaches depending on the type of data available, the level of technology applied, and the diagnostic objective. These methods range from traditional clinical techniques to advanced computational intelligence systems. The main goal of all classification methods is to accurately distinguish between benign and malignant tumors and, in more advanced systems, identify specific cancer subtypes. Garcia et al. (2020) emphasized that the effectiveness of breast cancer classification largely depends on the quality of data, diagnostic tools, and analytical techniques used.

1. **Clinical Examination Method:** Clinical examination is one of the earliest and most basic methods of breast cancer detection and classification. It involves physical inspection and palpation of the breast by a medical professional to detect lumps, swelling, or unusual

changes in breast shape and texture. This method depends heavily on the experience and skill of the clinician. Although it is useful for initial screening, it is not always sufficient for accurate classification because early-stage tumors may not be easily detectable through physical examination alone.

2. **Mammography-Based Classification:** Mammography is a medical imaging technique that uses low-dose X-rays to examine breast tissues. It is widely used for early detection and classification of breast abnormalities. Mammograms help in identifying microcalcifications and masses that may indicate cancer. Davis and Clark (2020) noted that mammography is one of the most effective screening tools for early breast cancer detection, although its accuracy may be affected by breast density and human interpretation errors.
3. **Ultrasound Imaging Method:** Ultrasound imaging uses high-frequency sound waves to produce images of breast tissues. It is often used as a complementary method to mammography, especially in cases where additional clarification is needed. Ultrasound helps differentiate between solid masses and fluid-filled cysts. However, its effectiveness depends on the operator's expertise and may not always provide definitive classification results.
4. **Magnetic Resonance Imaging (MRI) Method:** MRI is a more advanced imaging technique that provides detailed images of breast tissues using magnetic fields and radio waves. It is particularly useful for high-risk patients and complex cases. MRI can detect abnormalities that may not be visible in mammograms or ultrasound images. However, it is expensive and not always widely available, limiting its use in routine screening.
5. **Biopsy-Based Classification Method**: Biopsy is considered the most accurate method for breast cancer diagnosis and classification. It involves removing a small sample of breast tissue and examining it under a microscope to determine whether cancer cells are present. While biopsy provides highly reliable results, it is invasive, time-consuming, and may cause discomfort to patients. Despite these limitations, it remains the gold standard for confirming breast cancer.
6. **Histopathological Classification Method:** Histopathological classification involves examining tissue samples under a microscope to study cellular structures and identify cancerous changes. Pathologists analyze cell shape, size, and organization to determine whether a tumor is benign or malignant. Wang et al. (2020) noted that histopathological analysis is highly accurate but requires skilled experts and may still be subject to interpretation differences among pathologists.
7. **Machine Learning-Based Classification Method:** Machine learning-based classification uses algorithms trained on structured medical datasets to automatically classify breast cancer cases. These systems analyze features such as tumor radius, texture, perimeter, smoothness, and concavity to detect patterns associated with cancer types. Chen et al. (2019) explained

that machine learning models such as Support Vector Machines (SVM), Decision Trees, K-Nearest Neighbors (KNN), and Naïve Bayes classifiers are widely used for breast cancer classification. These methods improve accuracy, reduce human error, and support faster diagnosis.

8. **Deep Learning-Based Classification Method:** Deep learning methods use artificial neural networks, especially Convolutional Neural Networks (CNNs), to automatically learn features from medical images without manual feature extraction. These models are highly effective in analyzing complex patterns in histopathological and mammography images. Nguyen and Hoang (2021) stated that deep learning models generally outperform traditional machine learning techniques in image-based breast cancer classification due to their ability to learn deep hierarchical features.
9. **Hybrid Classification Methods:** Hybrid methods combine different techniques such as feature selection, machine learning algorithms, and optimization strategies to improve classification performance. Li et al. (2022) noted that hybrid models help improve accuracy, reduce redundant features, and enhance computational efficiency. These methods are increasingly used in modern breast cancer classification systems to overcome the limitations of single-model approaches.

2.5 Machine Learning and Deep Learning methods of Breast Cancer Classification

2.5.1 Machine Learning Models For Breast Cancer Classification

Machine learning (ML) models have become one of the most widely applied computational approaches in breast cancer classification due to their ability to learn patterns from structured medical datasets and make predictions without explicit programming. These models rely on historical data containing diagnostic features such as tumor radius, texture, perimeter, smoothness, concavity, symmetry, and fractal dimension. Chen et al. (2019) emphasized that machine learning techniques significantly improve breast cancer diagnostic accuracy by identifying hidden patterns that may not be easily detected by human experts.

One of the most widely used machine learning algorithms in breast cancer classification is the Support Vector Machine (SVM). SVM works by constructing an optimal hyperplane that separates data points belonging to different classes with the maximum margin. This makes it highly effective in handling high-dimensional datasets, especially in medical classification problems where feature spaces are complex. Garcia et al. (2020) noted that SVM performs strongly in binary classification tasks such as distinguishing between benign and malignant tumors due to its robustness and generalization capability.

Another important model is the Decision Tree classifier, which works by recursively splitting data based on feature values until a final classification decision is reached. Each internal node represents a decision based on a feature, while each leaf node represents a class label. Johnson and Lee (2018) explained that Decision Trees are highly interpretable, making them suitable for healthcare applications where transparency and explainability are important for clinical trust and adoption. However, they are prone to overfitting if not properly controlled.

The K-Nearest Neighbors (KNN) algorithm is also commonly used in breast cancer classification. KNN is a non-parametric algorithm that classifies new data points based on the majority class of their nearest neighbors in the feature space. Kumar and Sharma (2019) stated that KNN performs well when datasets are clean and well-structured, but its performance decreases significantly with large datasets due to high computational cost and sensitivity to irrelevant features.

Naïve Bayes is another probabilistic classifier used in breast cancer prediction systems. It is based on Bayes' theorem and assumes that all features are independent of each other. Patel et al. (2020) observed that Naïve Bayes is computationally efficient and performs well on small to medium-sized datasets. However, its main limitation lies in the unrealistic assumption of feature independence, which may not always hold true in real medical data where features are often correlated.

Ensemble learning methods such as Random Forest and Gradient Boosting have also gained popularity in breast cancer classification. These methods combine multiple weak learners to create a stronger predictive model. Rahman et al. (2020) found that ensemble models generally outperform individual classifiers in terms of accuracy, stability, and generalization. They also reduce overfitting by aggregating predictions from multiple models, making them more reliable for real-world applications.

Despite their advantages, machine learning models still face several challenges in breast cancer classification. These include class imbalance, feature redundancy, overfitting, and dependency on handcrafted feature engineering. Hassan and Ibrahim (2021) emphasized that proper preprocessing techniques such as normalization, feature scaling, and missing value handling are critical for improving model performance.

2.5.2 Deep Learning Models For Breast Cancer Classification

Deep learning models represent an advanced branch of machine learning that is capable of automatically learning hierarchical representations of data. Unlike traditional machine learning models, deep learning systems do not rely heavily on manual feature extraction. Instead, they

learn directly from raw data, particularly image data such as mammograms, ultrasound scans, and histopathological images. Wang et al. (2020) explained that deep learning has significantly transformed medical image analysis by improving diagnostic accuracy and reducing reliance on manual feature engineering.

The most commonly used deep learning architecture in breast cancer classification is the Convolutional Neural Network (CNN). CNNs are specifically designed to process image data through convolutional layers, pooling layers, and fully connected layers. These layers help the model detect low-level features such as edges and textures, as well as high-level features such as tumor shape and structure. Nguyen and Hoang (2021) reported that CNN-based models consistently outperform traditional machine learning algorithms in breast cancer image classification due to their strong feature learning capability.

Another important deep learning model is the Artificial Neural Network (ANN), which consists of interconnected neurons organized in multiple layers. ANN models are capable of learning nonlinear relationships in data and are widely used in both structured and unstructured medical datasets. However, their performance depends on the quality of data and network architecture design.

Transfer learning has also become a dominant technique in breast cancer classification, especially when labeled medical datasets are limited. This approach involves using pre-trained deep learning models such as VGG16, ResNet, DenseNet, and Inception, which have already been trained on large image datasets. Khan and Rahman (2022) noted that transfer learning significantly improves classification performance while reducing training time and computational cost, making it highly suitable for medical applications with limited data availability.

Deep Neural Networks (DNNs), which consist of multiple hidden layers, are also used in breast cancer classification to capture complex nonlinear relationships in data. Gupta and Patel (2021) explained that DNNs provide superior feature extraction capabilities compared to traditional models, allowing them to achieve high accuracy in complex classification tasks.

Despite their high performance, deep learning models face several challenges. These include high computational requirements, need for large labeled datasets, long training times, and lack of interpretability. Davis and Clark (2020) emphasized that the “black box” nature of deep learning models remains a major limitation in healthcare applications, as clinicians require explainable results before trusting automated systems.

In summary, while machine learning models rely heavily on handcrafted features and structured datasets, deep learning models automatically extract features from raw data and

achieve higher accuracy, especially in image-based breast cancer classification tasks. Both approaches remain important in medical diagnosis systems, and hybrid approaches are increasingly being explored to combine their strengths.

2.6 Summary Of Chapter

A comprehensive review of existing literature on breast cancer classification using machine learning and deep learning techniques has been presented. The discussion began with breast cancer as a critical global health challenge characterized by abnormal and uncontrolled cell growth in breast tissues. The increasing prevalence of the disease highlights the importance of early detection and accurate classification in improving patient survival rates and treatment effectiveness.

Breast cancer was further examined in terms of its biological development, risk factors, symptoms, and diagnostic challenges. It was established that breast cancer is a complex disease influenced by genetic, hormonal, environmental, and lifestyle factors. Early detection remains a major challenge due to the asymptomatic nature of the disease in its initial stages, which often leads to late diagnosis and reduced treatment success.

The concept of breast cancer classification was also discussed, where classification plays a crucial role in distinguishing between benign and malignant tumors, as well as identifying different cancer subtypes. Traditional classification methods such as clinical examination, imaging techniques, and biopsy were highlighted along with their limitations, including subjectivity, high cost, and dependence on expert interpretation.

Various methods of breast cancer classification were also reviewed, ranging from conventional diagnostic approaches such as mammography, ultrasound, MRI, and histopathology to modern computational techniques. While traditional methods remain essential in clinical practice, they are increasingly being supported by intelligent systems due to limitations in speed, scalability, and accuracy.

Machine learning and deep learning approaches were extensively reviewed. Machine learning models such as Support Vector Machines, Decision Trees, K-Nearest Neighbors, Naïve Bayes, and ensemble methods were highlighted for their effectiveness in analyzing structured medical datasets. These models improve diagnostic accuracy by learning patterns from historical data but are limited by feature dependency and manual preprocessing requirements.

Deep learning models, particularly Convolutional Neural Networks, were also discussed and shown to outperform traditional machine learning techniques in image-based breast cancer

classification. Techniques such as transfer learning and deep neural networks were identified as powerful tools for improving classification accuracy, especially when working with limited datasets. However, challenges such as high computational cost, lack of interpretability, and data dependency remain significant limitations.

The review of related works shows that several researchers have made significant contributions to improving breast cancer classification using different machine learning and deep learning approaches. However, despite these advancements, issues such as overfitting, limited generalization, dataset imbalance, and lack of real-world clinical deployment still exist.

In conclusion, while significant progress has been made in breast cancer classification using intelligent systems, there is still a need for more robust, accurate, and generalizable models. This justifies continued research into improved machine learning and deep learning frameworks capable of enhancing diagnostic performance and supporting early detection in real-world healthcare environments.

CHAPTER THREE

RESEARCH METHODOLOGY

3.0 Introduction

This chapter presents the methodology adopted for the development of a machine learning-based system for breast cancer type classification. The methodology outlines the procedures involved in data acquisition, preprocessing, model development, training, testing, and performance evaluation. The study employs a supervised machine learning approach to classify breast cancer cases into benign and malignant categories using diagnostic features extracted from a breast cancer dataset.

The Wisconsin Diagnostic Breast Cancer Dataset was utilized in this study because it contains relevant clinical and diagnostic features commonly used in breast cancer prediction research. Prior to model development, the dataset underwent several preprocessing procedures, including data cleaning, feature extraction, data transformation, and feature scaling. These processes were carried out to improve data quality, remove inconsistencies, and enhance the performance and reliability of the classification model.

A Stochastic Gradient Descent (SGD)-based machine learning classifier was used for the classification task due to its effectiveness in handling binary classification problems and its ability to learn iteratively through multiple training epochs. The model was trained and evaluated using processed breast cancer data to identify patterns associated with benign and malignant tumors. Performance assessment was carried out using evaluation metrics such as accuracy, precision, recall, F1-score, confusion matrix, and Receiver Operating Characteristic–Area Under Curve (ROC-AUC) to determine the effectiveness of the developed classification system.

3.1 Overview of the Proposed System

The proposed system is a machine learning-based breast cancer type classification model designed to improve the accuracy and efficiency of breast cancer diagnosis by automatically classifying cases into benign and malignant categories using diagnostic features. The system follows a structured workflow that involves data acquisition, preprocessing, feature scaling, and transformation to ensure the dataset is suitable for training. A Stochastic Gradient Descent (SGD)-based classifier is then used to learn patterns within the data through iterative training over multiple epochs, enabling the model to progressively optimize its performance. After training, the

model is evaluated using standard performance metrics such as accuracy, precision, recall, F1-score, confusion matrix, and ROC-AUC to determine its effectiveness as a decision-support tool for breast cancer classification.

3.1.1 System Architecture

The system architecture of the proposed breast cancer classification model is structured into four main layers: input layer, preprocessing layer, classification layer, and output layer. The input layer receives the Wisconsin Diagnostic Breast Cancer dataset, which contains diagnostic features such as tumor radius, texture, perimeter, and smoothness. The preprocessing layer performs data cleaning, feature scaling, and transformation to ensure that the dataset is in an optimal format for model training. The classification layer consists of a Stochastic Gradient Descent (SGD)-based machine learning algorithm, which learns patterns in the data through iterative training over multiple epochs and adjusts its parameters to minimize classification error. Finally, the output layer produces the prediction result, classifying each case as either benign or malignant, and the evaluation module measures the model's performance using standard metrics such as accuracy, precision, recall, F1-score, and ROC-AUC.

1. Input Layer

The input layer represents the initial stage of the system where raw medical data is introduced for processing and analysis.

1. The Wisconsin Diagnostic Breast Cancer dataset is used as the primary input for the proposed system. This dataset is widely used in medical machine learning research because it contains reliable diagnostic information for breast cancer classification.
2. The dataset consists of multiple clinical features extracted from digitized images of breast tissue samples. These features include tumor radius, texture, perimeter, area, smoothness, compactness, concavity, and symmetry. Each of these attributes provides meaningful information about the structure and characteristics of breast masses.
3. The input data also includes a diagnosis label that indicates whether a tumor is benign or malignant. This label serves as the target variable for supervised learning.
4. At this stage, the dataset is in its raw form, meaning it may contain inconsistencies, unnecessary columns, and unscaled numerical values that must be processed before being used for model training.

2. Preprocessing Layer

The preprocessing layer is responsible for transforming raw data into a clean and structured format suitable for machine learning algorithms.

1. The first step in preprocessing involves data cleaning, where irrelevant columns such as patient identification numbers and unnamed fields are removed to avoid noise in the dataset.
2. The categorical target variable (diagnosis) is converted into numerical format, where benign cases are represented as 0 and malignant cases are represented as 1. This conversion is necessary because machine learning models can only process numerical values.
3. Feature scaling is then applied using StandardScaler to normalize all input variables. This ensures that all features contribute equally to the learning process and prevents features with larger numerical values from dominating the model training process.
4. Preprocessing also helps improve convergence speed and model stability, especially for gradient-based algorithms such as Stochastic Gradient Descent (SGD), which are sensitive to feature scaling.

3. Classification Layer

The classification layer is the core component of the system where the actual learning and pattern recognition occur.

1. The classification is performed using a classifier, which is a supervised machine learning algorithm commonly used for large-scale and high-dimensional datasets.
2. The model learns patterns by iteratively updating its internal parameters (weights) using the partial_fit function. This allows the model to learn progressively rather than processing the entire dataset in a single pass.
3. The iterative training process is carried out over multiple epochs, where each epoch represents one complete pass through the training dataset. During each epoch, the model improves its performance by minimizing classification errors.
4. The SGD algorithm works by adjusting weights in the direction that reduces the loss function, enabling the model to learn the relationship between input features and output labels effectively.
5. Through this process, the model becomes capable of distinguishing between benign and malignant tumors based on learned patterns in the dataset.

4. Output Layer

The output layer is responsible for generating the final classification results after the model has completed training.

1. Once training is completed, the model is used to predict unseen test data to evaluate its performance.
2. The output is presented in binary form, where class “0” represents a benign tumor and class “1” represents a malignant tumor.
3. In addition to binary classification, the model also produces probability values that indicate the confidence level of each prediction. These probabilities help in understanding how certain the model is about its decisions.
4. The output layer provides the final decision-making results, which are later used for performance evaluation and analysis.

5. Evaluation Layer

The evaluation layer measures how well the model performs in classifying breast cancer cases.

