Project Report

On

BREAST CANCER DETECTION USING MACHINE LEARNING

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MASTER OF SCIENCE

in

APPLIED STATISTICS AND DATA ANALYTICS

by

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CERTIFICATE

This is to certify that the dissertation entitled, **BREAST CANCER DETECTION USING MACHINE LEARNING** is a bonafide record of the work done by **Ms. MEGHA SUNIL** under my guidance as partial fulfillment of the award of the degree of **Master of Science in Applied Statistics and Data Analytics** at St. Teresa's College (Autonomous), Ernakulam affiliated to Mahatma Gandhi University, Kottayam. No part of this work has been submitted for any other degree elsewhere.

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DECLARATION

I hereby declare that the work presented in this project is based on the original work done by me under the guidance of **Mrs. Mary Andrews**, Assistant Professor, Department of Mathematics and Statistics, St. Teresa's College (Autonomous), Ernakulam and has not been included in any other project submitted previously for the award of any degree.

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ABSTRACT

Breast cancer is one of the most common cancers affecting women worldwide. Early detection plays a crucial role in improving survival rates and treatment outcomes. This study aims to develop and evaluate machine learning and deep learning models for the classification of benign and malignant tumors using mammographic images and clinical data. The project also incorporates survival analysis to estimate patient survival probabilities based on clinical parameters. Various machine learning models, including logistic regression, support vector machines, and ensemble learning techniques, are employed. Additionally, deep learning-based convolutional neural networks (CNNs) are trained on mammographic images. The results are analyzed to determine the most effective model for accurate breast cancer detection and prognosis.

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Contents

Chapter 1 : Preliminaries

1.1 Introduction

Breast cancer remains one of the most prevalent malignancies affecting women worldwide. Early detection is crucial in improving survival rates, as timely intervention significantly enhances treatment effectiveness. Over the past decade, rapid advancements in machine learning (ML) and deep learning (DL) have revolutionized breast cancer diagnosis, offering automated, highly accurate tumor classification methods (Yala et al., 2019). Traditional diagnostic techniques, including mammography and biopsy, while widely used, can be time-consuming and subject to human error. However, AI-driven approaches have shown superior accuracy, robustness, and efficiency in analyzing mammographic images and clinical patient data, making early detection and prognosis more reliable (Alshammari, Almuhanna, & Alhiyafi, 2021).

Recent studies emphasize the significance of Convolutional Neural Networks (CNNs) in medical imaging, particularly for their ability to extract deep spatial features from mammograms, thereby improving classification accuracy (Wang, 2024). Additionally, integrating statistical survival analysis models—such as the Kaplan-Meier estimator and the Cox Proportional-Hazards Model—enables oncologists to estimate patient survival probabilities and identify key prognostic factors that influence outcomes (Tatap Perets, 2023). The combination of ML and DL with survival analysis holds great promise for optimizing clinical decision-making and enhancing patient care (Mangukiya et al., 2022).

A significant challenge in breast cancer detection is the availability of large, diverse, and well-annotated datasets. Research indicates that imbalanced datasets and limited training samples may result in biased models, emphasizing the need for effective data augmentation and feature selection techniques to improve model performance (Sengar et al., 2020). Moreover, analyzing

the correlation between clinical factors and tumor progression provides valuable insights into the pathophysiology of breast cancer (Fatima et al., 2020). Advanced ML algorithms such as XGBoost and Random Forest have been widely adopted to improve classification accuracy by leveraging feature importance rankings (Chen, 2015). Similarly, deep learning architectures like VGG16 and ResNet50 have demonstrated exceptional accuracy in classifying mammographic images, further enhancing early detection capabilities (Faradmal et al., 2012).

This study focuses on developing an AI-powered framework for breast cancer detection and survival analysis by utilizing ML and DL techniques on mammography images and clinical datasets. The key objectives include: (1) classifying tumors as benign or malignant using supervised learning algorithms, (2) implementing deep learning models for mammography-based detection, and (3) conducting survival analysis to estimate patient prognosis. By incorporating advanced AI methodologies, this research aims to improve early detection, optimize treatment strategies, and contribute to more effective breast cancer management.

1.2 Breast Cancer

Breast cancer is a complex and life-threatening disease, affecting millions of women globally. It is estimated that approximately 10% of women will develop breast cancer at some point in their lives, making it the most common cancer among females. Recent statistics reveal an alarming rise in breast cancer cases; however, survival rates remain promising, with 88% of patients surviving at least five years post-diagnosis and around 80% surviving for a decade. Early detection plays a crucial role in managing breast cancer, as it remains the second leading cause of cancer-related deaths among women, following heart disease.

Breast tumors can be categorized as benign or malignant. Benign tumors are non-cancerous, slow-growing, and do not invade surrounding tissues, whereas malignant tumors are aggressive, spreading to nearby tissues and potentially metastasizing to other parts of the body. The abnormal proliferation of fatty and fibrous tissues in the breast contributes to cancer

development. As these cancerous cells multiply within tumors, the disease progresses through various stages.

Different types of breast cancer are classified based on how the abnormal cells spread within the body:

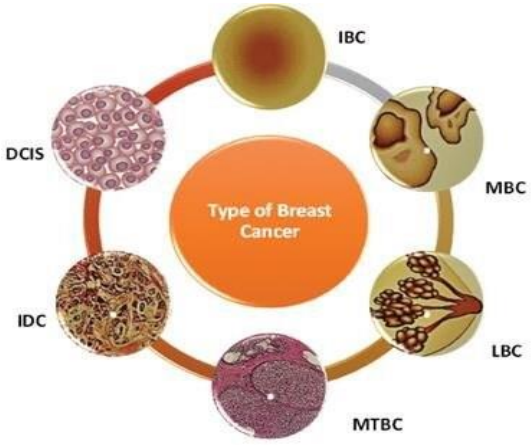

Figure 1: Major types of Breast Cancer

1. Ductal Carcinoma in Situ (DCIS): A non-invasive form where abnormal cells remain confined within the milk ducts of the breast.
2. Invasive Ductal Carcinoma (IDC): The most common type, where cancerous cells spread beyond the milk ducts into surrounding breast tissues. This type can also occur in men.
3. Mixed Tumors Breast Cancer (MTBC): Also known as invasive mammary carcinoma, this type arises from abnormal ductal and lobular cells.
4. Lobular Breast Cancer (LBC): Originates in the lobules (milk-producing glands) and may increase the likelihood of developing other invasive cancers.
5. Mucinous Breast Cancer (MBC): Also referred to as colloid breast cancer, this type occurs when abnormal ductal cells spread into surrounding tissues.

6. Inflammatory Breast Cancer (IBC): A rare but aggressive form characterized by rapid tumor growth, leading to swelling and redness, often due to blocked lymph vessels.

1.3 Symptoms of Breast Cancer

Breast cancer symptoms can vary from person to person. While some individuals may experience multiple warning signs, others may not exhibit any noticeable symptoms. The most commonly observed indicators include:

- A lump or thickened area in the breast or underarm region
- Swollen lymph nodes in the armpit
- Changes in the size, shape, texture, or color of the breast
- Unexplained discomfort or pain in the breast
- Skin redness, dimpling, or puckering
- Nipple discharge (other than breast milk), particularly if bloody
- Scaly, red, or swollen skin on the breast, nipple, or areola
- Nipple inversion or an unusual change in direction

1.4 Diagnosis of Breast Cancer

Breast cancer can be diagnosed through several medical techniques, including:

1. Breast Ultrasound: Uses sound waves to create detailed images (sonograms) of internal breast structures.
2. Diagnostic Mammogram: A specialized X-ray of the breast, recommended when abnormalities such as lumps are detected during a routine screening mammogram.
3. Breast MRI (Magnetic Resonance Imaging): A high-resolution imaging method that utilizes a magnetic field and computer technology to generate detailed breast images.
4. Biopsy: A procedure that involves extracting tissue or fluid from the breast for microscopic examination. There are different types of biopsies, including fine-needle aspiration, core biopsy, and open biopsy. Recently, AI-based diagnostic techniques have been introduced to enhance accuracy in cancer detection.

1.5 Objectives

1. To create a ML model to classify malignant and benign tumor using supervised machine learning classifier algorithm.

2. To develop and evaluate deep learning models for mammography-based breast cancer detection.

3. To perform survival analysis on patient data to estimate survival probabilities.

Chapter 2 : Literature Review

This chapter gives the recent research work and contributions done in the field of breast cancer detection with machine learning techniques, deep learning models for mammography-based breast cancer detection and survival analysis.