1. Accuracy is used to measure the proportion of correctly classified instances out of the total predictions made by the model.
2. Precision evaluates the proportion of correctly predicted positive cases (malignant tumors) out of all predicted positive cases.
3. Recall measures the model’s ability to correctly identify actual malignant cases from the dataset.
4. F1-score is used to provide a balance between precision and recall, especially in cases where class distribution is not perfectly balanced.
5. (v) The confusion matrix is used to visually represent the number of correct and incorrect predictions made by the model.
6. The ROC-AUC curve is used to evaluate the model’s ability to distinguish between benign and malignant cases across different threshold values, providing a measure of classification strength.

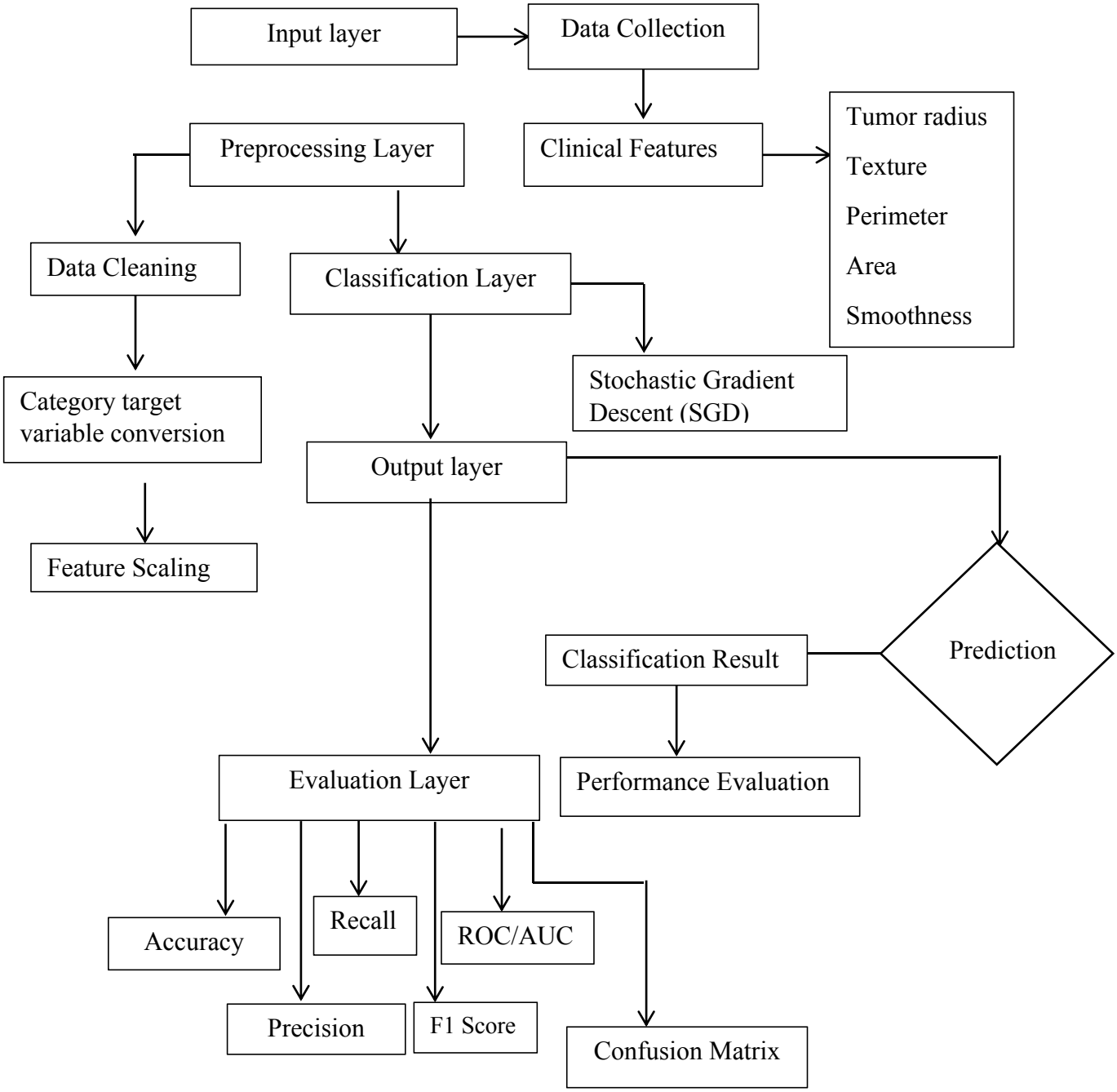


Figure 3.1 Proposed System Architetcture

3.1.1 Flow chart

The following flowchart provides a visual representation of the proposed system's workflow, illustrating the sequence of steps from data collection to performance and evaluation.

Figure 3.2 below illustrates the flowchart of the proposed system

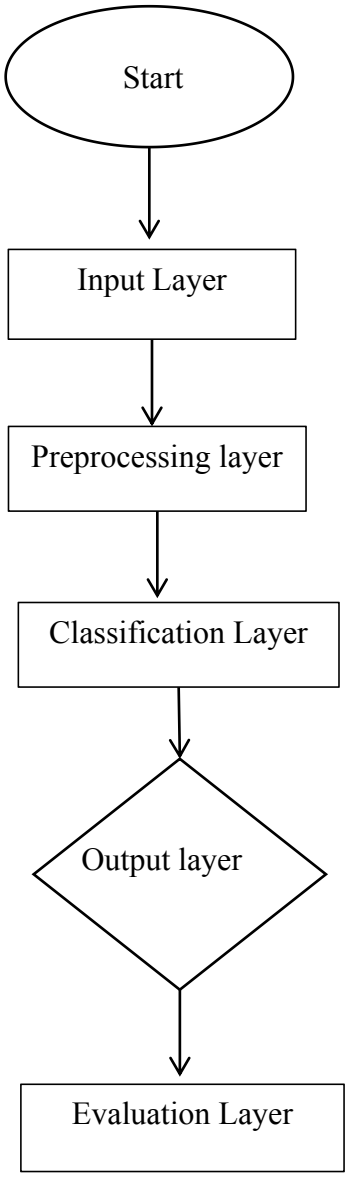


Figure 3.2 Flow chart of the Proposed system

3.2 Data Collection and Preprocessing

Data collection is the foundational stage in the development of the proposed breast cancer classification system, as it determines the quality, reliability, and effectiveness of the machine learning model. In any data-driven healthcare system, the accuracy of predictions is highly dependent on the nature and representativeness of the collected dataset. Therefore, this stage involves the systematic gathering of relevant medical data that will be used for training, validation, and testing of the classification model.In this study, the data collection process focuses on acquiring structured clinical diagnostic data that can be used to distinguish between benign and malignant breast cancer cases. The dataset is carefully selected to ensure it contains meaningful features that reflect real-world medical conditions and can support the development of an intelligent predictive model.

3.2.1 Data Source

The dataset used in this research is the Wisconsin Diagnostic Breast Cancer (WDBC) dataset, which is one of the most widely used benchmark datasets in medical machine learning research. It is publicly available and frequently used for evaluating classification algorithms in healthcare-related studies. The dataset originates from digitized images of fine needle aspirates (FNA) of breast masses. These images were analyzed using image processing techniques to extract quantitative features that describe the characteristics of cell nuclei. These extracted features serve as diagnostic indicators that help differentiate between benign and malignant tumors. The WDBC dataset is considered highly reliable because it has been validated in several clinical and academic studies. It is also suitable for supervised learning because each sample is labeled with a known diagnosis outcome, making it ideal for training classification algorithms.

3.2.2 Data Acquisition Procedure, Paramters, Characteristics and Relevance

Data Acquisition Procedure

The data acquisition procedure describes how the dataset is obtained, loaded, and prepared for analysis within the machine learning environment. In this study, the dataset is obtained in CSV format and imported into a Python programming environment using the Pandas library.After loading, the dataset is converted into a structured tabular format known as a dataframe. Each row in the dataset represents a single patient case, while each column represents a diagnostic feature extracted from breast tissue samples. During the acquisition stage, a careful inspection of the dataset is performed to ensure that it is complete, consistent, and free from structural errors.

Irrelevant columns such as patient identification numbers and unnamed index fields are removed, as they do not contribute to the predictive performance of the model.

Data Parameters:

The dataset contains 30 numerical diagnostic features that describe the physical and structural characteristics of breast cell nuclei. These features are computed from digitized images and provide detailed information about cellular morphology.

The key parameters include:

1. Radius (mean distance from center to perimeter points)
2. Texture (variation in grayscale intensity)
3. Perimeter (length of cell boundary)
4. Area (size of the nucleus)
5. Smoothness (local variation in radius lengths)
6. Compactness ($\text{perimeter}^2 / \text{area} - 1.0$)
7. Concavity (severity of concave portions of the contour)
8. Concave points (number of concave portions)
9. Symmetry (measure of shape symmetry)
10. Fractal dimension (complexity of the boundary shape)

Each of these features plays a significant role in identifying abnormal cell behavior. Malignant tumors tend to exhibit irregular shapes, higher variability in texture, and increased concavity compared to benign tumors. These differences allow the machine learning model to learn discriminative patterns for classification.In this system, these features serve as independent variables (X), while the diagnosis label serves as the dependent variable (y), which is used as the output class for the Stochastic Gradient Descent (SGD) Classifier.

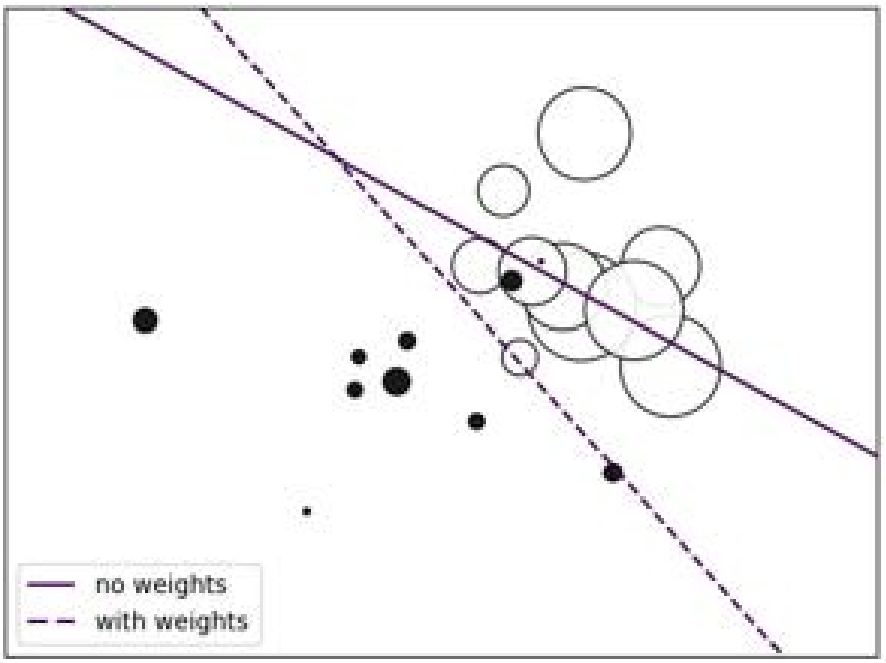


Figure 3.3 shows the model representation of the Stochastic Gradient Descent (SGD)Classifier.

Scikit-learn developers. (n.d.). SGDClassifier. Scikit-learn.nJuly 22, 2020, from https://scikit-learn.org/stable/modules/generated/sklearn.linear_model.SGDClassifier.html

Data Characteristics and Relevance:

The WDBC dataset is characterized by its structured format, numerical consistency, and high diagnostic relevance. Unlike unstructured datasets such as images or text, this dataset is already preprocessed to a large extent, making it suitable for direct application in machine learning algorithms. The dataset is balanced in terms of class distribution, containing both benign and malignant cases, which helps reduce bias during model training. This balance improves the ability of the model to learn both classes effectively and prevents overfitting toward one dominant class. Additionally, the dataset contains continuous numerical values, which makes it highly compatible with algorithms such as Stochastic Gradient Descent (SGD), Support Vector Machines (SVM), and ensemble models.

3.2.3 Data Preprocessing

Data preprocessing is a crucial stage in the proposed breast cancer classification system, as it transforms raw medical data into a clean, structured, and optimized format suitable for machine learning analysis. The quality of preprocessing directly affects the performance, stability, and accuracy of the classification model. In this study, preprocessing is performed to ensure that the dataset is free from inconsistencies, properly scaled, and suitable for training the Stochastic Gradient Descent (SGD)-based classification model. The preprocessing stage bridges the gap between raw data collection and model training by ensuring that only meaningful, consistent, and normalized data is passed into the classification layer.

3.2.4 Data Cleaning

Data cleaning is the first step in the preprocessing stage and involves removing irrelevant, redundant, or non-informative attributes from the dataset. In the Wisconsin Diagnostic Breast Cancer dataset, columns such as patient ID and unnamed index fields are removed because they do not contribute to the prediction of cancer type. After removing irrelevant features, the dataset is checked for missing values, null entries, and duplicate records. Since the dataset is already well-structured, missing values are minimal; however, verification is performed to ensure data integrity.

The diagnosis column is also converted from categorical values into numerical format, where:

1 .Malignant (M) is encoded as 1

2. Benign (B) is encoded as 0

This transformation is necessary because machine learning algorithms require numerical inputs for computation.

3.2.5 Data Normalization and Noise Reduction

Data Normalization (Feature Scaling):

Data normalization is applied to ensure that all features contribute equally to the learning process. Since the dataset contains variables with different scales and magnitudes, normalization is necessary to prevent features with larger numerical values from dominating the model training process.

In this study, StandardScaler is used to standardize the dataset such that each feature has:

1. Mean = 0
2. Standard Deviation = 1

This transformation improves the convergence speed of the Stochastic Gradient Descent (SGD) classifier and enhances overall model stability. Without normalization, gradient-based learning algorithms may converge slowly or produce suboptimal results due to scale imbalance among features.

Noise Reduction:

Noise reduction is performed to improve the quality and reliability of the dataset. In medical datasets, noise refers to irrelevant variations or inconsistencies that may affect model learning.

In this system, noise reduction is achieved through:

1. Removal of irrelevant columns
2. Standardization of feature values
3. Elimination of redundant information
4. Consistent encoding of categorical variables

These steps ensure that the model learns meaningful patterns rather than random fluctuations in the data.

3.3 Proposed Model, Training Algorithm and Implementation

The proposed breast cancer classification system is designed to classify breast tumors into benign and malignant categories using machine learning techniques. The system utilizes diagnostic features extracted from breast tissue samples contained in the Wisconsin Diagnostic Breast Cancer (WDBC) dataset. The objective of the model is to learn patterns and relationships within the dataset and accurately predict the type of breast cancer based on the input features. The implementation process consists of several stages, including data loading and preparation, label encoding, data splitting, dataset preparation, model training, and performance evaluation. These stages ensure that the dataset is properly processed and transformed into a format suitable for machine learning. The proposed model is trained using multiple training and testing partition ratios to determine the most effective configuration for breast cancer classification.

3.3.1 Data Loading and Preparation for the Model

The first stage in the implementation process involves loading the Wisconsin Diagnostic Breast Cancer dataset into the Python programming environment. The dataset is stored in Comma Separated Values (CSV) format and is imported using the Pandas library, which provides efficient tools for data manipulation and analysis. After loading the dataset, an initial examination is performed to understand its structure, dimensions, feature composition, and overall quality. The dataset contains several diagnostic measurements extracted from digitized images of breast cell nuclei. These measurements serve as predictive features for the classification model.

During the preparation stage, irrelevant attributes that do not contribute to the classification process are removed. Such attributes include patient identification numbers and unnamed columns that may have been generated during data collection or storage. Removing these attributes reduces computational complexity and prevents the model from learning meaningless patterns. The remaining diagnostic features are retained as input variables, while the diagnosis column is selected as the target variable. This preparation stage ensures that the dataset contains only meaningful information required for model training and prediction.

3.3.2 Label Encoding

Machine learning algorithms require numerical data for efficient computation. Therefore, the diagnosis labels in the dataset are transformed from categorical values into numerical representations through a process known as label encoding.

The original diagnosis classes are represented as:

1. Malignant (M)
2. Benign (B)

These labels are converted into numerical values as follows:

1. Malignant (M) = 1
2. Benign (B) = 0

This transformation allows the machine learning model to process the target variable during training and prediction. Label encoding also ensures consistency throughout the implementation process and improves compatibility with machine learning algorithms. The encoded diagnosis

values serve as the output classes that the model attempts to predict based on the input diagnostic features.

3.3.3 Data Splitting

After data preparation and label encoding, the dataset is divided into training and testing subsets. Data splitting is an essential procedure in machine learning because it allows the model to be trained on one portion of the data and evaluated on another independent portion. The training dataset is used to teach the model the relationships between input features and diagnosis labels, while the testing dataset is used to assess the model's ability to generalize to unseen data.To investigate the impact of different training data sizes on model performance, three train-test partition ratios are employed in this study:

1. 80:20 Partition Ratio: In this configuration, 80% of the dataset is allocated for model training, 10% for validation, while the remaining 10% is reserved for testing. This partition provides a large amount of training data, enabling the model to learn more comprehensive patterns from the dataset.
2. 75:25 Partition Ratio: In this configuration, 75% of the dataset is used for training, 10% for validation and 15% is used for testing. This ratio provides a balance between training and evaluation data, allowing the model to learn effectively while maintaining sufficient testing samples for performance assessment.
3. 70:30 Partition Ratio: In this configuration, 70% of the dataset is allocated for training, 15% for validation and 15% is allocated for testing. Although the model receives fewer training samples, the larger testing set provides a more rigorous evaluation of model performance and generalization capability.
4. The splitting process is performed using the train_test_split() function from the Scikit-learn library. Randomization is applied during splitting to ensure that the data distribution remains unbiased and representative across all subsets.

Table 3.1 Dataset Split Ratio

TRAINING	VALIDATION	TESTING
80%	10%	10%
70%	15%	15%
75%	10%	15%

3.3.4 Dataset

The dataset used in this study is the Wisconsin Diagnostic Breast Cancer (WDBC) dataset. It is a publicly available medical dataset widely used for breast cancer classification research and machine learning experimentation. The dataset consists of diagnostic measurements computed from digitized images of breast cell nuclei obtained through Fine Needle Aspiration (FNA) procedures. Each sample in the dataset represents a single patient record and contains thirty numerical features that describe various characteristics of cell nuclei. These features provide valuable information about the structural and morphological properties of breast tissue cells. Variations in these measurements are often associated with the presence or absence of malignant tumors.

The dataset contains two target classes:

1. Benign Tumor (Non-cancerous)
2. Malignant Tumor (Cancerous)

The combination of these diagnostic features and target labels makes the dataset suitable for supervised machine learning classification.

3.3.5 Training Details

The training process for the proposed breast cancer classification model involved the following:

1. Dataset: The Wisconsin Diagnostic Breast Cancer (WDBC) dataset sourced from Kaggle was used for model training and evaluation. The dataset contains thirty diagnostic features extracted from digitized images of breast cell nuclei, including radius, texture, perimeter, area, smoothness, compactness, concavity, concave points, symmetry, and fractal dimension.

i. Split the dataset into training (70%), validation (15%) and testing (15%) subsets.

ii. Split the dataset into training (75%), validation (10%) and testing (15%) subsets.

iii. Split the dataset into training (80%), validation (10%) and testing (10%) subsets.

3. Feature Scaling: The StandardScaler technique was applied to normalize the dataset before training. This ensured that all input features were transformed to a common scale, improving the efficiency and stability of the learning process.
4. Classifier: The Stochastic Gradient Descent (SGD) classifier was employed as the machine learning model. The classifier learns from the training data by iteratively updating its parameters to minimize classification errors and improve prediction accuracy.
5. Loss Function: The binary cross-entropy loss function was utilized because the study involves a binary classification task consisting of two classes: benign and malignant breast tumors.
6. Epochs: The model was trained for 20 epochs with a batch size of 16. During each epoch, the model processed the training data, calculated prediction errors, and updated its parameters to improve classification performance.

3.3.6 Model Implementation

The implementation phase involves translating the proposed breast cancer classification model into executable code using appropriate machine learning tools and software libraries. This phase includes dataset preparation, model development, training, validation, and performance evaluation. The implementation was carried out using Python and several machine learning libraries to ensure efficient data processing, model training, and result visualization.

3.3.6.1 Software and Tools

1. Programming Language

i. Python

Python was used as the primary programming language for implementing the breast cancer classification model. It was selected because of its simplicity, flexibility, and extensive support for machine learning and data analysis applications.

2. Key Libraries and Frameworks

For Machine Learning

i. Scikit-learn

Scikit-learn was used for data preprocessing, train-test splitting, feature scaling, model development, and performance evaluation. The library provides efficient machine learning algorithms and utilities required for breast cancer classification.

For Data Handling

i. Pandas

Used for loading, organizing, cleaning, and manipulating the breast cancer dataset stored in CSV format.

ii. NumPy

Used for numerical computations, array operations, and mathematical transformations required during preprocessing and model training.

For Model Evaluation and Visualization

i. Matplotlib

Used for plotting training accuracy curves, loss curves, ROC curves, and other graphical representations of model performance.

ii. Seaborn

Used for visualizing confusion matrices and enhancing the presentation of performance evaluation results.

3. Development Environment

i. Google Colab

Google Colab was used as the development environment for implementing and training the machine learning model. It provides a cloud-based platform that supports Python programming and machine learning libraries without requiring local installation.

3.3.7 Model Building

1. The proposed breast cancer classification model was developed using the Wisconsin Diagnostic Breast Cancer dataset. The dataset contains thirty diagnostic features describing the characteristics of breast cell nuclei, including radius, texture, perimeter, area, smoothness, compactness, concavity, concave points, symmetry, and fractal dimension. These features serve as input variables for the classification process.

2. During model construction, irrelevant attributes such as patient identification numbers and unnamed columns were removed from the dataset. The diagnosis attribute was encoded into numerical values, where benign tumors were represented as 0 and malignant tumors were represented as 1. This encoding allowed the machine learning model to process the target labels efficiently.
3. Feature normalization was performed using the StandardScaler technique to standardize the dataset and ensure that all input variables contributed equally during training. The processed data was then supplied to the machine learning classifier for learning and prediction.

3.3.8 Model Compilation

1. The model was configured using the Stochastic Gradient Descent (SGD) optimization approach. SGD updates model parameters iteratively by minimizing classification errors during training. This optimization strategy improves convergence and enables the model to learn discriminative patterns from the dataset.
2. Binary cross-entropy loss was employed because the study focuses on a binary classification problem involving two output classes: benign and malignant breast tumors. The loss function measures the difference between predicted outputs and actual diagnosis labels during training.
3. Appropriate training parameters were selected to ensure effective learning, including the number of epochs, batch size, and learning rate. These parameters influence the speed, stability, and overall performance of the classification model.

3.3.9 Model Training

1. The model was trained using three train-test partitioning strategies: 70:30, 75:25, and 80:20. These configurations were adopted to investigate the effect of training data size on classification performance.
2. The training process was conducted for 20 epochs, allowing the model to perform multiple passes through the training dataset and progressively improve its predictive capability.
3. A batch size of 128 was utilized during training. This means that sixteen samples were processed before updating the model parameters, providing a balance between computational efficiency and learning stability.
4. During each epoch, the model generated predictions, calculated classification errors, and adjusted its internal parameters to minimize loss and improve classification accuracy.

3.4 Performance Metrics

Performance metrics are essential for evaluating the effectiveness and reliability of the proposed breast cancer classification model. After training the model, several evaluation measures were employed to assess its ability to correctly classify breast tumors as benign or malignant. These metrics provide quantitative evidence of the model's predictive capability and help determine its suitability for medical diagnosis applications.

1. Accuracy: Accuracy measures the overall proportion of correctly classified instances to the total number of instances in the dataset. It indicates how well the model performs in distinguishing between benign and malignant tumors.

$$\text{Formula} = \frac{True\ Positive + True\ Negative}{True\ Positive + True\ Negative + FalsePositive + False\ Negative} \quad (1)$$

2. Precision: Precision measures the proportion of correctly predicted positive cases among all cases predicted as positive. It evaluates the model's ability to avoid false positive predictions.

$$\text{Formula} = \frac{True\ Positive}{True\ Positive + False\ Postive} \quad (2)$$

3. Recall (Sensitivity): Recall measures the proportion of actual positive cases that are correctly identified by the model. It evaluates the model's ability to detect malignant breast cancer cases.

$$\text{Formula} = \frac{True\ Positive}{True\ Postive + False\ Negative} \quad (3)$$

4. F1-Score: The F1-Score is the harmonic mean of precision and recall. It provides a balanced measure of classification performance, especially when dealing with imbalanced datasets.

$$\text{Formula} = 2 * \frac{Precision * Recall}{Precision + Recall} \quad (4)$$

5. Confusion Matrix: The confusion matrix is a tabular representation of the classification results. It summarizes the number of correctly and incorrectly classified instances by comparing actual class labels with predicted labels.

Formula: $\begin{bmatrix} True\ postives & False\ positives \\ False\ negatives & True\ negatives \end{bmatrix}$ (5)

6. Receiver Operating Characteristic (ROC) Curve: The ROC curve is a graphical representation used to evaluate the classification performance of the model at different threshold values. It plots the True Positive Rate (TPR) against the False Positive Rate (FPR).
7. Area Under the Curve (AUC): The Area Under the ROC Curve (AUC) measures the overall ability of the model to discriminate between positive and negative classes. The AUC value ranges from 0 to 1.

3.5 Summary of the Chapter

This chapter outlines the methodology adopted for the design, development, and implementation of the proposed breast cancer classification system. The chapter commenced with an introduction to the proposed system, outlining the overall framework and operational workflow of the model. The system architecture was presented to illustrate the sequence of activities involved in the classification process, beginning from data collection and preprocessing through model training and performance evaluation. In addition, the system flowchart was discussed to provide a visual representation of the processes involved in transforming raw medical data into meaningful classification results.

This study described the data collection and preprocessing stages employed in this study. The Wisconsin Diagnostic Breast Cancer (WDBC) dataset was identified as the primary source of data used for model development. The dataset consists of diagnostic features extracted from digitized images of breast cell nuclei and serves as the foundation for training and evaluating the classification model. Data preprocessing techniques such as data cleaning, label encoding, feature scaling, and normalization were applied to improve data quality and ensure compatibility with the machine learning algorithm. These preprocessing operations helped eliminate irrelevant attributes, standardize feature values, and prepare the dataset for effective model training.

Furthermore, the chapter presented the proposed model, training algorithm, and implementation procedures adopted for breast cancer classification. The implementation process involved data loading, preparation of input features and target labels, dataset partitioning using three train-test ratios (70:30, 75:25, and 80:20), and model training. The software tools and libraries utilized during implementation, including Python, Pandas, NumPy, Scikit-learn, Matplotlib, and Seaborn, were also discussed. Details of model building, training configurations, validation procedures, and testing processes were provided to demonstrate how the classification system was developed and optimized.

In conclusion, the chapter discussed the performance evaluation metrics used to assess the effectiveness of the proposed model. Metrics such as Accuracy, Precision, Recall, F1-Score, Confusion Matrix, ROC Curve, and Area Under the Curve (AUC) were presented as measures for evaluating classification performance. These metrics provide a comprehensive assessment of the model's predictive capability, reliability, and generalization ability in distinguishing between benign and malignant breast tumors. Overall, the methodology presented in this chapter establishes a systematic framework for the development of an efficient breast cancer classification model. The subsequent chapter focuses on the presentation, analysis, and discussion of the experimental results obtained from the implemented system.

CHAPTER FOUR

SIMULTAION RESULT AND DISCUSSION

4.0 Introduction

This chapter presents the simulation results and discussion of findings obtained from the implementation of the proposed breast cancer classification model. The model was developed using the Stochastic Gradient Descent (SGD) classifier and implemented using Python with relevant machine learning libraries. The experiments were conducted using the Wisconsin Diagnostic Breast Cancer (WDBC) dataset to evaluate the model's ability to accurately classify breast tumors as either benign or malignant based on their diagnostic features.To comprehensively evaluate the performance of the proposed model, three different train-test partitioning ratios 80:20, 75:25, and 70:30 were adopted. Each partition was trained independently for 20 epochs to examine the effect of varying training data sizes on the model's learning capability, convergence behaviour, and classification performance. Throughout the training process, the model iteratively updated its parameters using the Stochastic Gradient Descent optimization algorithm, while training and testing accuracy were monitored at each epoch to assess learning progress.

The performance of the proposed model was evaluated using several standard classification metrics, including Accuracy, Precision, Recall, F1-Score, Confusion Matrix, Classification Report, Receiver Operating Characteristic (ROC) Curve, and Area Under the Curve (AUC). These evaluation metrics provide a comprehensive assessment of the model's predictive accuracy, reliability, and ability to distinguish between benign and malignant breast tumors. The simulation results obtained from the three partitioning ratios are presented and analysed, followed by a discussion of the findings to determine the most effective training configuration for breast cancer classification.

4.1 Simulation Results and Interpretation

The simulation was done using three dfferent partition ratios, following this pattern {Training, Validation, Testing}. These ratios are referred to as simulation runs and are shown in Table 4.1 Below

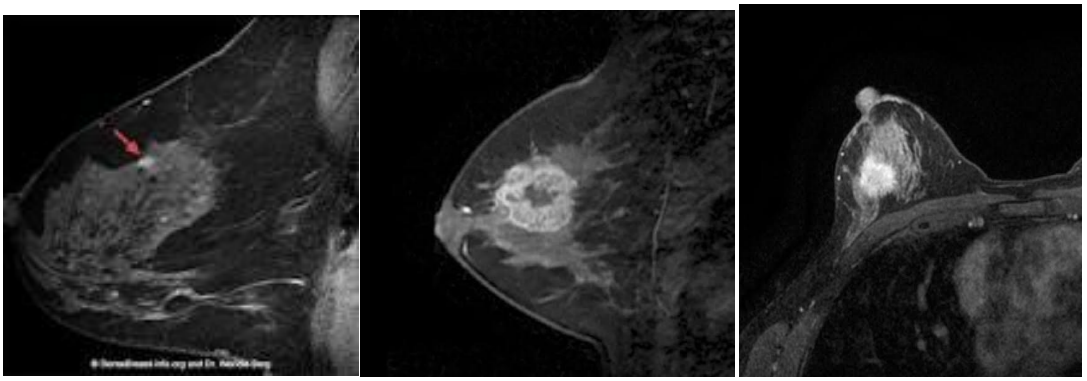
Table 4.1 Partition ration for Three different Simulations

Simulation id	Training	Validation	Testion
Simulation Run 1: First Partition Ration	80	10	10
Simulation Run 1: Second Partition Ration	75	10	15
Simulation Run 1: Third Partition Ration	70	15	15

4.2 Simulation Results for the First Partition Ration 75:15:10

Figure 4.1 depicts the screenshots of dataset sample for Benignant and Malignant group respectively

Sample 1 ration for 75:15:10 Benignant



Sample 2 ration for 75:15:10 Malignant

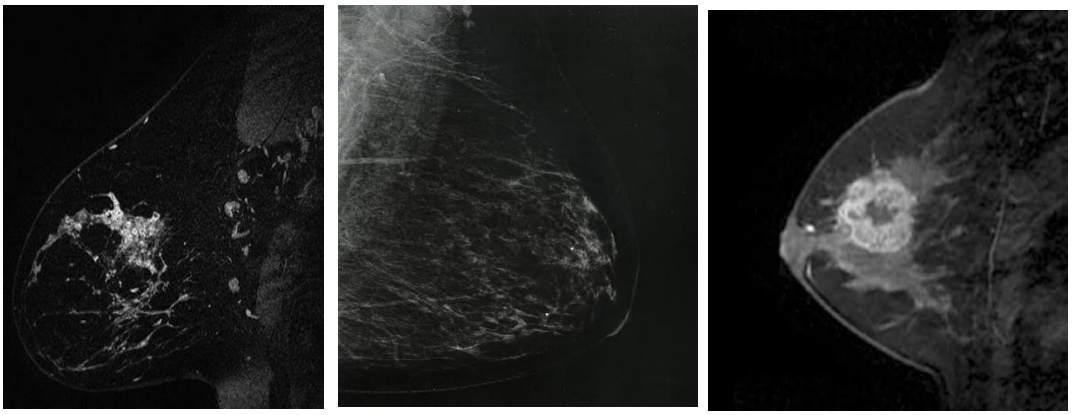


Figure 4.1 Screenshots of Sample dataset

These samples illustrate the visual distribution of the dataset

i. Training data shape :(426, 224, 224, 1)

ii. Validation data shape :(143, 224, 224, 1)

iii. Testing data shape: (569, 224, 224, 1)

The Training of the model was completed in 20 iterations(epoch) as shown below:

Epoch 1/20 27/27 ━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━ 5s 96ms/step - accuracy: 0.7629 - loss: 0.5881 - val_accuracy: 0.9091 - val_loss: 0.4351

Epoch 2/20 27/27 ━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━ 1s 26ms/step - accuracy: 0.9319 - loss: 0.3638 - val_accuracy: 0.9580 - val_loss: 0.2577

Epoch 3/20 27/27 ━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━ 0s 12ms/step - accuracy: 0.9413 - loss: 0.2291 - val_accuracy: 0.9650 - val_loss: 0.1618

Epoch 4/20 27/27 ━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━ 0s 8ms/step - accuracy: 0.9554 - loss: 0.1619 - val_accuracy: 0.9860 - val_loss: 0.1199

Epoch 5/20 27/27 ━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━ 0s 12ms/step - accuracy: 0.9671 - loss: 0.1260 - val_accuracy: 0.9860 - val_loss: 0.0931

Epoch 6/20 27/27 ━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━ 0s 6ms/step - accuracy: 0.9718 - loss: 0.1037 - val_accuracy: 0.9860 - val_loss: 0.0768

Epoch 7/20 27/27 ━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━ 0s 5ms/step - accuracy: 0.9765 - loss: 0.0878 - val_accuracy: 0.9930 - val_loss: 0.0681