- Faradmal, Javad, et al. (2012) compared the results of CPH and frailty models in breast cancer (BC) patients. A historical cohort study was carried out using medical records gathered from the Fars Province Cancer Registry. The dataset consisted of 769 women having BC referred to Shiraz Namazi Hospital, south of Iran. These patients had been followed for 6 years. After selecting the most important prognostic risk factors on survival, CPH and gamma-frailty Cox models were used to estimate the effects of the risk factors. The results of CPH model showed that, tumor characteristics and number of involved lymph nodes increase the mortality hazard of BC (P = 0.05). In addition, the frailty model showed that there is at least a latent factor in the model (P = 0.005)

- Chen, W., Zheng, R. (2015) retrieved cancer data from the National Central Cancer Registry Database and the new diagnosis situation and the number of deaths due to breast cancers were estimated. The time trend and survival for breast cancer were also analyzed. About 249,000 new cases, with a 37.86/100,000 crude incidence rate, of female breast cancer were diagnosed in China in 2011. The crude incidence rate increased over the past ten years, and the trend for age-standardized rate increased gradually. Approximately 60,000 deaths were caused by breast cancer in China in 2011, with a crude mortality rate of 9.21/100,000. The crude mortality for females with breast cancer in China increased over the past several decades.

- Yala, Adam, et al. (2019) studied 88994 consecutive screening mammograms in 39571 women between January 1, 2009, and December 31, 2012. For each patient, all examinations were assigned to either training, validation, or test sets, resulting in

71 689, 8554, and 8751 examinations, respectively. Cancer outcomes were obtained through linkage to a regional tumor registry. By using risk factor information from patient questionnaires and electronic medical records review, three models were developed to assess breast cancer risk within 5 years: a risk-factor-based logistic regression model (RF-LR) that used traditional risk factors, a DL model (image only DL) that used mammograms alone, and a hybrid DL model that used both traditional risk factors and mammograms.

- Noreen Fatima et al. (2020) performed a comparative review or machine learning techniques and analyzed their accuracy across various journals. Her main focus is to comparatively analyze different existing Machine Learning and Data Mining techniques in order to find out the most appropriate method that will support the large dataset with good accuracy of prediction. She concluded by saying that each technique is suitable under different conditions and on different type of dataset, after the comparative analysis of these algorithms we came to know that machine learning algorithm SVM is the most suitable algorithm for prediction of breast
  cancer.

- Sengar et al. (2020) attempted to detect breast cancer using ML algorithms, namely RF, Bayesian Networks and SVM. The researchers obtained the Wisconsin original breast cancer dataset from the UCI repository and utilized it for comparing the learning models in terms of key parameters such as accuracy, recall, precision, and area of ROC graph. The classifiers were tested using K-fold validation method, where the chosen value of K is equal to 10.

- Alshammari, M. M., Almuhanna, A., Alhiyafi, J. (2021) applied machine learning based techniques to assist the radiologist in reading mammogram images and classifying the tumor in a very reasonable time interval. They extracted several features from the region of interest in the mammogram, which the radiologist manually annotated. These features

are incorporated into a classification engine to train and build the proposed structure classification models. They used a dataset that was not previously seen in the model to evaluate the accuracy of the proposed system following the standard model evaluation schemes. This study finally recommends using the optimized Support Vector Machine or Naïve Bayes, which produced 100% accuracy after integrating the feature selection and hyper-parameter optimization schemes.

- Manav Mangukiya et al. (2022) evaluated the accuracy in the classification of data in terms of efficiency and effectiveness of each algorithm in terms of accuracy, precision, sensitivity and specificity. The researchers reviewed various Techniques to detect early, efficiently and accurately Using Machine Learning. In this paper, Data Visualization and performance comparisons between different machine learning algorithms: Support Vector Machine (SVM), Decision Tree, Naive Bayes (NB), K Nearest Neighbors (k-NN), Adaboost, XGboost and Random Forest was conducted on Wisconsin breast cancer Dataset .Experimental results show that XGboost offers the highest accuracy (98.24%) with the lowest error rate.

- Tatap Perets (2023) aims to develop a more accurate way of diagnosing breast cancer using machine learning. The solution involves the use of artificial intelligence methods like Convolutional Neural Networks to diagnose breast cancer. The algorithm is realized in Python environment. The result shows that this method is far more efficient than all other techniques, achieving accuracy above 97%. Moreover, a web app is also deployed for user-friendliness, in order to detect any subsequent sample patient image.

- Wang, L. (2024) aims to study the recent achievements of deep learning-based mammography for breast cancer detection and classification. This review paper highlights the potential of deep learning-assisted X-ray mammography in improving the accuracy of breast cancer screening. While the potential benefits are clear, it is essential to address the challenges associated with implementing this technology in clinical

settings. Future research should focus on refining deep learning algorithms, ensuring data privacy, improving model interpretability, and establishing generalizability to successfully integrate deep learning-assisted mammography into routine breast cancer screening programs.

Chapter 3 : Materials and Methods

This chapter carefully explains the various methods and processes taken to realize the project. It reveals the model used, the training of the model in the software, and several other parameters.

3.1 Dataset

This research relies on three distinct datasets, each corresponding to a specific objective:

1. **Machine Learning-Based Tumor Classification**: The dataset for this objective was sourced from Kaggle and was originally assembled by Dr. William H. Wolberg from the University of Wisconsin Hospitals in Madison. It includes data from over 500 patients, with 30 numerical features describing various tumor characteristics. The target variable is binary, where 0 represents benign tumors and 1 represents malignant ones.
2. **Deep Learning-Based Mammography Analysis**: For this part of the study, the dataset is obtained from the University of South Florida's Digital Mammography Home Page. It consists of mammogram images that are used to train Convolutional Neural Network (CNN) models for detecting and classifying abnormalities like masses and other related classifications.
3. **Survival Analysis**: The survival analysis is based on a dataset provided by the National Institutes of Health (NIH). This collection includes patient records that document survival times, tumor features, treatment history, and biomarker information. These records are essential for performing Kaplan-Meier survival estimates and Cox Proportional-Hazards regression modeling.

3.2 Overview on Artificial Intelligence

Artificial Intelligence (AI) is a branch of computer science dedicated to creating systems and software that can perform tasks that typically require human intelligence. These tasks

range from learning and perception to problem-solving, language understanding, and logical reasoning. Within the AI field, two key areas are machine learning and deep learning.

Advantages of Artificial Intelligence

AI is revolutionizing numerous sectors of life. By leveraging machine learning, AI-powered systems and devices mimic human cognitive abilities, driving digital transformation in various industries. These intelligent systems analyze their environment, respond to stimuli, solve problems, and assist with day-to-day activities, simplifying life in the process. Below are some notable ways AI is making an impact:

1. **Voice Assistants**: AI-driven voice assistants, such as Siri, Google Home, and Alexa, interpret voice commands through Voice User Interfaces (VUI). These systems go beyond simple voice recognition, tapping into cloud databases for a more comprehensive experience.
2. **Streaming Services**: Platforms like Netflix, Spotify, and Hulu use machine learning algorithms to constantly improve user experience by processing vast amounts of data, which helps to personalize recommendations.
3. **Tailored Marketing**: Businesses are using AI-based personalized marketing strategies, fueled by customer data, to enhance engagement and connect with users on a more individualized level.
4. **Smart Keyboards**: AI-powered mobile keyboards come equipped with features like autocorrection and language recognition to make typing smoother and more efficient.
5. **Navigation and Travel**: Navigation apps, such as Google Maps and Waze, process large amounts of geographic data, constantly updating with real-time information via machine learning algorithms that analyze satellite imagery.
6. **Autonomous Vehicles**: The field of self-driving cars is advancing rapidly, with investments from major companies pushing the boundaries beyond features like cruise control to fully autonomous vehicles.

7. **Security and Surveillance**: AI's ability to monitor multiple CCTV feeds at once has made it indispensable in surveillance, improving security by automating the detection of potential threats.
8. **Internet of Things (IoT)**: The integration of AI and IoT is creating smart home technologies that require minimal human interaction. While IoT focuses on connecting devices, AI enhances these devices' ability to learn and adapt based on data.
9. **Facial Recognition**: Technologies like Face ID in smartphones are common examples of facial recognition, but concerns around biases related to race and gender in areas like forensic use still need to be addressed.
10. **Healthcare**: AI is increasingly being used in the healthcare sector, helping doctors and medical professionals diagnose, treat, and manage patient care more effectively and efficiently.

3.3 Overview on Machine Learning Algorithms

Machine Learning (ML), a subset of AI, involves statistical techniques that enable systems to learn from data and improve performance without explicit programming. Unlike traditional linear models, deep learning techniques involve hierarchical layers of increasing complexity, allowing more advanced decision-making.