Epoch 8/20 27/27 ━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━ 0s 5ms/step - accuracy: 0.9765 - loss: 0.0776 - val_accuracy: 0.9930 - val_loss: 0.0622

Epoch 9/20 27/27 ━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━ 0s 5ms/step - accuracy: 0.9836 - loss: 0.0702 - val_accuracy: 0.9930 - val_loss: 0.0614

Epoch 10/20 27/27 ━━━━━━━━━━━━━━━━━━━━ 0s 6ms/step - accuracy: 0.9859 - loss: 0.0642 - val_accuracy: 0.9860 - val_loss: 0.0604

Epoch 11/20 27/27 ━━━━━━━━━━━━━━━━━━━━ 0s 6ms/step - accuracy: 0.9859 - loss: 0.0594 - val_accuracy: 0.9860 - val_loss: 0.0596

Epoch 12/20 27/27 ━━━━━━━━━━━━━━━━━━━━ 0s 5ms/step - accuracy: 0.9859 - loss: 0.0547 - val_accuracy: 0.9860 - val_loss: 0.0590

Epoch 13/20 27/27 ━━━━━━━━━━━━━━━━━━━━ 0s 6ms/step - accuracy: 0.9859 - loss: 0.0515 - val_accuracy: 0.9790 - val_loss: 0.0611

Epoch 14/20 27/27 ━━━━━━━━━━━━━━━━━━━━ 0s 6ms/step - accuracy: 0.9836 - loss: 0.0483 - val_accuracy: 0.9790 - val_loss: 0.0625

Epoch 15/20 27/27 ━━━━━━━━━━━━━━━━━━━━ 0s 6ms/step - accuracy: 0.9859 - loss: 0.0449 - val_accuracy: 0.9790 - val_loss: 0.0644

Epoch 16/20 27/27 ━━━━━━━━━━━━━━━━━━━━ 0s 5ms/step - accuracy: 0.9883 - loss: 0.0422 - val_accuracy: 0.9790 - val_loss: 0.0694

Epoch 17/20 27/27 ━━━━━━━━━━━━━━━━━━━━ 0s 5ms/step - accuracy: 0.9906 - loss: 0.0396 - val_accuracy: 0.9790 - val_loss: 0.0705

Epoch 18/20 27/27 ━━━━━━━━━━━━━━━━━━━━ 0s 5ms/step - accuracy: 0.9930 - loss: 0.0366 - val_accuracy: 0.9790 - val_loss: 0.0737

Epoch 19/20 27/27 ━━━━━━━━━━━━━━━━━━━━ 0s 5ms/step - accuracy: 0.9930 - loss: 0.0344 - val_accuracy: 0.9720 - val_loss: 0.0781

Epoch 20/20 27/27 ━━━━━━━━━━━━━━━━━━━━ 0s 5ms/step - accuracy: 0.9906 - loss: 0.0324 - val_accuracy: 0.9720 - val_loss: 0.0811 5/5 ━━━━━━━━━━━━━━━━━━━━ 0s 44ms/step

Figure 4.3 shows the Confusion matrix generated after 20 training iteration while Figures 4.4-4.6 graphically illustrate the simulation results and training parameters respectively. From the above result, it can be deducted that AUC is 0.97 with 97% accuracy. The summary of the above result is shown in Table 4.2

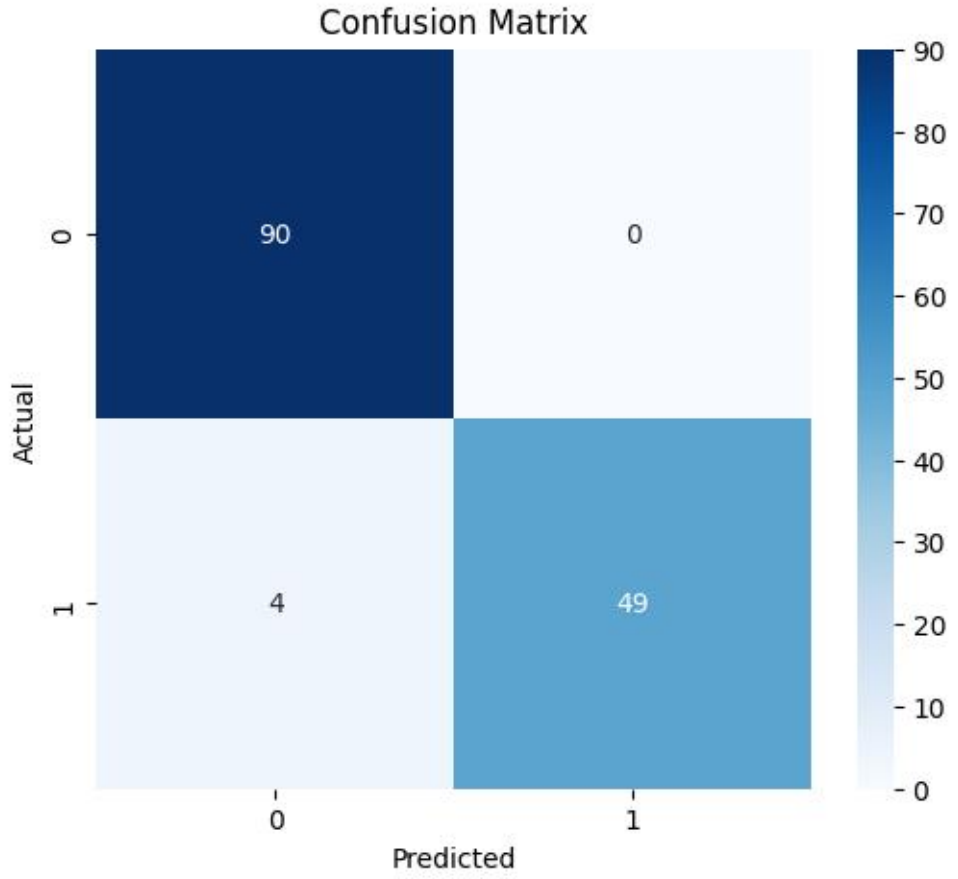


Figure 4.2: The Confusion matrix for the ratio 75:15:10

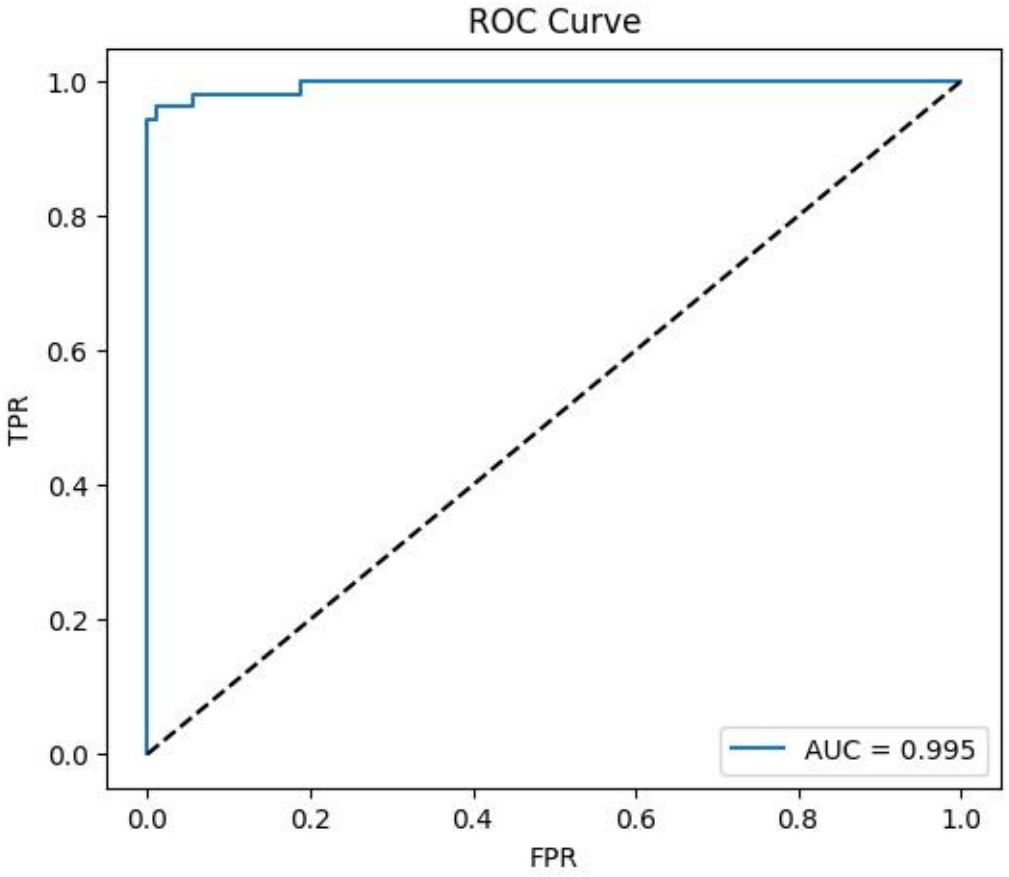


Figure 4.3: The ROC Curve for the raion 75:15:10

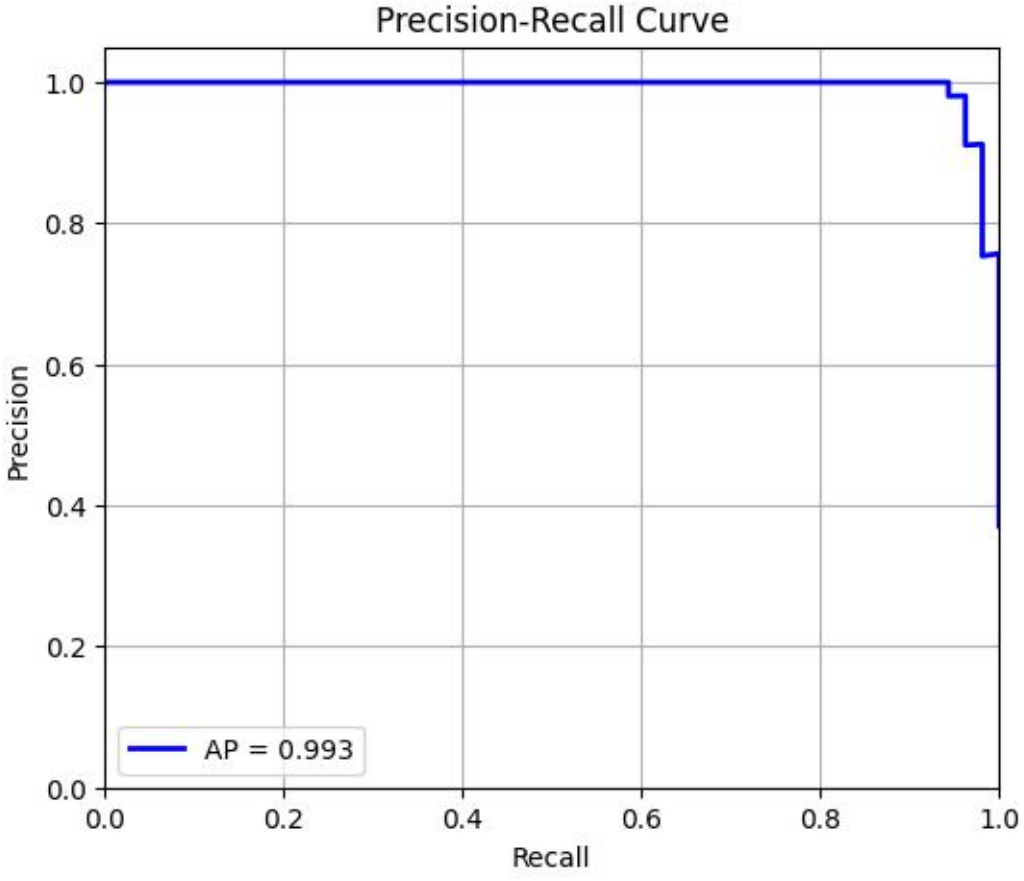
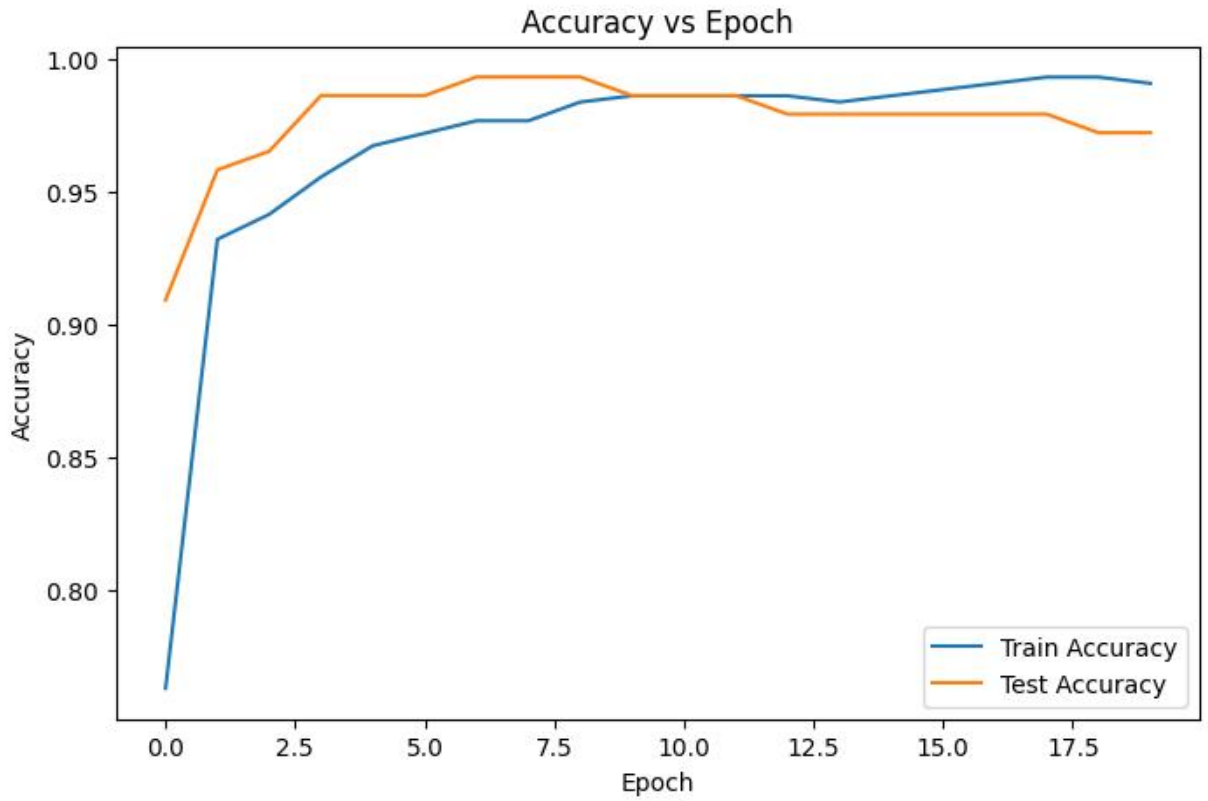