ML algorithms can generally be categorized into three main types:

1. **Supervised Learning:** The model is trained on labeled data, where each input corresponds to a known output. This is widely used in classification tasks such as tumor detection in medical imaging.
2. **Unsupervised Learning:** The algorithm explores patterns in unlabeled data to discover underlying structures, such as clustering patients based on similar characteristics.
3. **Semi-Supervised Learning:** A hybrid approach that leverages both labeled and unlabeled data, improving learning efficiency while reducing reliance on extensive labeled datasets.

Figure 2.1 shows a diagram illustrating the classification of these algorithms. Various machine learning techniques are also employed in detecting breast cancer, showcasing their broad applications in healthcare.

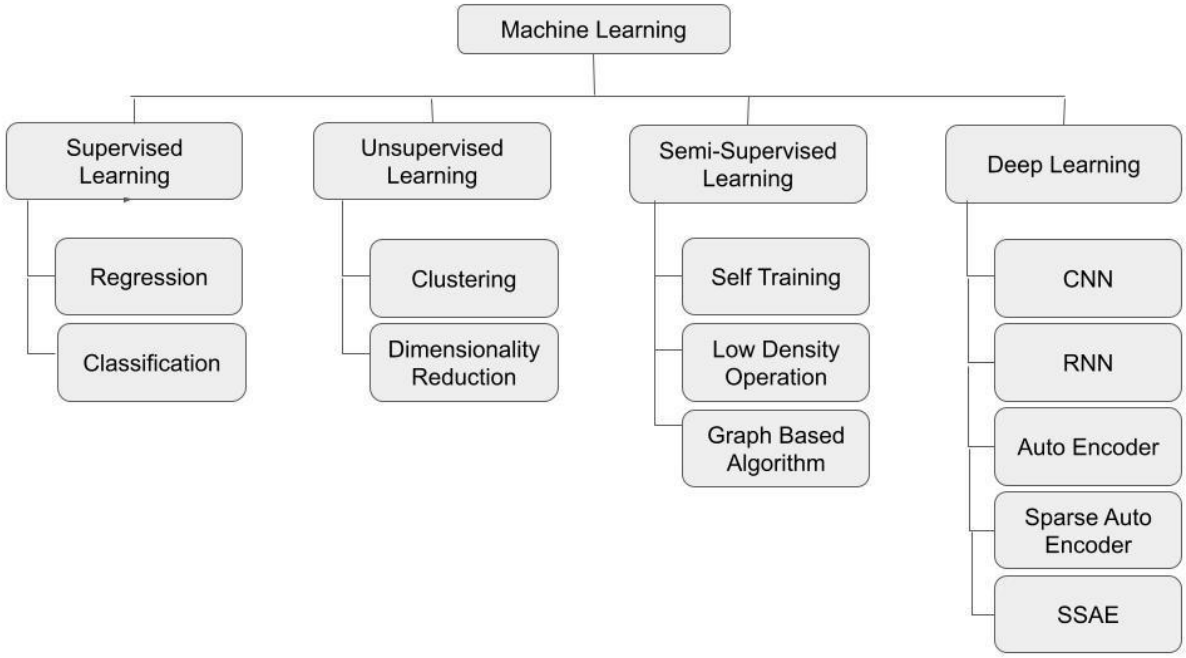

Figure 2: Classification of Machine Learning algorithms

3.3.1 Supervised Machine Learning Algorithms

Supervised machine learning is a technique in which a model is trained using labeled data, meaning each input is associated with a known output. The goal is to help the model recognize patterns and make predictions based on past examples. One of the most common applications of supervised learning is classification, where data is sorted into predefined categories. Algorithms such as decision trees and artificial neural networks (ANNs) are widely used for this purpose. Decision trees help determine the most relevant attributes in a dataset, while ANNs learn from past data to classify new inputs accurately.

1. **Logistic Regression (LR)**

Logistic regression is a simple yet powerful method used for classification tasks. It is designed to predict binary outcomes, such as whether a patient has a disease (1) or not (0). The model

calculates the probability of an event occurring by applying a mathematical function called the sigmoid function. The output is always a value between 0 and 1, and a predefined threshold (typically 0.5) is used to classify the input. If the probability is above 0.5, it is classified as one category; otherwise, it falls into the other. The probability of a class label $Y = 1$ given an input feature vector X is modeled using the sigmoid function:

$$P(Y = 1/X) = \frac{1}{1 + e^{-(wX+b)}} \tag{1}$$

where, w = weight vector, X = feature vector, b = bias

2. Support Vector Machine (SVM)

Support Vector Machines (SVMs) are effective classification algorithms that work well with both linear and non-linear data. The core idea behind SVM is to map data points into a higher-dimensional space and identify a boundary (hyperplane) that best separates different classes. The objective is to maximize the margin between the hyperplane and the closest data points from each class, ensuring accurate classification with minimal errors. SVM is especially powerful in high-dimensional datasets, making it a preferred choice for applications like image classification and text categorization.

SVM finds an optimal hyperplane $wX + b = 0$ that maximizes the margin between two classes.

$$\min_{w,b} \quad \frac{1}{2}\|w\|^2$$

subject to

$$y_i(wX_i + b) \geq 1, \forall i \tag{2}$$

3. Decision Tree (DT)

Decision Trees are one of the most intuitive machine learning models. They organize data into a tree-like structure where each internal node represents a decision based on a specific attribute. The process starts at the root node and moves through branches based on conditions until reaching a final classification. Decision trees are popular in decision-making applications, such as diagnosing medical conditions, predicting customer behavior, and credit scoring.

4. Random Forest (RF)

Random Forest is an advanced version of decision trees that enhances accuracy by creating multiple trees and combining their outputs. Instead of relying on a single tree (which can sometimes lead to overfitting), random forests generate several trees using different subsets of the data. Each tree makes a prediction, and the final classification is determined by majority voting. This ensemble technique reduces variance, improves stability, and is widely used in fraud detection, financial forecasting, and medical diagnoses.

5. Naive Bayes (NB)

Naïve Bayes is a classification algorithm based on probability theory. It operates on Bayes' theorem, which calculates the likelihood of an event occurring given certain conditions. Despite its name, the model makes a simplifying assumption that all features are independent, even though real-world data often contains correlations. However, this assumption allows the algorithm to be extremely fast and efficient. Naïve Bayes is commonly used in spam filtering, sentiment analysis, and text classification.

6. K-Nearest Neighbors (KNN)

The K-Nearest Neighbors (KNN) algorithm is a straightforward yet powerful classification method. It assigns a new data point to the category most common among its 'K' closest neighbors in the dataset. The choice of 'K' is crucial—if it's too small, the model may be sensitive to noise, and if it's too large, it might overlook important local patterns. KNN is widely used in recommendation systems, handwriting recognition, and image classification.

7. Artificial Neural Networks (ANN)

Artificial Neural Networks (ANNs) are inspired by the structure of the human brain. They consist of multiple interconnected layers of neurons that process information and learn patterns. Initially developed by McCulloch and Pitts and later improved by researchers like Rumelhart, ANNs are excellent at recognizing complex patterns in data. They use learning mechanisms such as backpropagation to improve accuracy over time. ANNs are widely used in areas like image and speech recognition, natural language processing, and medical diagnostics.

8. XGBoost (Extreme Gradient Boosting)

XGBoost is a high-performance machine learning algorithm designed for both speed and accuracy. It builds decision trees sequentially, with each tree learning from the mistakes of the previous one. This boosting technique helps in reducing errors and improving performance. Additionally, XGBoost includes regularization methods to prevent overfitting and uses parallel processing to enhance efficiency. Due to its high accuracy, XGBoost is a favorite choice in machine learning competitions and is extensively used in finance, healthcare, and predictive analytics. XGBoost uses an ensemble of decision trees to optimize a regularized loss function:

$$L(\theta) = \sum_{i=1}^{n} l(y_i, \hat{y}_i) + \sum_{k=1}^{K} \Omega(f_k) \tag{3}$$

where, $l(y_i, \hat{y}_i)$ is the loss function and $\Omega(f_k)$ is a regularization term to reduce overfitting.

9. AdaBoost (Adaptive Boosting)

AdaBoost is another boosting algorithm that improves classification performance by combining multiple weak classifiers into a strong one. It assigns different weights to data points, giving more importance to those that were misclassified in previous rounds. As a result, the model progressively focuses on difficult cases and improves its accuracy with each iteration.

AdaBoost works particularly well with decision trees and is widely used in fraud detection, face recognition, and bioinformatics.