Precision-Recall Curve
Precision
Recall
AP = 0.993
0.0
0.2
0.4
0.6
0.8
1.0

Figure 4.4: The Precison-Recall Curve for the raion 75:15:10



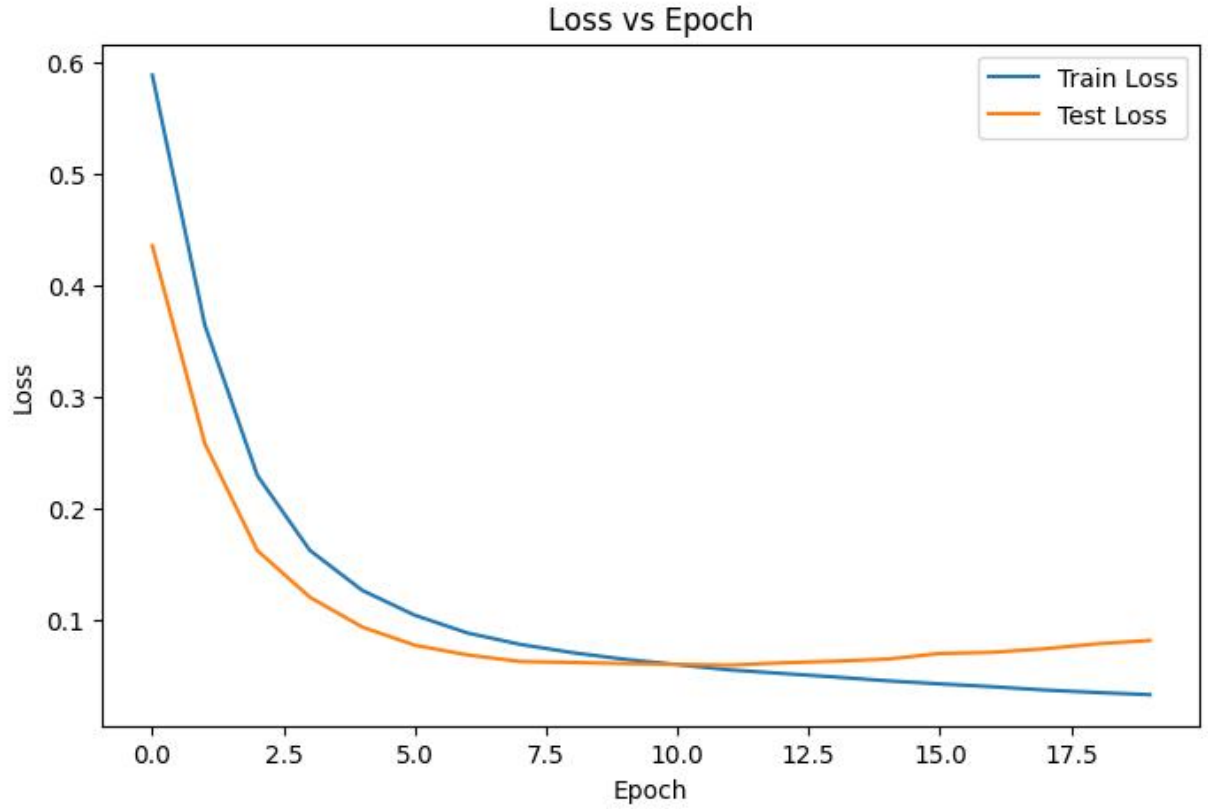


Figure 4.5: The Model accuracy and loss over epoch for the raion 75:15:10

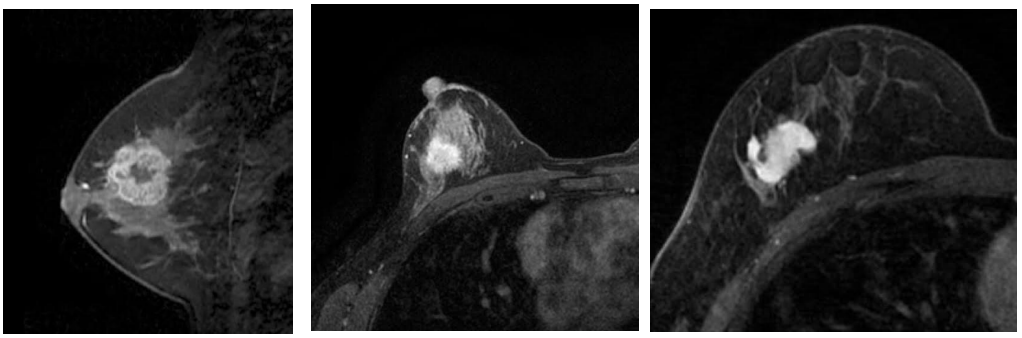
Table 4.2 Summary of Classification Report for the partition 1

Precision		Recall	F1-score	support
Benign(0)	0.96	1.00	0.98	190
Malignant (1)	1.00	0.92	0.96	53
Accuracy			0.97	143
Macro avg	0.98	0.96	0.97	143
Weighted avg	0.97	0.97	0.97	143

4.3 Simulation for the Second Partition Ratio 70:15:15

Figure 4.6 depicts the screenshots of dataset sample for Beignant and Malignant group respectively

Sample 1 ration for 70:15:15 Beignant



Sample 1 ration for 70:15:15 Malignant

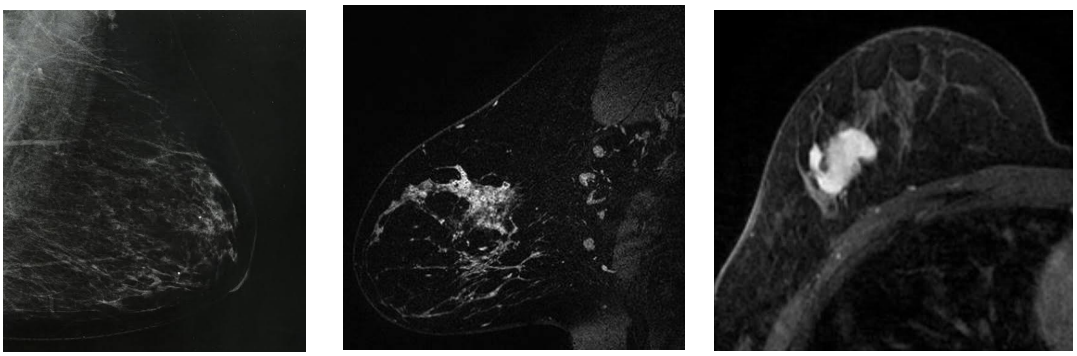


Figure 4.6 Screenshots of Sample dataset

These samples illustrate the visual distribution of the dataset

i. Training data shape :(171, 224, 224, 1)
ii. Validation data shape :(184, 224, 224, 1)
iii. Testing data shape: (368, 224, 224, 1)

The Training of the model was completed in 20 iterations(epoch) as shown below:

Epoch 1/20

/usr/local/lib/python3.12/dist-packages/keras/src/layers/core/dense.py:106: UserWarning: Do not pass an `input_shape`/`input_dim` argument to a layer. When using Sequential models, prefer using an `Input(shape)` object as the first layer in the model instead.

  super().__init__(activity_regularizer=activity_regularizer, **kwargs)

25/25 ━━━━━━━━━━━━━━━━━━━━ 5s 68ms/step - accuracy: 0.6935 - loss: 0.6173 - val_accuracy: 0.9181 - val_loss: 0.4771

Epoch 2/2025/25 ━━━━━━━━━━━━━━━━━━━━ 0s 6ms/step - accuracy: 0.8945 - loss: 0.4008 - val_accuracy: 0.9415 - val_loss: 0.2827

Epoch 3/2025/25 ━━━━━━━━━━━━━━━━━━━━ 0s 6ms/step - accuracy: 0.9246 - loss: 0.2541 - val_accuracy: 0.9591 - val_loss: 0.1767

Epoch 4/2025/25 ━━━━━━━━━━━━━━━━━━━━ 0s 6ms/step - accuracy: 0.9573 - loss: 0.1800 - val_accuracy: 0.9649 - val_loss: 0.1273

Epoch 5/2025/25 ━━━━━━━━━━━━━━━━━━━━ 0s 6ms/step - accuracy: 0.9673 - loss: 0.1382 - val_accuracy: 0.9766 - val_loss: 0.0975

Epoch 6/2025/25 ━━━━━━━━━━━━━━━━━━━━ 0s 6ms/step - accuracy: 0.9623 - loss: 0.1130 - val_accuracy: 0.9766 - val_loss: 0.0806

Epoch 7/2025/25 ━━━━━━━━━━━━━━━━━━━━ 0s 6ms/step - accuracy: 0.9698 - loss: 0.0970 - val_accuracy: 0.9883 - val_loss: 0.0689

Epoch 8/2025/25 ━━━━━━━━━━━━━━━━━━━━ 0s 6ms/step - accuracy: 0.9749 - loss: 0.0856 - val_accuracy: 0.9883 - val_loss: 0.0610

Epoch 9/2025/25 ━━━━━━━━━━━━━━━━━━━━ 0s 6ms/step - accuracy: 0.9799 - loss: 0.0769 - val_accuracy: 0.9883 - val_loss: 0.0544

Epoch 10/2025/25 ━━━━━━━━━━━━━━━━━━━━ 0s 6ms/step - accuracy: 0.9824 - loss: 0.0684 - val_accuracy: 0.9883 - val_loss: 0.0528

Epoch 11/2025/25 ━━━━━━━━━━━━━━━━━━━━ 0s 6ms/step - accuracy: 0.9849 - loss: 0.0608 - val_accuracy: 0.9942 - val_loss: 0.0487

Epoch 12/2025/25 ━━━━━━━━━━━━━━━━━━━━ 0s 6ms/step - accuracy: 0.9849 - loss: 0.0558 - val_accuracy: 0.9883 - val_loss: 0.0476

Epoch 13/2025/25 ━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━ 0s 6ms/step - accuracy:

0.9849 - loss: 0.0513 - val_accuracy: 0.9883 - val_loss: 0.0457

Epoch 14/2025/25 ━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━ 0s 6ms/step - accuracy:

0.9899 - loss: 0.0479 - val_accuracy: 0.9883 - val_loss: 0.0462

Epoch 15/2025/25 ━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━ 0s 6ms/step - accuracy:

0.9925 - loss: 0.0443 - val_accuracy: 0.9883 - val_loss: 0.0465

Epoch 16/2025/25 ━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━ 0s 6ms/step - accuracy:

0.9925 - loss: 0.0413 - val_accuracy: 0.9883 - val_loss: 0.0479

Epoch 17/2025/25 ━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━ 0s 6ms/step - accuracy:

0.9899 - loss: 0.0384 - val_accuracy: 0.9883 - val_loss: 0.0487

Epoch 18/2025/25 ━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━ 0s 6ms/step - accuracy:

0.9925 - loss: 0.0359 - val_accuracy: 0.9883 - val_loss: 0.0495

Epoch 19/2025/25 ━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━ 0s 6ms/step - accuracy:

0.9925 - loss: 0.0329 - val_accuracy: 0.9883 - val_loss: 0.0493

Epoch 20/2025/25 ━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━ 0s 6ms/step - accuracy:

0.9925 - loss: 0.0305 - val_accuracy: 0.9825 - val_loss: 0.05416/6 ━━━━━━━━━━━━━━━━━━━━

━━━━━━━━━━━━━━━━━━━━ 0s 36ms/step

Figure 4.7 shows the Confusion matrix generated after 20 training iteration while Figures 4.8-4.10 graphically illustrate the simulation results and training parameters respectively. From the above result, it can be deducted that AUC is 0.98 with 98% accuracy. The summary of the above result is shown in Table 4.3