3.3.2 Unsupervised Machine Learning Algorithms

Unsupervised learning is a machine learning approach where a model is trained using only input data, without any labeled outputs. Unlike supervised learning, these algorithms work without predefined categories and instead analyze the data to identify hidden patterns and structures. One of the most common applications of unsupervised learning is clustering, where similar data points are grouped together. This technique is particularly useful when labeled data is unavailable. Popular unsupervised learning methods include K-Means Clustering, Principal Component Analysis (PCA), and Hierarchical Clustering.

1. **K-Means Clustering**

K-Means is a widely used clustering algorithm that divides a dataset into distinct groups based on similarity. The algorithm assigns each data point to the most suitable cluster, ensuring that points within the same cluster are more alike than those in different clusters. The process continues until the clusters are optimized, meaning the data points within each group are as close to each other as possible. K-Means is particularly useful for large datasets and is commonly applied in customer segmentation, image compression, and market analysis. The goal is to partition n data points into K clusters by minimizing intra-cluster variance:

$$J = \sum_{i=1}^{K} \sum_{x_j \in C_i} \| x_j - \mu_i \| \quad (4)$$

where, x_j is data points in cluster C_i and μ_i is centroid of cluster C_i

2. C-Means Clustering

C-Means clustering is another clustering method where each data point is assigned to a specific group. Unlike K-Means, which uses hard clustering (where each data point belongs to only one cluster), C-Means allows for more flexible classification. This algorithm is especially useful in fields like medical image processing and disease prediction, where detecting subtle similarities between cases can improve diagnoses.

3. Hierarchical Clustering

Hierarchical clustering organizes data into a structured hierarchy, forming a tree-like representation of relationships between data points. Instead of dividing the data into a fixed number of clusters, this method creates a hierarchy of nested clusters, which can be visualized as a dendrogram. This makes it easier to explore relationships between data points at different levels of similarity. Hierarchical clustering is often used in genetic research, market segmentation, and document classification.

4. Gaussian Mixture Model (GMM)

The Gaussian Mixture Model (GMM) is a soft clustering technique that classifies data points based on probability distributions. Unlike K-Means, which assigns each data point to a single cluster, GMM allows points to belong to multiple clusters with varying degrees of certainty. The model operates using the Expectation-Maximization (EM) algorithm, which iteratively refines the probability estimates to find the best-fit clusters. GMM is particularly effective for applications like anomaly detection, speech recognition, and financial risk analysis.

3.3.3 Semi-Supervised Machine Learning Algorithms

Semi-supervised learning is a hybrid approach that combines elements of both supervised and unsupervised learning. It uses a small amount of labeled data alongside a large volume of unlabeled data to improve model performance. This technique is especially useful when

collecting labeled data is costly or time-consuming. Instead of manually labeling an entire dataset, a model can learn from a few labeled examples and generalize patterns across the unlabeled data. One common application of semi-supervised learning is speech recognition, where manually labeling thousands of hours of audio recordings is impractical. Another example is web content classification, where labeling every single webpage would be inefficient. By leveraging a mix of labeled and unlabeled data, semi-supervised learning provides a more scalable and effective solution for real-world machine learning problems.

3.3.4 Deep Learning Algorithms

Deep learning has gained immense popularity across various industries due to its ability to handle highly complex tasks. At its core, deep learning relies on different types of neural network architectures, each designed for specific applications. Below are some of the most widely used deep learning models:

1. **Convolutional Neural Networks (CNNs)**

Convolutional Neural Networks (CNNs), or ConvNets, are primarily used in image recognition and object detection. Originally introduced by Yann LeCun in 1988 as LeNet, CNNs have since evolved into powerful models used in medical image analysis, satellite imagery processing, time-series forecasting, and anomaly detection. These networks use convolutional filters to extract important features from images, allowing them to recognize patterns such as edges, shapes, and textures. This ability makes CNNs a fundamental technology behind applications like facial recognition, self-driving cars, and medical diagnostics. CNNs apply convolutional filters to extract features from images:

$$X'_{ij} = \sum_m \sum_n W_{mn} X_{i-m,j-n} + b \tag{5}$$

where, X'_{ij} is output pixel value, W_{mn} is convolution kernel, $X_{i-m,j-n}$ is input pixel values and b is bias.

2. Long Short-Term Memory Networks (LSTMs)

LSTMs are a type of Recurrent Neural Network (RNN) designed to process sequential data while preserving long-term dependencies. Unlike traditional RNNs, which struggle with remembering information over long sequences, LSTMs use memory cells to retain important details over extended periods. Because of this, LSTMs are widely applied in speech recognition, financial forecasting, and drug discovery, where analyzing sequential patterns is crucial.

3. Recurrent Neural Networks (RNNs)

RNNs are designed with cyclic connections that allow information from past inputs to influence the current output. This makes them highly effective for tasks such as natural language processing, image captioning, handwriting recognition, and language translation.

4. Generative Adversarial Networks (GANs)

Recurrent Neural Networks (RNNs) are designed with feedback loops that allow past information to influence the present output. This makes them highly effective for tasks that require context awareness, such as natural language processing, handwriting recognition, and language translation. RNNs are often used in applications like chatbots, voice assistants, and real-time captioning, where the model needs to remember previous inputs to generate meaningful responses.

5. Radial Basis Function Networks (RBFNs)

Radial Basis Function Networks (RBFNs) are a type of feed-forward neural network that employs radial basis functions as activation mechanisms. These networks are commonly

applied in classification, regression, and time-series forecasting, making them valuable for tasks like financial modeling and control systems.

6. Multilayer Perceptrons (MLPs)

Multilayer Perceptrons (MLPs) are one of the most fundamental deep learning models. They consist of multiple layers of perceptrons, each with an activation function, and are fully connected, meaning every neuron in one layer is linked to every neuron in the next. MLPs are widely used in speech and image recognition, machine translation, and predictive analytics, providing a strong foundation for many AI-driven applications.

7. Self-Organizing Maps (SOMs)

Developed by Teuvo Kohonen, Self-Organizing Maps (SOMs) are a type of neural network used for data visualization and dimensionality reduction. They help uncover patterns in high-dimensional datasets by organizing similar data points into clusters, making the information easier to interpret. SOMs are commonly used in market analysis, customer segmentation, and fraud detection, where large volumes of complex data need to be structured meaningfully.

8. Deep Belief Networks (DBNs)

Deep Belief Networks (DBNs) are generative models composed of multiple layers of hidden variables, often built using Restricted Boltzmann Machines (RBMs). These networks are effective in applications such as image recognition, video analysis, and motion-capture processing. DBNs are particularly useful when working with large datasets, as they can uncover hidden structures in the data without requiring extensive labeled inputs.

9. Restricted Boltzmann Machines (RBMs)

Restricted Boltzmann Machines (RBMs), originally developed by Geoffrey Hinton, are probabilistic neural networks used for tasks like dimensionality reduction, collaborative filtering, classification, and regression. RBMs serve as a foundational building block for Deep Belief Networks (DBNs) and are widely used in recommendation systems, such as those found in streaming services and e-commerce platforms.

10. Autoencoders

Autoencoders are a special type of feed-forward neural network designed to reconstruct input data. First introduced by Geoffrey Hinton in the 1980s, autoencoders learn to encode data efficiently and then reconstruct it, making them useful for tasks like image denoising, pharmaceutical research, and trend prediction. These networks are widely applied in feature extraction, anomaly detection, and reducing the complexity of high-dimensional datasets.

3.4 Overview on Survival Analysis

Survival analysis is a statistical method used to study the time until a specific event occurs, such as disease recurrence, progression, or patient survival. In the case of breast cancer, it helps in understanding:

1. The duration before cancer returns after treatment.
2. The overall probability of survival following a diagnosis.
3. How clinical factors like tumor size or treatment type influence patient survival.

A unique challenge in survival analysis is censored data, which occurs when some patients either drop out of the study or live beyond the observation period, making it impossible to determine their exact survival time.

Key Terms in Survival Analysis

1. Survival Function

   The survival function, S(t), represents the probability that a patient survives past a given time t. Mathematically, it is expressed as:

$$S(t) = P(T > t) \tag{6}$$

   where, T is the random variable denoting survival time and t is a specific time. The survival function is monotonically decreasing, meaning $S(0) = 1$ and $S(\infty) = 0$

2. Hazard Function

   The hazard function, h(t), represents the instantaneous risk of an event occurring at a specific time, given that the individual has survived up until that point. It helps in identifying risk factors that influence survival duration.

$$h(t) = \lim_{\Delta t \to 0} \frac{P(t \leq T < t + \Delta t | T \geq t)}{\Delta t} \tag{7}$$

Methods in Survival Analysis

1. Kaplan-Meier Estimator

   The Kaplan-Meier (KM) estimator is a non-parametric method used to estimate the survival probability over time. The formula is:

$$S(t) = \prod_{t_i \leq t} (1 - \frac{d_i}{n_i}) \tag{8}$$

where d_i is the number of patients who died at time t_i and n_i is the no. of patients at risk at t_i

   Kaplan-Meier curves are often used to visually compare survival rates between different patient groups, such as those receiving different treatments.

2. Cox Proportional Hazards Model

   The Cox regression model is a semi-parametric approach used to examine the relationship between survival time and one or more predictor variables, such as age, tumor stage, or treatment type.

   The hazard function in the Cox model is given by:

$$h\,(t\,|X) = h_0(t)\,e^{\beta X} \tag{9}$$

   where $h_0(t)$ is the baseline hazard function, X is the vector of predictor variables and β is the regression coefficients estimating risk.

3. Log-Rank Test

The log-rank test is used to compare survival distributions across different patient groups, such as those receiving different treatments. It assesses whether there is a statistically significant difference in survival rates between groups. The test statistic is:

$$Q = \frac{\sum_i (O_i - E_i)^2}{E_i} \tag{10}$$

where O_i is the observed number of deaths in group i and E_i is the expected number of deaths under the null hypothesis.

A low p-value (0.05) indicates a statistically significant difference between survival curves.

3.5 Project Methodology

This project utilized a combination of **machine learning and deep learning** approaches to classify tumors and analyze patient survival patterns. The methodology was structured into three main phases: machine learning for tumor classification, deep learning for mammography analysis, and survival analysis for breast cancer patients.

3.5.1 Machine Learning for Tumor Classification

The machine learning-based tumor classification followed a structured process, beginning with data preprocessing. The dataset was carefully examined for missing values, which were either filled using appropriate statistical techniques or removed to maintain data integrity. To ensure consistency across numerical features, Min-Max Scaling was applied, keeping all values within a standardized range for improved model performance. After preprocessing, the dataset was divided into 80% for training and 20% for testing.

Once the data was prepared, various supervised learning models were trained and evaluated, including: Logistic Regression, Support Vector Machine, Decision Tree, Random Forest, Naive Bayes, K-Nearest Neighbors, Artificial Neural Networks, XGBoost and AdaBoost.

Among these, XGBoost achieved the highest accuracy, reaching 98.24 %.

3.5.2 Deep Learning for Mammography Analysis

To classify mammograms using deep learning, Convolutional Neural Networks (CNNs) were utilized for image analysis. The process began with image preprocessing, where mammogram images were converted to grayscale, resized to a uniform 224×224 pixels, and normalized by scaling pixel values between 0 and 1. To enhance the model's ability to generalize to different cases, data augmentation techniques such as rotation, flipping, and contrast adjustments were applied.

The CNN architecture was structured with three convolutional layers, each followed by max-pooling layers to reduce the dimensionality while preserving key features. Fully connected dense layers were added to process extracted features, and dropout regularization was implemented to mitigate overfitting. The final classification layer used a sigmoid activation function to distinguish between malignant and benign cases. Training was carried out over 20 epochs with a batch size of 16, balancing model performance and computational efficiency. Evaluation metrics included accuracy, loss curves, confusion matrices, and F1-score, ensuring a comprehensive assessment of the model's performance.

3.5.3 Survival Analysis on Breast Cancer Patients

To assess patient survival probabilities based on tumor progression and clinical factors, survival analysis was conducted. In the data preprocessing stage, missing survival times were handled appropriately, censored data was labeled correctly, and categorical variables—such as tumor stage, treatment type, and biomarker presence—were encoded for analysis.

The Kaplan-Meier estimator was applied to estimate survival probabilities over time, allowing comparisons across different patient groups, such as those with varying tumor stages. Additionally, the Cox Proportional-Hazards model was used to examine the impact of clinical and demographic factors on survival time, identifying significant predictors that influence patient outcomes.

Chapter 4 : Data Description And Exploratory Data Analysis

4.1 Data Description

The datasets used in this study come from three different sources:

1. Breast Cancer Wisconsin Dataset (Kaggle) – for Machine Learning-based Tumor Classification.
2. University of South Florida Digital Mammography Dataset – for Deep Learning-based Breast Cancer Detection.
3. National Institute of Health (NIH) Dataset – for Survival Analysis of Breast Cancer Patients.

Each dataset contains various attributes that play a significant role in breast cancer detection and analysis. The following section provides a detailed description of the attributes in each dataset

Attributes

1. Breast Cancer Wisconsin Dataset (Kaggle)

This dataset, obtained from Dr. William H. Wolberg of the University of Wisconsin, consists of 30 numerical features extracted from digitized images of fine needle aspirate (FNA) biopsies of breast masses. The dataset is commonly used for binary classification (Benign vs. Malignant).

- Diagnosis – Target variable (0 = Benign, 1 = Malignant)
- Radius (mean, worst, and standard error) – Measures the distance from the center to the perimeter of the tumor.
- Texture (mean, worst, and standard error) – Describes variations in the gray-scale intensity of the cells.
- Perimeter (mean, worst, and standard error) – The total outer boundary of the tumor cells.

- Area (mean, worst, and standard error) – The overall space occupied by the tumor cells.
- Smoothness (mean, worst, and standard error) – Measures the difference between local radius lengths.
- Compactness (mean, worst, and standard error) – Captures how closely packed the cells are.
- Concavity (mean, worst, and standard error) – Measures the severity of concave portions of the tumor contour.
- Concave Points (mean, worst, and standard error) – Number of concave portions in the tumor contour.
- Symmetry (mean, worst, and standard error) – Measures how symmetrical the tumor shape is.
- Fractal Dimension (mean, worst, and standard error) – Captures the complexity of the tumor boundary.

2. University of South Florida Digital Mammography Dataset

This dataset contains mammographic images categorized into different diagnostic classes, which are used for deep learning-based breast cancer detection. The key attributes include:

- Image ID – Unique identifier for each mammogram.
- Breast Density – Indicates the density of the breast tissue (Fatty, Scattered, Heterogeneously Dense, Extremely Dense).
- Calcification Type – Describes whether calcifications are benign or suspicious for malignancy.

- Mass Shape – Characterizes the morphology of the detected mass (Round, Oval, Lobular, Irregular).
- Mass Margins – Determines the boundaries of the mass (Circumscribed, Micro lobulated, Obscured, Ill-defined, Spiculated).
- Assessment Score – BI-RADS assessment score used by radiologists to classify risk.

3. **National Institute of Health (NIH) Dataset**

This dataset is used for survival analysis and contains patient information regarding breast cancer diagnosis, treatment, and outcomes.

- Patient ID – Unique identifier for each patient.
- Age – Age of the patient at the time of diagnosis.
- Tumor Stage – Staging classification based on tumor progression (Stage I-IV).
- Lymph Node Involvement – Number of lymph nodes affected by cancer.
- Tumor Size – Measurement of the tumor in millimeters.
- Estrogen Receptor (ER) Status – Indicates whether the tumor cells have estrogen receptors.
- Progesterone Receptor (PR) Status – Indicates the presence of progesterone receptors.
- HER2 Status – Identifies HER2-positive or negative breast cancer cases.
- Treatment Type – Chemotherapy, radiation therapy, or surgery.
- Survival Time – Time (in months) the patient survived after diagnosis.
- Survival Status – Binary outcome (0 = Deceased, 1 = Alive)

4.2 Exploratory Data Analysis

4.2.1 Exploratory Data Analysis of the Breast Cancer Wisconsin Dataset

1. **Count Plot**

A count plot is used to visualize the number of benign and malignant cases in the dataset.

The target variable ”Diagnosis” has two categories:

0 (Benign) – Non-cancerous tumors

1 (Malignant) – Cancerous tumors

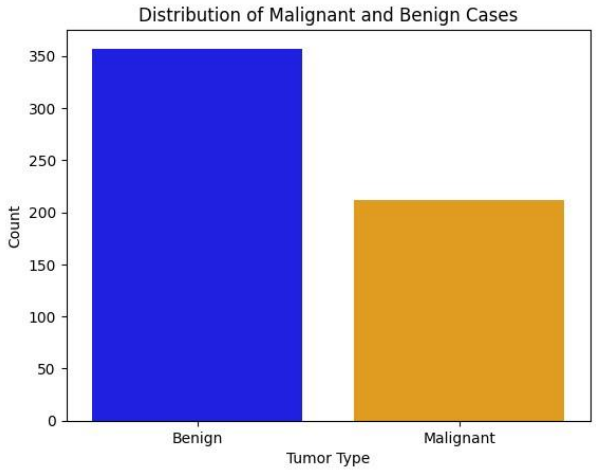

Figure 3: Count Plot

2. **Pair Plot**

A pair plot (scatter plot matrix) is used to visualize the relationships between different numerical features. It helps in:

-Understanding the separation between benign and malignant tumors.