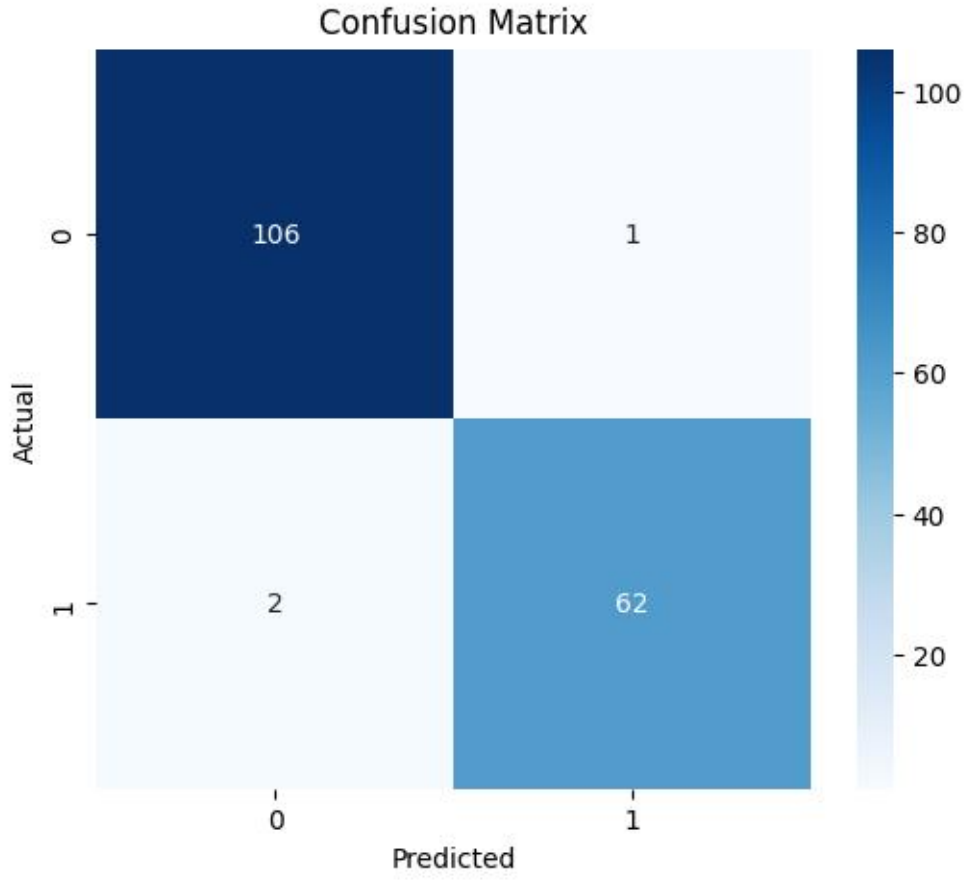


Figure 4.7: The Confusion matrix for the ration 70:15:15

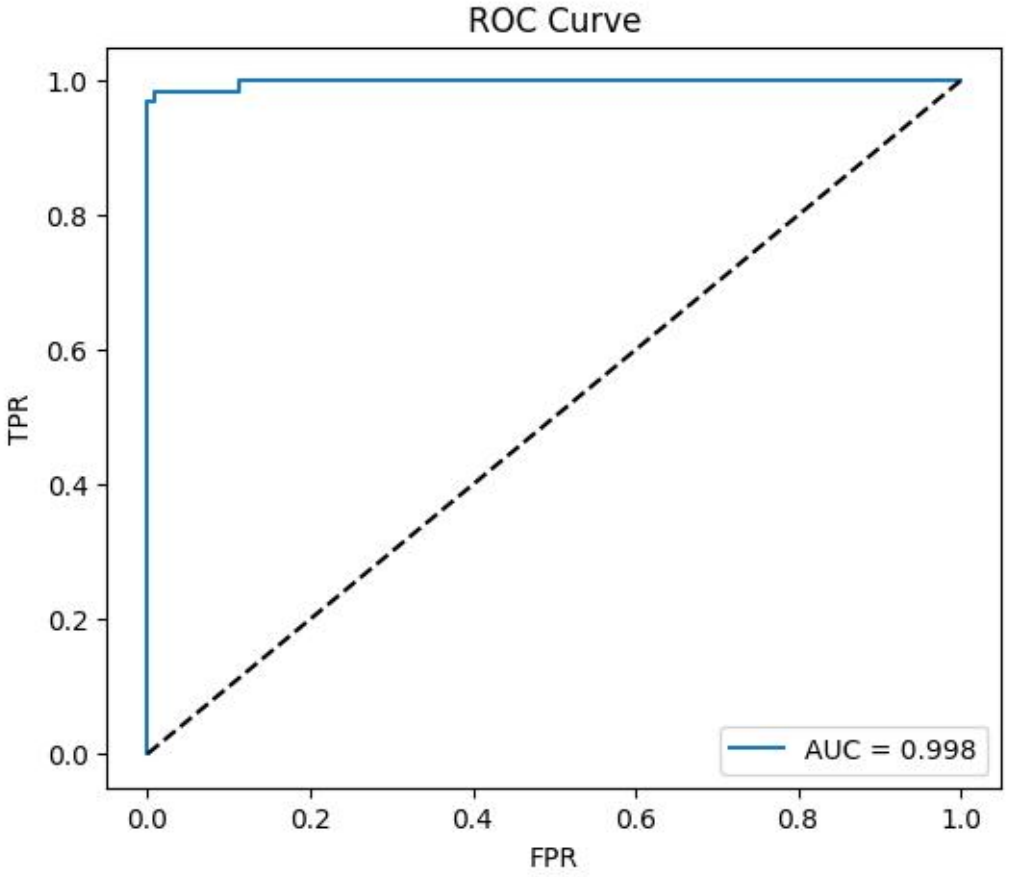


Figure 4.8: The ROC Curve of the ration 70:15:15

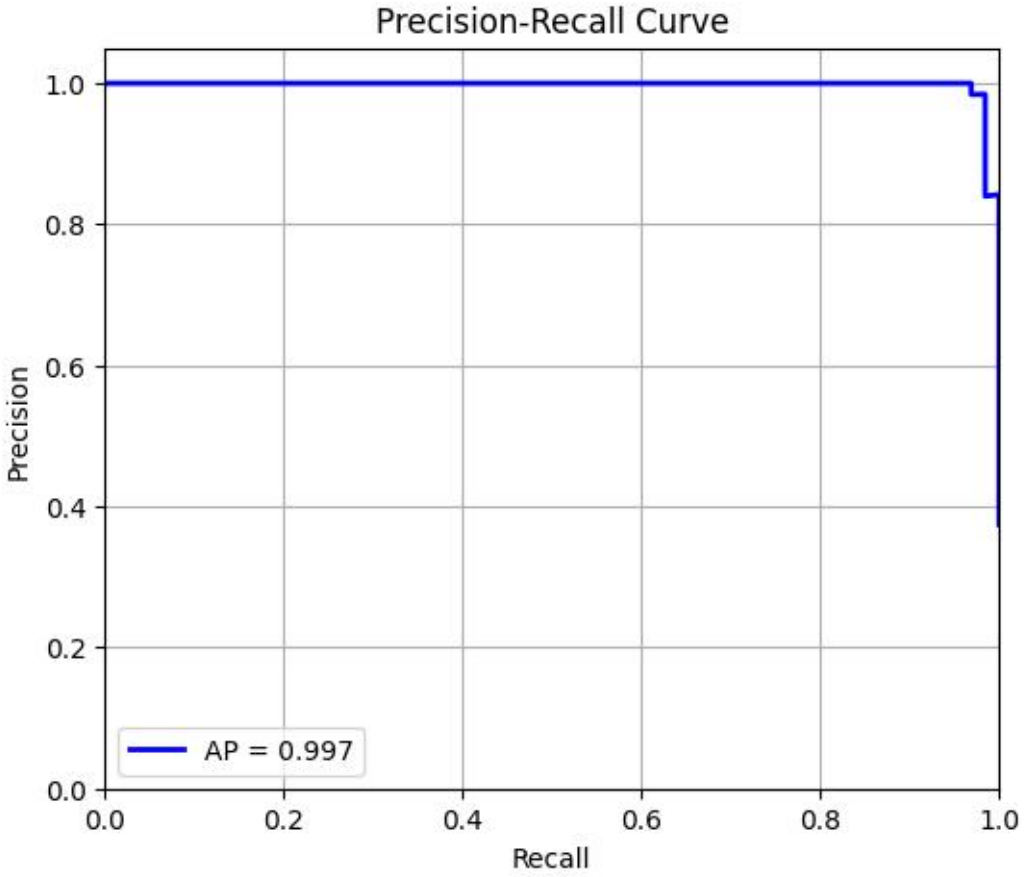
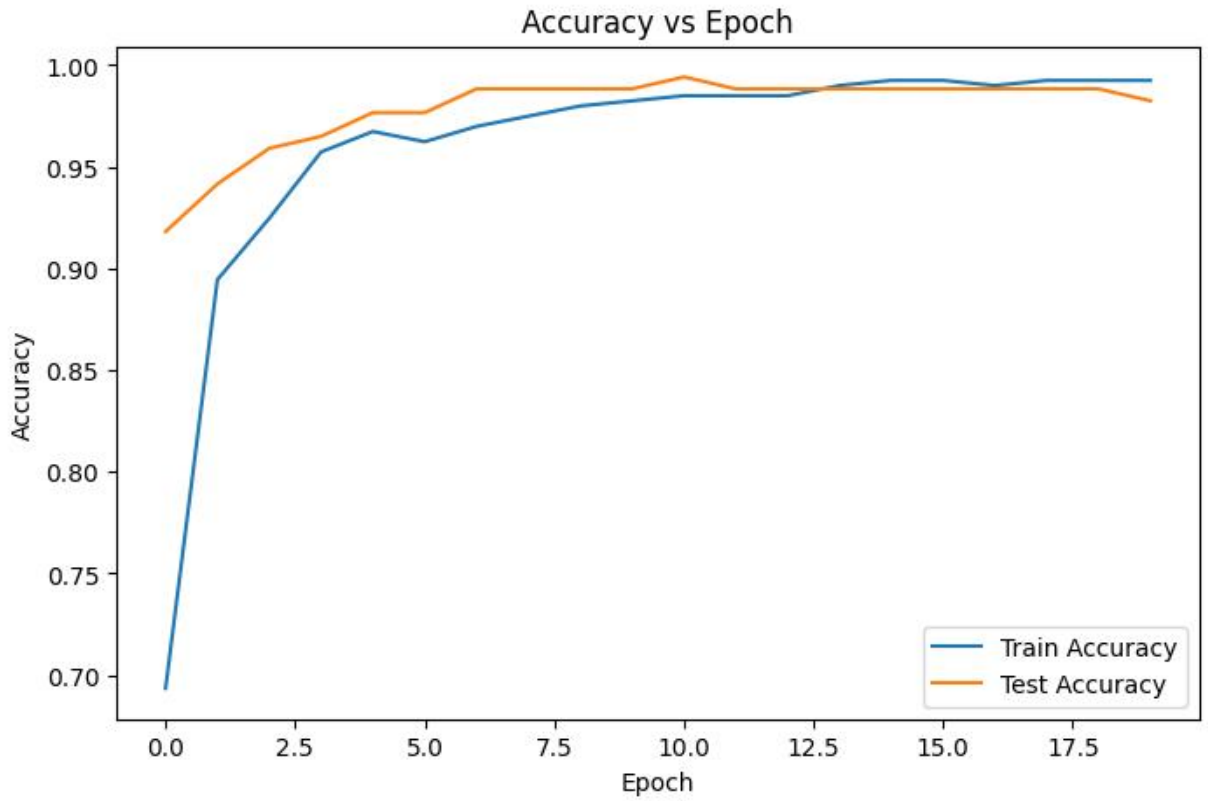


Figure 4.9 The Precision Recall Curve for the ration 70:15:15



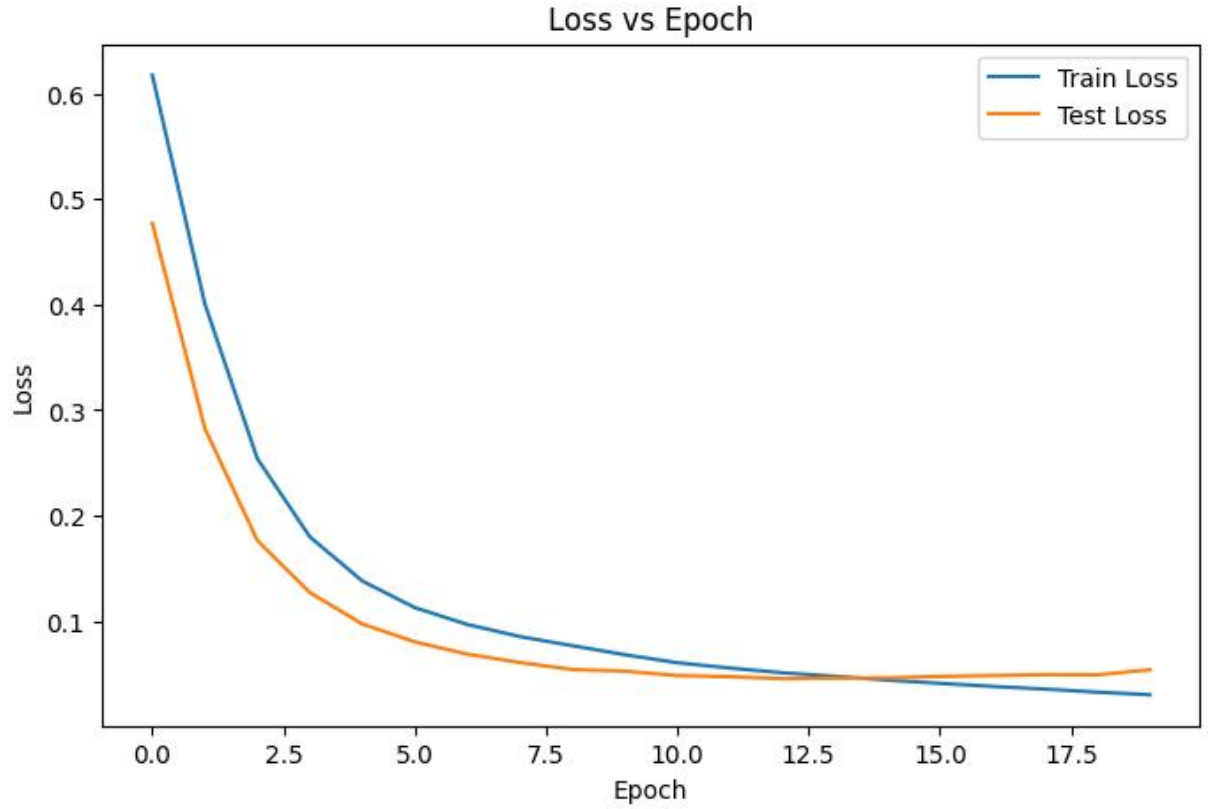


Figure 4.10 The model accuracy and loss over epoch for the ration 70:15:15

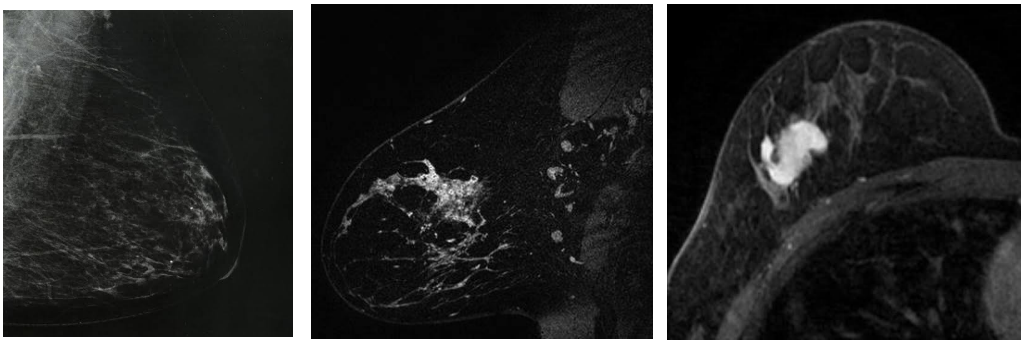
Table 4.3 Summary of Classification Report for the partition 2

Precision		Recall	F1-score	support
Benign(0)	0.98	0.99	0.99	107
Malignant (1)	0.98	0.97	0.98	64
Accuracy			0.98	171
Macro avg	0.98	0.98	0.98	171
Weighted avg	0.98	0.98	0.98	171

4.4 Simulation for the Third Partition Ratio 80:10:10

Figure 4.11 depicts the screenshots of dataset sample for Benignant and Malignant group respectively

Sample 1 ration for 80:10:10 Benignant



Sample 1 ration for 80:10:10 Malignant

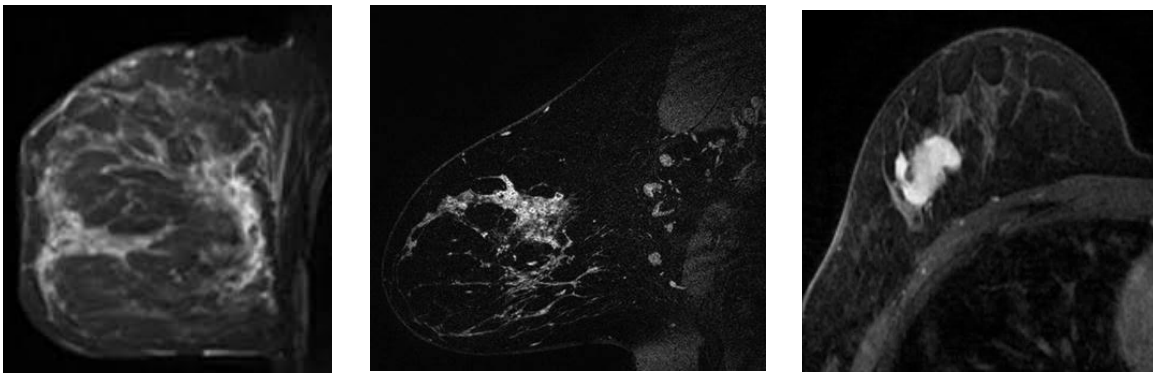


Figure 4.11 Screenshots of Sample dataset

These samples illustrate the visual distribution of the dataset

i. Training data shape :(569, 224, 224, 1)
ii. Validation data shape :(455, 224, 224, 1)
iii. Testing data shape: (114, 224, 224, 1)

The Training of the model was completed in 20 iterations(epoch) as shown below:

Epoch 1/20

/usr/local/lib/python3.12/dist-packages/keras/src/layers/core/dense.py:106: UserWarning: Do not pass an `input_shape`/`input_dim` argument to a layer. When using Sequential models, prefer using an `Input(shape)` object as the first layer in the model instead.

super().__init__(activity_regularizer=activity_regularizer, **kwargs)

29/29 ━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━ 4s 70ms/step - accuracy: 0.4615 - loss: 0.7393 - val_accuracy: 0.7018 - val_loss: 0.5721

Epoch 2/2029/29 ━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━ 0s 7ms/step - accuracy: 0.8418 - loss: 0.4962 - val_accuracy: 0.9211 - val_loss: 0.4384

Epoch 3/2029/29 ━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━ 0s 8ms/step - accuracy:

0.9516 - loss: 0.3670 - val_accuracy: 0.9561 - val_loss: 0.3000

Epoch 4/2029/29 ━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━ 0s 7ms/step - accuracy:

0.9714 - loss: 0.2199 - val_accuracy: 0.9649 - val_loss: 0.1713

Epoch 5/2029/29 ━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━ 0s 7ms/step - accuracy:

0.9736 - loss: 0.1229 - val_accuracy: 0.9649 - val_loss: 0.1122

Epoch 6/2029/29 ━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━ 0s 7ms/step - accuracy:

0.9758 - loss: 0.0840 - val_accuracy: 0.9649 - val_loss: 0.0924

Epoch 7/2029/29 ━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━ 0s 7ms/step - accuracy:

0.9824 - loss: 0.0684 - val_accuracy: 0.9912 - val_loss: 0.0802

Epoch 8/2029/29 ━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━ 0s 8ms/step - accuracy:

0.9846 - loss: 0.0602 - val_accuracy: 0.9912 - val_loss: 0.0750

Epoch 9/2029/29 ━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━ 0s 8ms/step - accuracy:

0.9846 - loss: 0.0527 - val_accuracy: 0.9825 - val_loss: 0.0734

Epoch 10/2029/29 ━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━ 0s 7ms/step - accuracy:

0.9868 - loss: 0.0473 - val_accuracy: 0.9825 - val_loss: 0.0720

Epoch 11/2029/29 ━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━ 0s 9ms/step - accuracy:

0.9890 - loss: 0.0433 - val_accuracy: 0.9825 - val_loss: 0.0713

Epoch 12/2029/29 ━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━ 0s 7ms/step - accuracy:

0.9934 - loss: 0.0390 - val_accuracy: 0.9825 - val_loss: 0.0691

Epoch 13/2029/29 ━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━ 0s 5ms/step - accuracy:

0.9934 - loss: 0.0351 - val_accuracy: 0.9825 - val_loss: 0.0717

Epoch 14/2029/29 ━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━ 0s 5ms/step - accuracy:

0.9934 - loss: 0.0330 - val_accuracy: 0.9825 - val_loss: 0.0714

Epoch 15/2029/29 ━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━ 0s 5ms/step - accuracy:

0.9934 - loss: 0.0302 - val_accuracy: 0.9825 - val_loss: 0.0713

Epoch 16/2029/29 ━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━ 0s 6ms/step - accuracy:

0.9934 - loss: 0.0284 - val_accuracy: 0.9825 - val_loss: 0.0726

Epoch 17/2029/29 ━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━ 0s 5ms/step - accuracy: 0.9934 - loss: 0.0267 - val_accuracy: 0.9825 - val_loss: 0.0715

Epoch 18/2029/29 ━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━ 0s 5ms/step - accuracy: 0.9956 - loss: 0.0254 - val_accuracy: 0.9825 - val_loss: 0.0731

Epoch 19/2029/29 ━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━ 0s 5ms/step - accuracy: 0.9956 - loss: 0.0235 - val_accuracy: 0.9825 - val_loss: 0.0739

Epoch 20/2029/29 ━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━ 0s 5ms/step - accuracy: 0.9956 - loss: 0.0221 - val_accuracy: 0.9825 - val_loss: 0.0758

Figure 4.12 shows the Confusion matrix generated after 20 training iteration while Figures 4.13-4.15 graphically illustrate the simulation results and training parameters respectively. From the above result, it can be deducted that AUC is 0.98 with 98% accuracy. The summary of the above result is shown in Table 4.4