-Identifying highly correlated features that could be useful for classification.

-Detecting any overlapping patterns in the feature space.

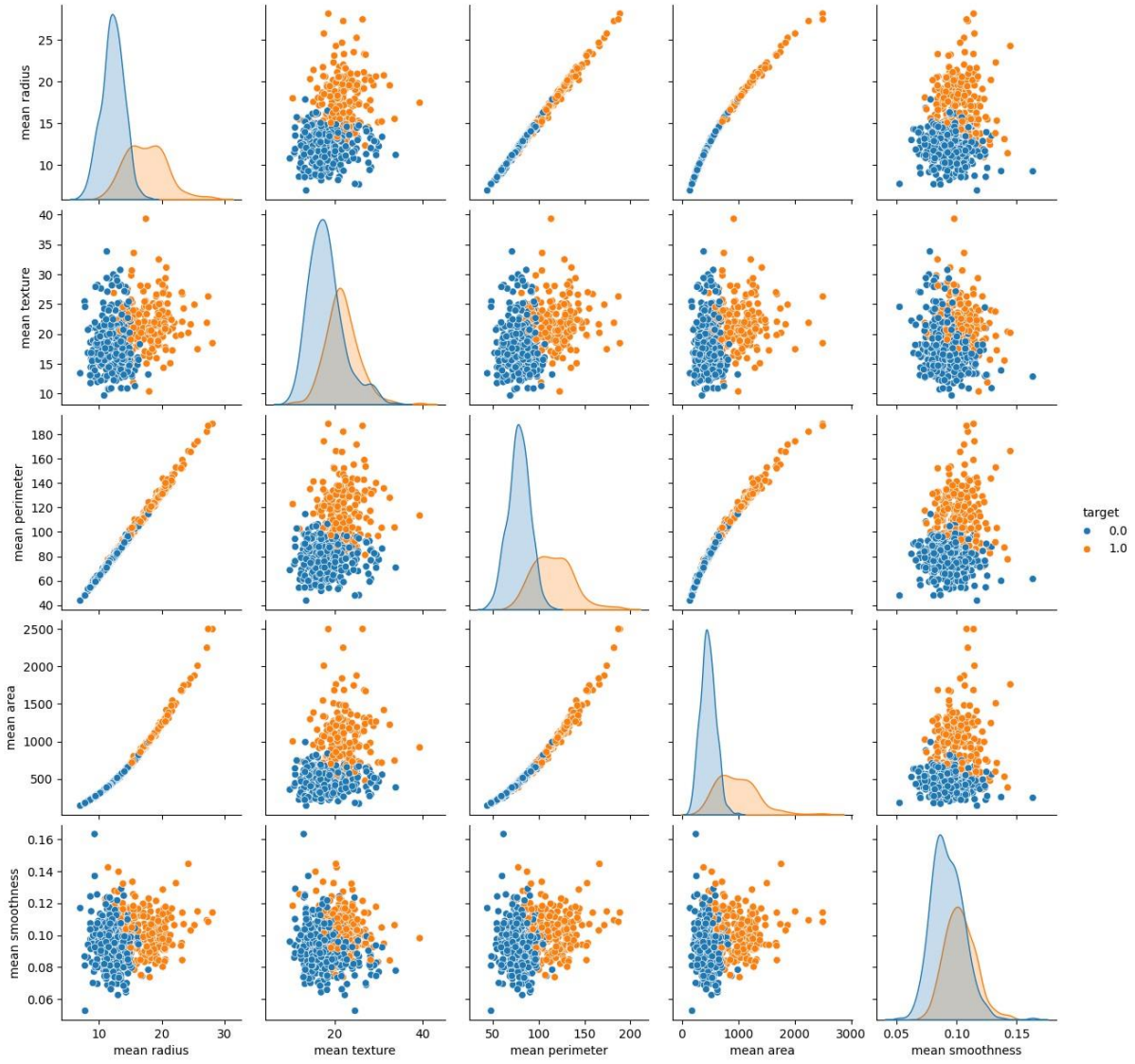

Figure 4: Pair Plot

3. **Heatmap of Correlation Matrix**

A correlation heatmap is a color-coded visualization of the correlation matrix that shows how strongly different features are related to each other. Correlation values range from -1 to +1, where:

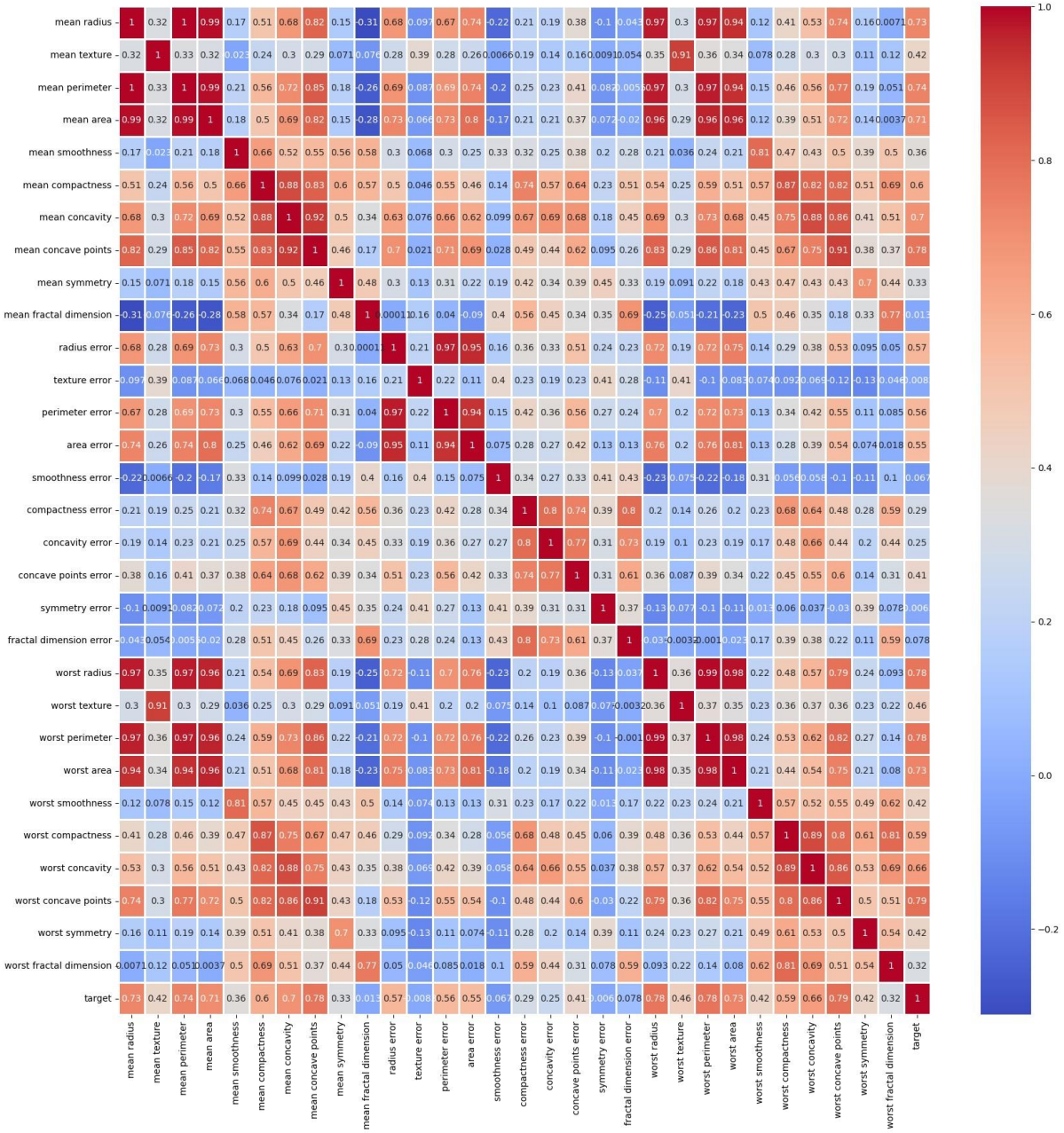

Figure 5: Heatmap of Correlation Matrix

- +1 indicates a strong positive correlation (both features increase together).
- -1 indicates a strong negative correlation (one feature increases while the other decreases).
- 0 means no correlation.

4. **Correlation Bar Plot**

A correlation bar plot helps in identifying the most influential features by plotting the correlation values of each feature with the target variable.

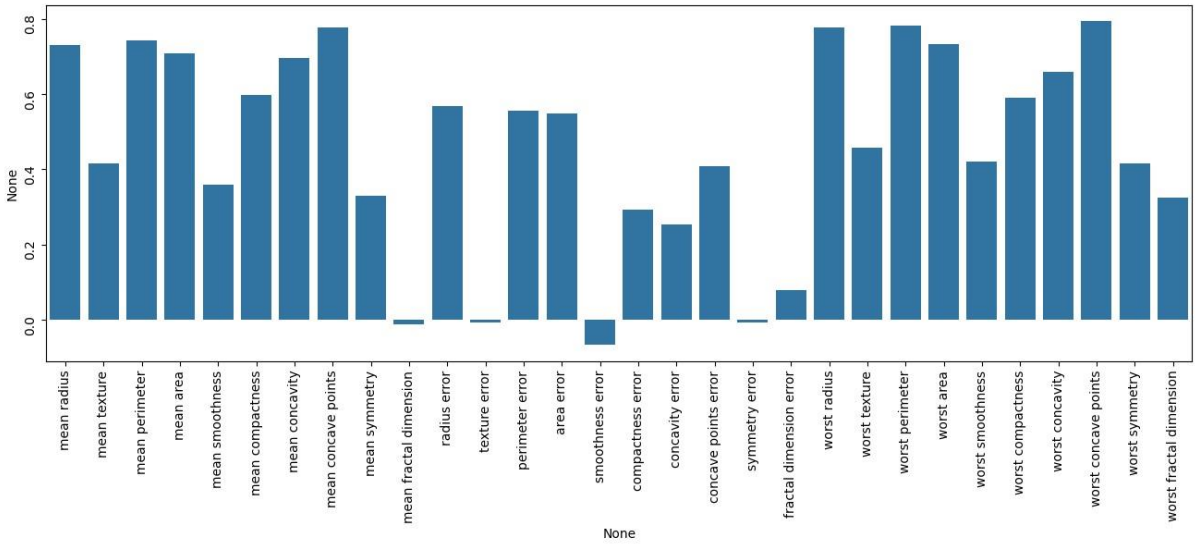

Figure 6: Correlation Bar Plot

4.2.2 Exploratory Data Analysis of Mammography-Based Breast Cancer Detection

1. **Image Preprocessing**

Since mammography images are obtained from different sources and may have variations in lighting, contrast, and resolution, preprocessing is essential to ensure consistency in the input data. The preprocessing steps included:

a) Grayscale Conversion:

- Mammographic images are originally in grayscale, but they may contain noise or unwanted artifacts.
- Converting all images to grayscale ensures uniformity and simplifies computation, as color information is not relevant for tumor detection.
- This step reduces the input dimensionality, making model training more efficient.

b) Normalization:

- Pixel values in mammograms typically range from 0 to 255. Normalization scales these values between 0 and 1 using:

$$I_{normalized} = \frac{I - I_{min}}{I_{max} - I_{min}} \tag{11}$$

- This step prevents large numerical differences from affecting the training process and ensures better convergence in deep learning models.

c) Data Augmentation:

Since deep learning models require large amounts of data for better generalization, data augmentation was applied to artificially increase the dataset size. The following augmentation techniques were used:

- Flipping: Horizontal and vertical flips help the model learn from different orientations of the same image.
- Rotation: Images were rotated randomly within a ±15° range to account for different breast positioning during mammography.
- Contrast Adjustments: Adjusting contrast enhances tumor visibility, making it easier for the model to learn important patterns.

2. **Dataset Splitting**

To ensure reliable model evaluation, the dataset was divided into:

80% Training Set: Used to train the deep learning model.

20% Testing Set: Used for final model evaluation.

The dataset split was performed randomly while maintaining a balanced ratio of malignant, benign, and normal images across both sets.

3. **Image Sample Visualization**

To understand the dataset characteristics, sample images from each category (benign and malignant) were visualized. The purpose of this step was to:

- Observe variations in brightness and contrast among images.
- Identify potential artifacts such as labels or noise that could affect model performance.
- Ensure that the preprocessing steps (grayscale conversion, normalization, augmentation) were correctly applied.

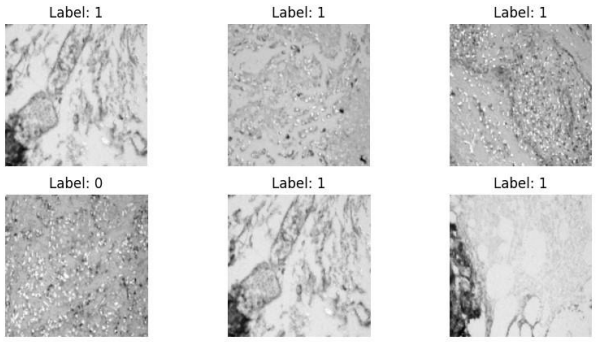

Figure 7: Sample Images

4.2.3 Exploratory Data Analysis for Survival Analysis on Breast Cancer Patients

1. Checking for Missing Values

Missing values in age, tumor size, or receptor status can bias survival analysis. No missing values were found.

2. Identifying Outliers

Outliers in tumor size can be detected using boxplots or Z-score analysis. If there were any outliers, they would appear as individual points outside the whiskers. Since the plot doesn't show any outliers, it means the tumor size data falls within a normal range.

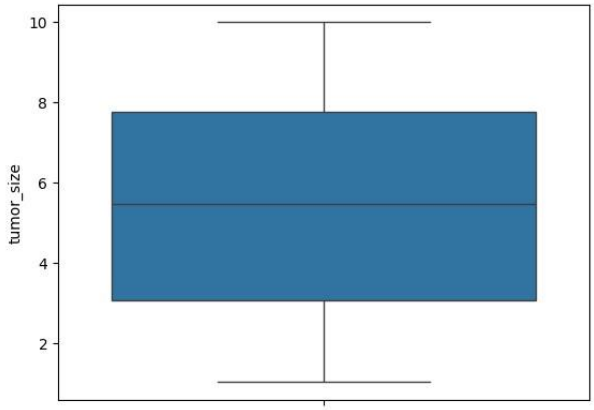

Figure 8: Boxplot for Tumor Size

3. Distribution of Survival Time

Histogram is used to visualize survival time distribution. This plot helps determine whether survival times are normally distributed or skewed, which impacts statistical modeling.

The distribution is right-skewed (positively skewed). Most patients have a short survival time, and fewer survive longer. The longer tail on the right indicates that a small number of patients survive much longer than the majority.

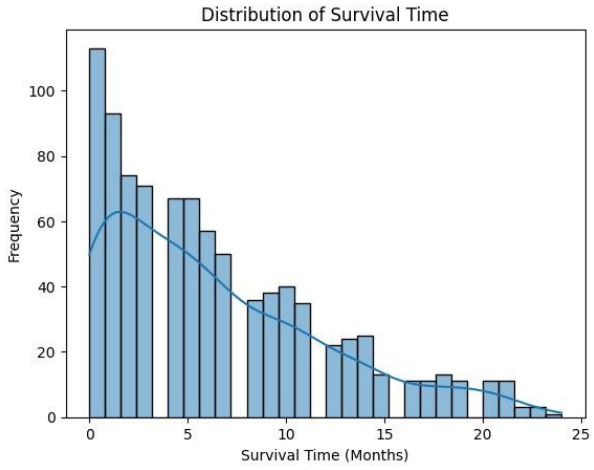

Figure 9: Distribution of Survival Time

Chapter 5 : Results and Findings

This section presents the key outcomes of the study, focusing on the three main objectives:

(1) Building Machine Learning model for breast cancer classification,

(2) Deep Learning models for mammography-based breast cancer detection, and

(3) Survival analysis to estimate survival probabilities.

5.1 Machine Learning Model for Breast Cancer Classification

The supervised machine learning models such as Support Vector Classifier (SVC), Logistic Regression, K-Nearest Neighbors (KNN) Classifier, Naive Bayes Classifier, Decision Tree Classifier, Random Forest Classifier, AdaBoost Classifier and XGBoost Classifier was trained on the breast cancer dataset to classify tumors as malignant or benign. The best-performing model, XGBoost, achieved an accuracy of 98% on the test set, outperforming other models.