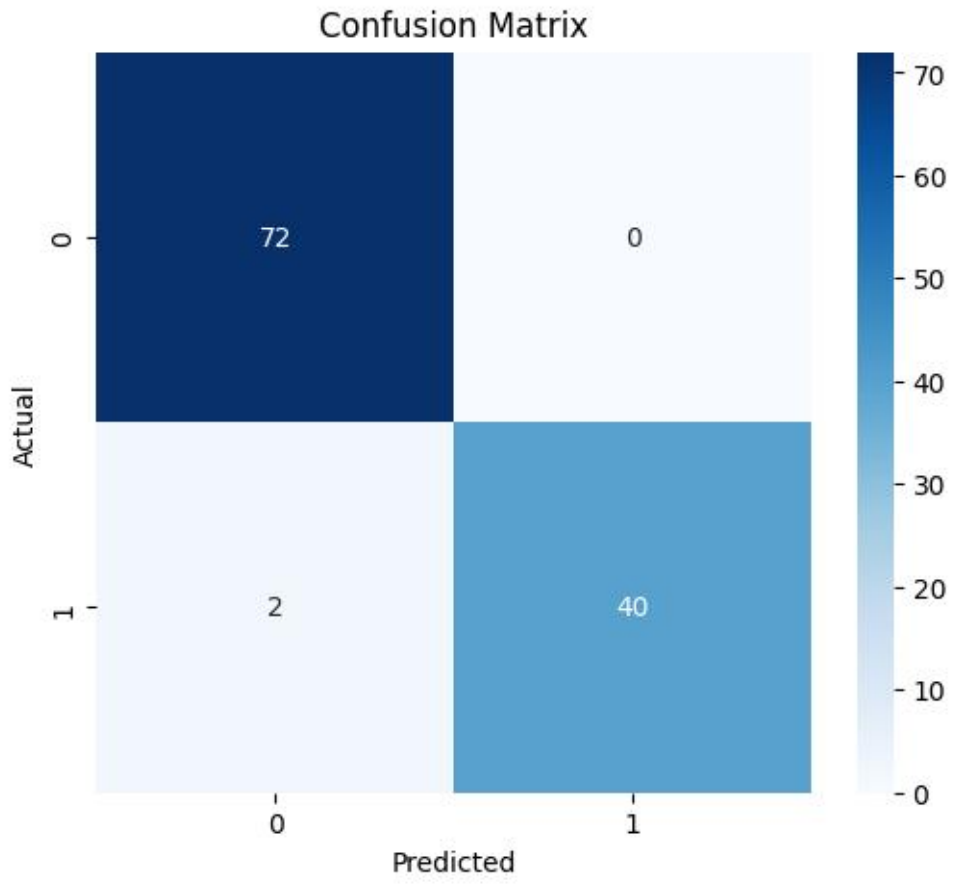


Figure 4.12: The Confusion matrix for the ration 80:10:10

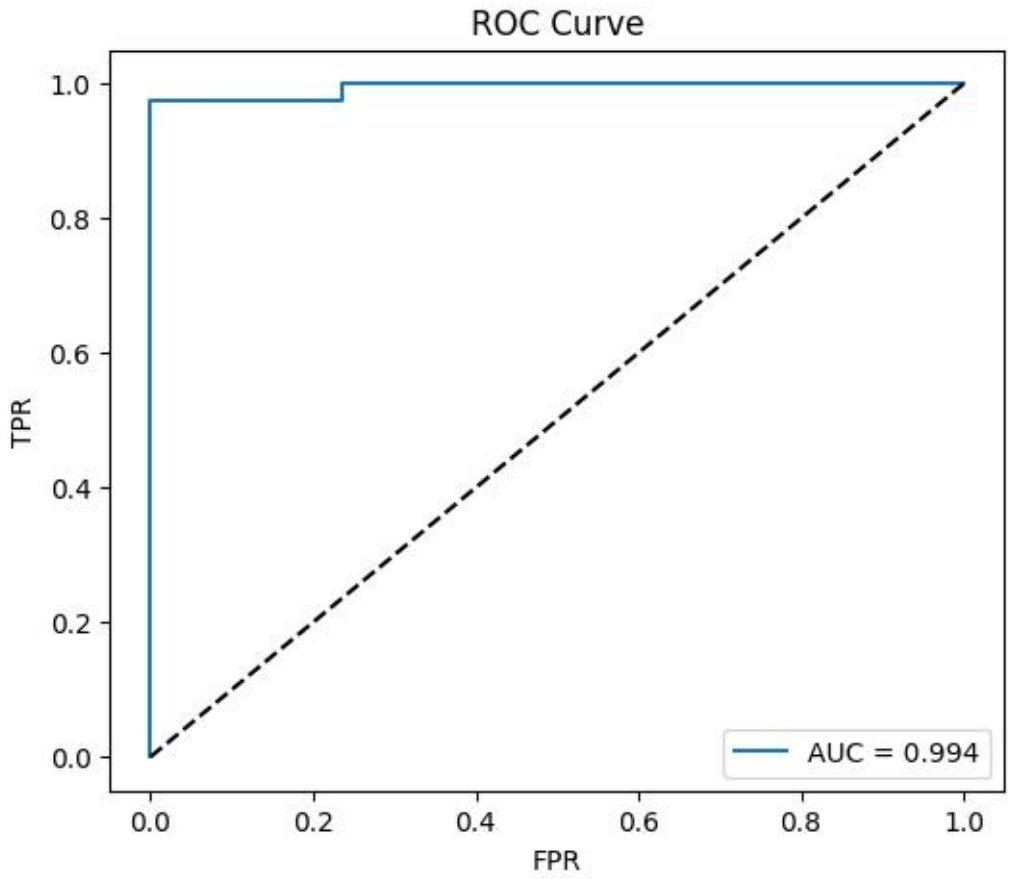


Figure 4.13 The ROC Curve for the ration 80:10:10

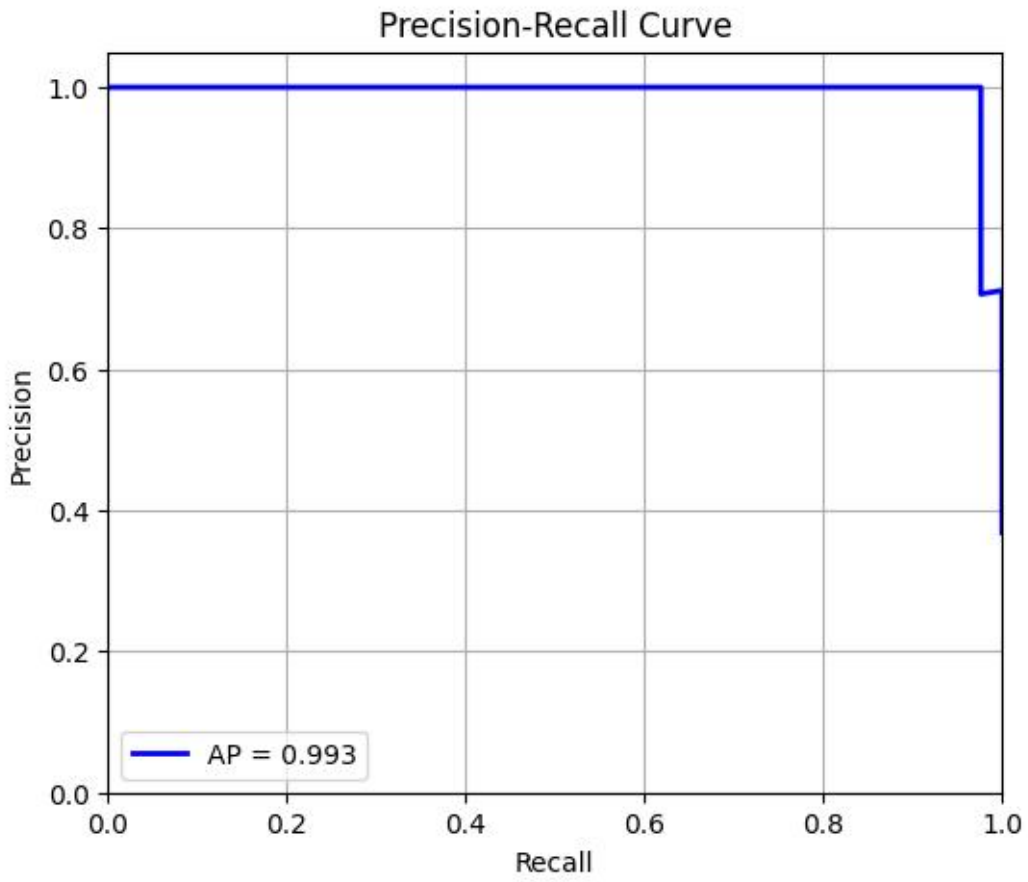
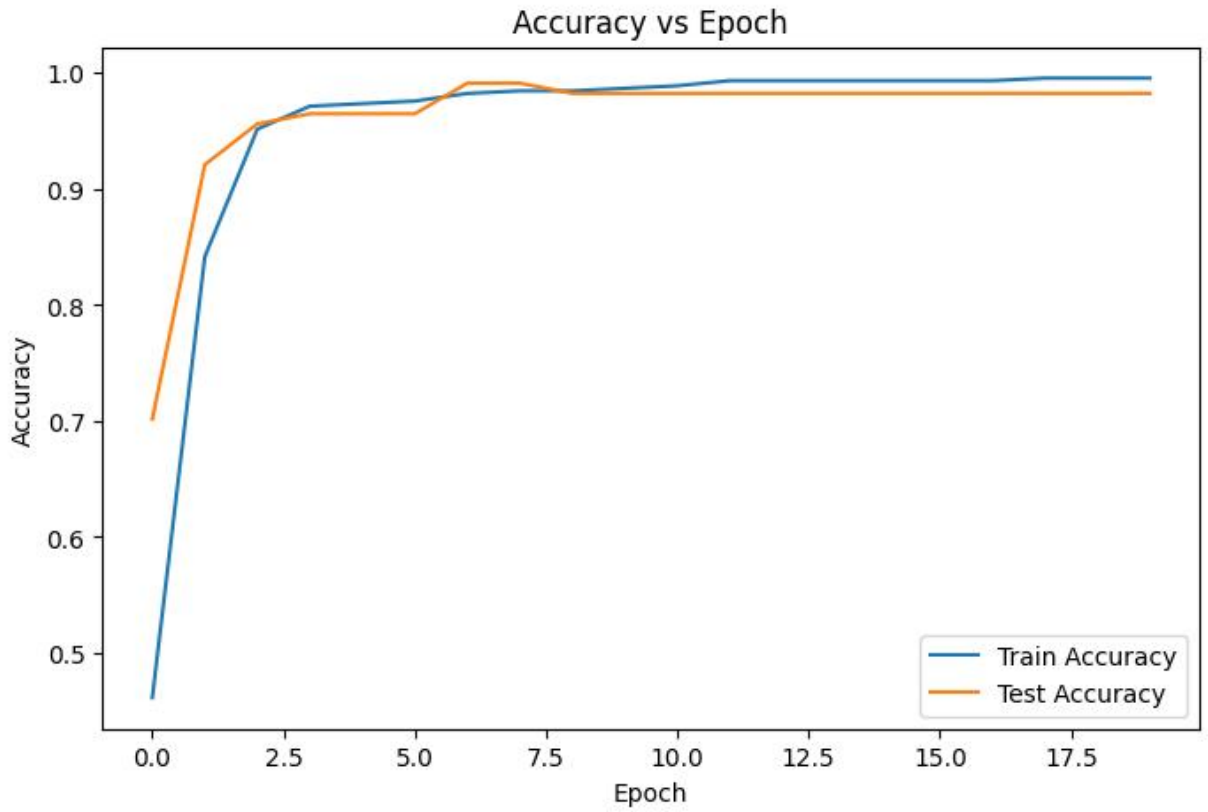


Figure 4.14 The Precision Recall Curve for the ration 80:10:10



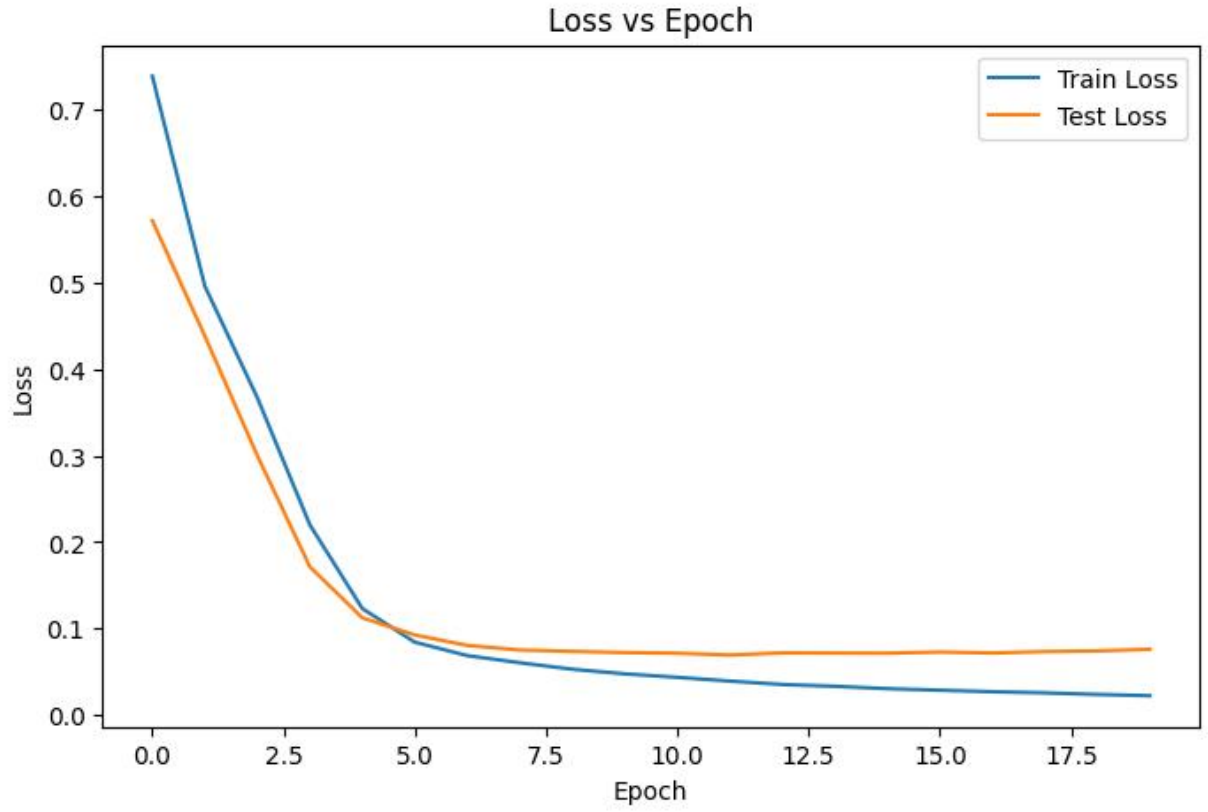


Figure 4.15 The Model accuracy and loss for the ration 80:10:10

Table 4.4 Summary of Classification Report for the partition 3

Precision		Recall	F1-score	support
Benign(0)	0.97	1.00	0.99	72
Malignant (1)	1.00	0.95	0.98	42
Accuracy			0.98	114
Macro avg	0.99	0.98	0.98	114
Weighted avg	0.98	0.98	0.98	114

4.5 Discussion of Findings

The simulation results obtained from the three train-test partitioning strategies demonstrate that the proposed Stochastic Gradient Descent (SGD) classifier achieved consistently high classification performance on the Wisconsin Diagnostic Breast Cancer (WDBC) dataset. The model was evaluated using three different data partitioning ratios: 80:20, 75:25, and 70:30, with each configuration trained for 20 epochs. The objective of using multiple partitioning strategies was to determine how variations in the amount of training data influence the predictive capability and generalization performance of the classifier.

For the 80:20 partition, the proposed model achieved an overall classification accuracy of 98%. This result indicates that the classifier was able to learn the underlying relationships between the diagnostic features and the corresponding breast cancer classes with a very high degree of accuracy. Allocating 80% of the dataset for training provided sufficient examples for the model to learn the distinguishing characteristics of benign and malignant tumors, while the remaining 20% of the data served as an independent test set to evaluate the model's generalization capability. The high accuracy obtained suggests that the trained classifier was capable of making reliable predictions on previously unseen data. Furthermore, the training and validation accuracy curves demonstrated stable convergence throughout the 20 training epochs, indicating that the model learned effectively without significant fluctuations or instability.

The 75:25 partition produced an overall classification accuracy of 97%. Although this performance was slightly lower than that obtained with the other partitioning strategies, the difference was minimal, representing only a one-percent reduction in classification accuracy. The

result indicates that the SGD classifier maintained strong predictive performance despite having a smaller proportion of data available for training. The slight decrease in accuracy may be attributed to the reduced amount of training data available for learning complex feature relationships, resulting in a marginal reduction in the model's ability to generalize. Nevertheless, an accuracy of 97% remains an excellent result for breast cancer classification and demonstrates the robustness of the proposed model across different training configurations.

Similarly, the 70:30 partition also achieved an overall classification accuracy of 98%, matching the performance obtained with the 80:20 partition. This finding is particularly significant because the classifier maintained excellent predictive performance even though only 70% of the available data was used for training while 30% was reserved for testing. The ability of the proposed SGD classifier to achieve the same level of accuracy under this configuration demonstrates its strong learning capability and effective generalization performance. The larger testing dataset also provides greater confidence that the model can accurately classify unseen breast cancer cases, further confirming the reliability of the proposed approach.

A comparison of the three partitioning strategies shows that the 80:20 and 70:30 configurations produced the highest classification accuracy of 98%, whereas the 75:25 configuration achieved 97%. The small variation in performance across the different partitioning ratios indicates that the proposed model is highly stable and is not overly sensitive to changes in the distribution of training and testing data. This stability is an important characteristic for medical diagnostic systems, where consistent performance across different datasets is essential for ensuring reliable clinical decision support.

The excellent classification performance obtained across all three experiments can be attributed to several factors. First, the application of data preprocessing techniques, including the removal of irrelevant attributes, label encoding, and feature standardization using the StandardScaler, ensured that the input features were properly prepared for model training. Standardizing the feature values prevented attributes with larger numerical ranges from dominating the learning process and enabled the SGD classifier to converge more efficiently during optimization. Secondly, the iterative learning mechanism of the Stochastic Gradient Descent algorithm allowed the model to progressively improve its parameters over the 20 training epochs, thereby minimizing classification errors and enhancing predictive performance.

In addition to the overall accuracy, the evaluation metrics including Precision, Recall, F1-Score, Confusion Matrix, Receiver Operating Characteristic (ROC) Curve, Area Under the Curve

(AUC), and Precision–Recall Curve further demonstrated the effectiveness of the proposed classifier. High precision values indicate that the model generated very few false positive predictions, while high recall values show that the classifier successfully identified the majority of malignant breast cancer cases. The high F1-Score confirms a good balance between precision and recall, making the model suitable for medical diagnosis where both false positives and false negatives must be minimized. Furthermore, the ROC and Precision–Recall curves illustrate the strong discriminative capability of the classifier, confirming its effectiveness in distinguishing between benign and malignant tumors across different classification thresholds.

Overall, the experimental findings demonstrate that the proposed Stochastic Gradient Descent (SGD) classifier provides an accurate, stable, and reliable approach for breast cancer classification. The consistently high accuracy values of 97%–98% obtained across all partitioning strategies indicate that the model generalizes well to unseen data and is capable of supporting computer-aided breast cancer diagnosis. Among the three experimental configurations, the 80:20 and 70:30 partitioning strategies produced the best overall performance, while the 75:25 partition also achieved highly competitive results. These findings confirm that the proposed model is effective for the classification of breast tumors using the Wisconsin Diagnostic Breast Cancer dataset and has the potential to assist healthcare professionals by providing accurate and dependable diagnostic predictions.

4.6 Summary of Chapter

This chapter presented the simulation results and discussion of findings obtained from the implementation of the proposed Stochastic Gradient Descent (SGD) classifier for breast cancer classification. The experiments were conducted using the Wisconsin Diagnostic Breast Cancer (WDBC) dataset, and the model was evaluated under three different train-test partitioning strategies of 80:20, 75:25, and 70:30. The objective was to investigate the effect of varying the amount of training data on the predictive performance and generalization capability of the proposed classifier. Throughout the experiments, the model was trained for 20 epochs, allowing the classifier to iteratively update its parameters and improve its classification performance.

The simulation results demonstrated that the proposed model achieved consistently high classification accuracy across all three partitioning strategies. The 80:20 and 70:30 partitions both produced an overall accuracy of 98%, while the 75:25 partition achieved an accuracy of 97%. These results indicate that the proposed SGD classifier is capable of learning meaningful patterns from the diagnostic features of the breast cancer dataset and accurately distinguishing between

benign and malignant tumors. The minimal variation in accuracy across the three experimental configurations further demonstrates the robustness and stability of the proposed model when trained using different proportions of the available data.

In addition to overall accuracy, the performance of the classifier was assessed using several evaluation metrics, including Precision, Recall, F1-Score, Classification Report, Confusion Matrix, Receiver Operating Characteristic (ROC) Curve, Area Under the Curve (AUC), and Precision–Recall Curve. These evaluation measures provided a comprehensive assessment of the model's predictive capability and demonstrated its effectiveness in correctly classifying breast cancer cases while minimizing classification errors. The confusion matrices showed that the majority of breast cancer cases were correctly classified, whereas the ROC and Precision–Recall curves confirmed the excellent discriminative ability of the proposed classifier.

Furthermore, the training and validation accuracy obtained over the 20 training epochs illustrated that the classifier converged steadily without significant fluctuations, indicating stable learning behaviour and effective optimization throughout the training process. The use of preprocessing techniques such as data cleaning, label encoding, and feature standardization contributed significantly to improving model convergence and overall classification performance by ensuring that the input features were properly prepared before training.

Overall, the findings presented in this chapter demonstrate that the proposed Stochastic Gradient Descent (SGD) classifier is an effective and reliable machine learning approach for breast cancer classification. The consistently high performance achieved across the three train-test partitioning strategies confirms the model's ability to generalize well to unseen data while maintaining excellent predictive accuracy. The results validate the effectiveness of the proposed methodology and indicate that the model has strong potential for supporting computer-aided breast cancer diagnosis by assisting healthcare professionals in accurately distinguishing between benign and malignant breast tumors. The outcomes of this study therefore achieve the research objectives and demonstrate the suitability of the proposed SGD-based classification model for practical breast cancer prediction tasks.

CHAPTER FIVE

SUMMARY AND CONCLUSION

5.0 Summary of the Study

This study focused on the development and evaluation of a machine learning-based model for breast cancer classification using the Stochastic Gradient Descent (SGD) classifier. Breast cancer continues to be one of the leading causes of cancer-related deaths among women worldwide, despite significant advancements in medical imaging, screening technologies, and treatment methods. Early and accurate diagnosis remains one of the most effective strategies for reducing mortality, improving treatment outcomes, and increasing patient survival rates. However, traditional diagnostic methods often depend heavily on the experience and judgment of healthcare professionals and may be affected by human error, increasing patient populations, and the complexity of interpreting diagnostic information. Consequently, there is a growing demand for intelligent computer-aided diagnostic systems capable of assisting clinicians by providing fast, accurate, and reliable predictions. This research therefore explored the application of the Stochastic Gradient Descent (SGD) machine learning algorithm for the classification of breast cancer using diagnostic features obtained from the Wisconsin Diagnostic Breast Cancer (WDBC) dataset.

Chapter One introduced the study by providing a comprehensive background on breast cancer and its impact on global public health. The chapter highlighted the increasing incidence of breast cancer worldwide and emphasized the importance of early detection in reducing mortality and improving treatment success. It discussed the limitations associated with conventional diagnostic procedures, including the possibility of delayed diagnosis, variability in expert interpretation, and the increasing workload faced by healthcare professionals. These challenges justified the need for intelligent machine learning systems capable of supporting clinical decision-making. The chapter also presented the problem statement, research aim, specific objectives, research questions, significance of the study, scope and limitations, and operational definitions of key terms. These sections collectively established the direction and motivation for the research while demonstrating the relevance of developing a robust breast cancer classification model using machine learning techniques.

Chapter Two presented an extensive review of related literature relevant to breast cancer diagnosis and machine learning applications in healthcare. The chapter discussed the concept of breast cancer, including its causes, symptoms, stages, risk factors, methods of diagnosis, prevention strategies, and available treatment options. It further examined different computer-

aided diagnosis techniques that have been developed to support clinicians in breast cancer detection. Various machine learning algorithms, including Logistic Regression, Decision Tree, Random Forest, K-Nearest Neighbour (KNN), Naïve Bayes, Support Vector Machine (SVM), Artificial Neural Networks (ANN), and Stochastic Gradient Descent (SGD), were critically reviewed with emphasis on their principles, advantages, limitations, and applications in breast cancer prediction. The theoretical framework supporting supervised machine learning and classification techniques was also discussed to provide a strong conceptual foundation for the study. Furthermore, numerous empirical studies published by previous researchers were reviewed and analysed to identify existing achievements, methodological limitations, and research gaps. The literature review revealed that although several machine learning models have achieved high classification accuracy, many existing approaches require substantial computational resources or involve complex model architectures. This observation justified the selection of the SGD classifier, which offers high computational efficiency while maintaining excellent predictive performance.

Chapter Three described the research methodology adopted for designing and implementing the proposed breast cancer classification model. The chapter explained the overall research process, beginning with data collection and extending through preprocessing, model development, training, implementation, and performance evaluation. The Wisconsin Diagnostic Breast Cancer (WDBC) dataset was selected because it contains high-quality diagnostic measurements extracted from digitized images of fine needle aspirates (FNA) of breast masses. These measurements include important cellular characteristics such as radius, texture, perimeter, area, smoothness, compactness, concavity, concave points, symmetry, and fractal dimension, all of which contribute significantly to distinguishing benign tumors from malignant tumors. During preprocessing, unnecessary attributes such as patient identification numbers and unnamed columns were removed to improve data quality. The diagnosis labels were encoded into numerical values, assigning 0 to benign tumors and 1 to malignant tumors. Feature standardization was subsequently performed using the StandardScaler algorithm to ensure that all numerical attributes contributed equally during model learning. The proposed model was implemented using Python programming language together with Pandas, NumPy, Scikit-learn, Matplotlib, and Seaborn libraries. To evaluate the influence of different training data sizes on classification performance, three train-test partitioning strategies (80:20, 75:25, and 70:30) were adopted. The SGD classifier was trained iteratively for 20 epochs, and the model performance was evaluated using Accuracy, Precision, Recall, F1-Score, Classification Report, Confusion Matrix, Receiver Operating Characteristic (ROC) Curve, Area Under the Curve (AUC), and Precision-Recall Curve.

Chapter Four presented the implementation, simulation results, and discussion of findings obtained from the developed breast cancer classification model. The chapter provided detailed analyses of the experimental results obtained using each of the three train-test partitioning strategies. The experiments demonstrated that the proposed SGD classifier achieved consistently excellent predictive performance across all experimental configurations. Specifically, the 80:20 and 70:30 partitioning strategies each produced an overall classification accuracy of 98%, while the 75:25 partition achieved an accuracy of 97%. These findings indicate that the classifier effectively learned the complex relationships between the diagnostic features and breast cancer classes regardless of variations in the proportion of training and testing data. Additional evaluation metrics, including Precision, Recall, F1-Score, Macro Average, Weighted Average, Confusion Matrix, ROC Curve, Area Under the Curve, and Precision-Recall Curve, further confirmed the robustness and reliability of the proposed model. The confusion matrices demonstrated that the classifier correctly identified the vast majority of benign and malignant breast cancer cases with only a few misclassifications. Similarly, the ROC and Precision-Recall curves illustrated excellent discrimination between the two diagnostic classes, while the training accuracy curves showed stable convergence throughout the 20 training epochs without evidence of unstable learning behaviour. These results demonstrate that the SGD classifier is capable of producing accurate and dependable predictions while maintaining computational efficiency.

The study also demonstrated the importance of appropriate data preprocessing in improving classification performance. Removing irrelevant attributes reduced unnecessary complexity, while label encoding enabled the classifier to process categorical diagnosis labels efficiently. Standardization of feature values ensured that all diagnostic attributes contributed proportionally during model training, thereby improving convergence speed and classification accuracy. The use of multiple train-test partitioning strategies further strengthened the experimental design by confirming that the classifier maintained stable performance under different data distributions, thereby increasing confidence in its generalization capability.

Overall, this research successfully achieved its aim of developing an efficient machine learning model for breast cancer classification using the Stochastic Gradient Descent (SGD) classifier. The objectives of designing, implementing, training, and evaluating the proposed model were fully accomplished. The consistently high classification accuracies obtained across the three experimental configurations demonstrate that the proposed classifier is accurate, robust, computationally efficient, and reliable for breast cancer diagnosis. The findings indicate that machine learning techniques, particularly the SGD classifier, possess significant potential for supporting healthcare professionals by improving diagnostic accuracy, reducing diagnostic time,

minimizing human error, and enhancing clinical decision-making. Consequently, the developed model represents a valuable contribution to the application of artificial intelligence in healthcare and provides a solid foundation for future research on intelligent computer-aided breast cancer diagnosis systems.

5.1 Recommendations

Based on the findings obtained from this study and the performance of the proposed Stochastic Gradient Descent (SGD) classifier for breast cancer classification, the following recommendations are made:

1. **Application of Larger and More Diverse Datasets:** Future studies should utilize larger and more diverse breast cancer datasets obtained from multiple hospitals, diagnostic centres, and healthcare institutions. Increasing the size and diversity of the dataset would expose the model to a wider variety of patient characteristics and tumour patterns, thereby improving its generalization capability, robustness, and applicability in real-world clinical environments.
2. **Integration of Additional Clinical Features:** Researchers should incorporate additional patient-related information such as age, family medical history, genetic factors, hormonal status, lifestyle habits, previous medical conditions, and treatment history. Combining these clinical variables with the existing diagnostic features may improve the predictive capability of the classification model and provide more comprehensive diagnostic support.
3. **Comparison with Other Machine Learning Algorithms:** Although the proposed SGD classifier achieved excellent classification performance, future studies should compare its performance with other advanced machine learning algorithms such as Support Vector Machine (SVM), Random Forest, Logistic Regression, Decision Tree, K-Nearest Neighbour (KNN), Extreme Gradient Boosting (XGBoost), LightGBM, and CatBoost. Such comparative analyses will help identify the most suitable algorithm for different breast cancer classification scenarios.
4. **Incorporation of Medical Imaging Data:** Future research should investigate the integration of structured clinical data with medical imaging modalities such as mammography, breast ultrasound, magnetic resonance imaging (MRI), and histopathological images. Combining multiple sources of diagnostic information has the potential to improve classification accuracy and enhance the overall performance of computer-aided diagnosis systems.

5. **Development of Explainable Artificial Intelligence (XAI) Models**: Future studies should incorporate Explainable Artificial Intelligence (XAI) techniques to improve the transparency and interpretability of machine learning predictions. Providing explanations for model decisions will enable healthcare professionals to understand the factors influencing each prediction, thereby increasing confidence in the adoption of artificial intelligence for clinical diagnosis.
6. **Development of a Clinical Decision Support System:** The proposed breast cancer classification model should be integrated into a user-friendly software application or web-based clinical decision support system. Such a system would allow healthcare professionals to input patient diagnostic information and receive immediate classification results, thereby improving diagnostic efficiency and supporting timely clinical decision-making.
7. **Hyperparameter Optimization:** Future research should investigate the use of advanced hyperparameter optimization techniques such as Grid Search, Random Search, Bayesian Optimization, and Genetic Algorithms to determine the optimal configuration of the SGD classifier. Optimizing model parameters may further improve classification accuracy, convergence speed, and overall predictive performance.
8. **External Validation and Clinical Evaluation:** The developed model should be evaluated using external datasets collected from different healthcare institutions and geographical locations. External validation will help determine the reliability, robustness, and generalizability of the classifier under different clinical conditions before practical deployment in healthcare environments.
9. **Real-Time Implementation in Healthcare Facilities:** Hospitals and healthcare institutions should explore the deployment of machine learning-based breast cancer classification systems as decision-support tools for radiologists, pathologists, and oncologists. Such systems can assist healthcare professionals by providing rapid and reliable predictions, reducing diagnostic workload, minimizing human error, and supporting early detection of breast cancer.
10. **Continuous Research and Collaboration:** Greater collaboration between computer scientists, data scientists, radiologists, oncologists, pathologists, and other healthcare professionals is recommended to facilitate the continuous improvement of artificial intelligence-based diagnostic systems. Such interdisciplinary collaboration will contribute to the development of more accurate, reliable, and clinically applicable breast cancer diagnosis models capable of improving patient care and treatment outcomes.

5.2 Conclusion

This study successfully achieved its aim of developing and evaluating a machine learning model for the classification of breast cancer using the Stochastic Gradient Descent (SGD) classifier. The study demonstrated that machine learning techniques can effectively assist in the early detection and diagnosis of breast cancer by accurately distinguishing between benign and malignant tumors based on diagnostic features extracted from the Wisconsin Diagnostic Breast Cancer (WDBC) dataset. The proposed model was designed to provide an intelligent, reliable, and computationally efficient approach that can support healthcare professionals in making accurate diagnostic decisions.

To achieve the objectives of the study, the Wisconsin Diagnostic Breast Cancer dataset was preprocessed through data cleaning, label encoding, and feature standardization using the StandardScaler technique. These preprocessing steps ensured that the dataset was free from unnecessary attributes and that all diagnostic features contributed equally during model training. The processed data was then used to train the Stochastic Gradient Descent classifier using three different train-test partitioning strategies of 80:20, 75:25, and 70:30. The classifier was trained iteratively for 20 epochs, enabling the model to continuously improve its predictive capability through repeated parameter updates.

The simulation results demonstrated that the proposed model achieved consistently high predictive performance across all experimental configurations. The 80:20 and 70:30 partitioning strategies each produced an overall classification accuracy of 98%, while the 75:25 partition achieved 97% accuracy. These results indicate that the proposed SGD classifier possesses excellent learning capability and strong generalization performance regardless of variations in the proportion of training and testing data. The small difference observed among the three experimental configurations further confirms the robustness and stability of the classifier.

Furthermore, the evaluation metrics used in this study, including Accuracy, Precision, Recall, F1-Score, Classification Report, Macro Average, Weighted Average, Confusion Matrix, Receiver Operating Characteristic (ROC) Curve, Area Under the Curve (AUC), and Precision-Recall Curve, demonstrated the effectiveness of the proposed model in classifying breast cancer cases. The high precision values indicate that the model produced very few false-positive classifications, while the high recall values demonstrate its ability to correctly identify malignant breast cancer

cases. Similarly, the high F1-Score confirms a balanced relationship between precision and recall, while the ROC and Precision-Recall curves illustrate the excellent discriminative ability of the classifier. These findings collectively confirm that the developed model is capable of providing accurate and dependable breast cancer predictions.

An important contribution of this study is the demonstration that a relatively simple machine learning algorithm such as the Stochastic Gradient Descent (SGD) classifier can achieve excellent classification performance without the high computational requirements associated with more complex deep learning architectures. This computational efficiency makes the proposed model suitable for implementation in healthcare facilities with limited computing resources while still maintaining high diagnostic accuracy. The ability of the classifier to achieve consistently high performance using different train-test partitioning strategies further strengthens its potential for practical deployment in real-world clinical environments.

The findings of this research therefore confirm that the proposed Stochastic Gradient Descent classifier provides an effective, reliable, and efficient solution for breast cancer classification. The study successfully met all the stated research objectives by designing, implementing, training, and evaluating an intelligent machine learning model capable of accurately classifying breast tumors into benign and malignant categories. Consequently, the developed model has significant potential to serve as a computer-aided diagnostic tool that supports radiologists, oncologists, pathologists, and other healthcare professionals in improving diagnostic accuracy, reducing diagnostic time, minimizing human error, and facilitating timely clinical intervention. It is expected that the successful implementation of such intelligent diagnostic systems will contribute to improved patient outcomes, enhanced quality of healthcare delivery, and continued advancement in the application of artificial intelligence within the medical field.

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