MODELS	INITIAL ACCURACY	TUNED ACCURACY
Support Vector Classifier (SVC)	93.85%	96.49%
Logistic Regression	96.49%	98.24%
K-Nearest Neighbors (KNN) Classifier	93.85%	57.89%
Naive Bayes Classifier	94.73%	93.85%
Decision Tree Classifier	94.73%	75.43%
Random Forest Classifier	97.36%	64.91%
AdaBoost Classifier	94.73%	94.73%
XGBoost Classifier	98.24%	98.24%

Table 3: Accuracy of models

Confusion Matrix

The confusion matrix provides a detailed breakdown of the model's predictions by comparing them to the actual tumor classifications in the test set. It serves as a valuable tool in assessing the model's ability to differentiate between benign and malignant tumors.

- True Negatives (TN): 66 cases were correctly classified as benign tumors, indicating the model's strong ability to recognize non-cancerous cases.
- True Positives (TP): 46 cases were accurately identified as malignant tumors, demonstrating its effectiveness in detecting cancerous growths.
- False Positives (FP): 0 cases—the model did not mistakenly classify any benign tumors as malignant, which is crucial as it prevents unnecessary medical interventions.
- False Negatives (FN): 2 cases—two malignant tumors were misclassified as benign, meaning there was a slight limitation in detecting all cancerous cases.

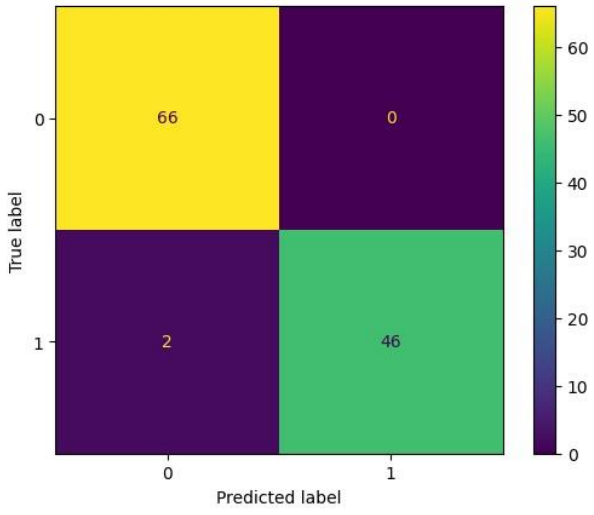

Figure 10: Confusion Matrix

The overall accuracy of the model was computed using the formula:

$$Accuracy = \frac{TP + TN}{TP + TN + FP + FN} = \frac{46 + 66}{46 + 66 + 0 + 2} = \frac{112}{114} = 98.25\% \quad (12)$$

This high accuracy score of 98.2% demonstrates the model's effectiveness in classifying tumors correctly, with minimal misclassification errors. The absence of false positives ensures that no unnecessary treatments would be recommended, while the presence of only two false negatives suggests a strong reliability in detecting malignant cases. However, despite its high accuracy, further optimization may be required to minimize the risk of false negatives, as failing to detect a malignant tumor could have serious medical consequences.

ROC Curve

The Receiver Operating Characteristic (ROC) Curve is a visual representation of the model's ability to distinguish between benign and malignant tumors at different classification thresholds. It plots the False Positive Rate (FPR) on the X-axis—indicating the proportion of benign tumors misclassified as malignant—against the True Positive Rate (TPR) on the Y-axis, which measures the model's ability to correctly identify malignant tumors.

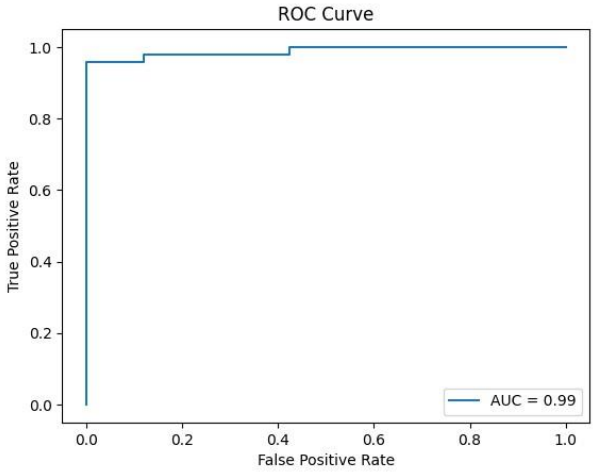

Figure 11: ROC Curve

A key performance metric derived from the ROC curve is the Area Under the Curve (AUC) score, which quantifies how effectively the model differentiates between the two tumor types. With an AUC score of 0.99, the model demonstrates exceptional classification performance, indicating a near-perfect ability to separate benign and malignant cases. A score close to 1

signifies that the model maintains high sensitivity (TPR) while keeping false positives (FPR) minimal, ensuring accurate diagnosis.

The sharp rise of the ROC curve toward the top-left corner further validates the model's strong performance across various threshold values, highlighting its reliability in real-world diagnostic scenarios. The high AUC score confirms that the model can accurately differentiate between tumor types with minimal compromises between sensitivity and specificity, reinforcing its effectiveness in medical decision-making.

5.2 Deep Learning Model for Mammography-Based Breast Cancer Detection

The deep learning model designed for breast cancer detection is based on a Convolutional Neural Network (CNN), a powerful architecture commonly used for image classification tasks. This model processes mammogram images through multiple convolutional layers, pooling layers, and fully connected layers to learn meaningful patterns and distinguish between malignant and benign tumors.

The architecture begins with a Conv2D layer containing 32 filters with a 3×3 kernel size, which captures basic image features such as edges and textures. A MaxPooling2D layer follows to reduce the spatial dimensions of the feature maps, helping to prevent overfitting. As the network progresses, additional Conv2D layers with 64 and 128 filters—each followed by max-pooling layers—are introduced, allowing the model to detect more complex structures within mammogram images. Once feature extraction is complete, a Flatten layer converts the extracted feature maps into a one-dimensional array, which is then passed through a fully connected (Dense) layer with 128 neurons. To mitigate overfitting, a Dropout layer is included, which randomly deactivates certain neurons during training. The final output layer consists of a single neuron that predicts whether the given mammogram indicates a malignant or benign tumor, making it a binary classification model.

Training Performance and Accuracy

The model comprises 11,168,513 trainable parameters, occupying approximately 42.60MB of memory. During training, the network was trained for 20 epochs, with key performance metrics recorded at each step. Initially, at Epoch 1, the training accuracy was 48.91% while the validation accuracy was 58.33%. The corresponding loss values were 1.1724 for training loss and 0.6833 for validation loss. As training progressed, the accuracy improved, with Epoch 5 showing 57.16% training accuracy and 58.33% validation accuracy, accompanied by a training loss of 0.6872 and validation loss of 0.6812. However, a notable observation is that validation accuracy remains constant at 58.33% throughout training, suggesting that the model is struggling to generalize well to unseen data, possibly due to overfitting or a capacity bottleneck in feature learning.

Layer (type)	Output Shape	Param
conv2d (Conv2D)	(None, 222, 222, 32)	320
max pooling2d (MaxPooling2D)	(None, 111, 111, 32)	0
conv2d$_1$(*Conv2D*)	(None, 109, 109, 64)	18,496
max pooling2d$_1$(*MaxPooling2D*)	(None, 54, 54, 64)	0
conv2d$_2$(*Conv2D*)	(None, 52, 52, 128)	73,856
max pooling2d$_2$(*MaxPooling2D*)	(None, 26, 26, 128)	0
flatten (Flatten)	(None, 86528)	0
dense (Dense)	(None, 128)	11,075,712
dropout (Dropout)	(None, 128)	0
dense$_1$(*Dense*)	(None, 1)	129

To improve performance, several strategies can be explored. Increasing the dataset size or applying data augmentation techniques may enhance generalization. Hyperparameter tuning,

such as adjusting the learning rate, batch size, or dropout rate, could also lead to improved results. Additionally, experimenting with deeper architectures, such as

ResNet or VGG, or utilizing transfer learning with pre-trained models on medical imaging datasets may yield better accuracy and stability. Further analysis of the loss curves and misclassified cases may also provide insights into refining the model for more reliable breast cancer detection.

Training vs. Validation Accuracy and Loss

The Training vs. Validation Accuracy plot (left) illustrates that training accuracy increases rapidly, reaching approximately 60%. However, the validation accuracy remains stagnant at around 58%, indicating that while the model is learning from the training data, it struggles to generalize to unseen validation samples. This discrepancy between training and validation accuracy suggests a case of overfitting, where the model memorizes patterns from the training set rather than learning meaningful features that generalize well to new data. Additionally, the overall accuracy remains relatively low, highlighting the need for improvements such as hyperparameter tuning, data augmentation, or a more sophisticated model architecture to enhance performance and reduce overfitting.

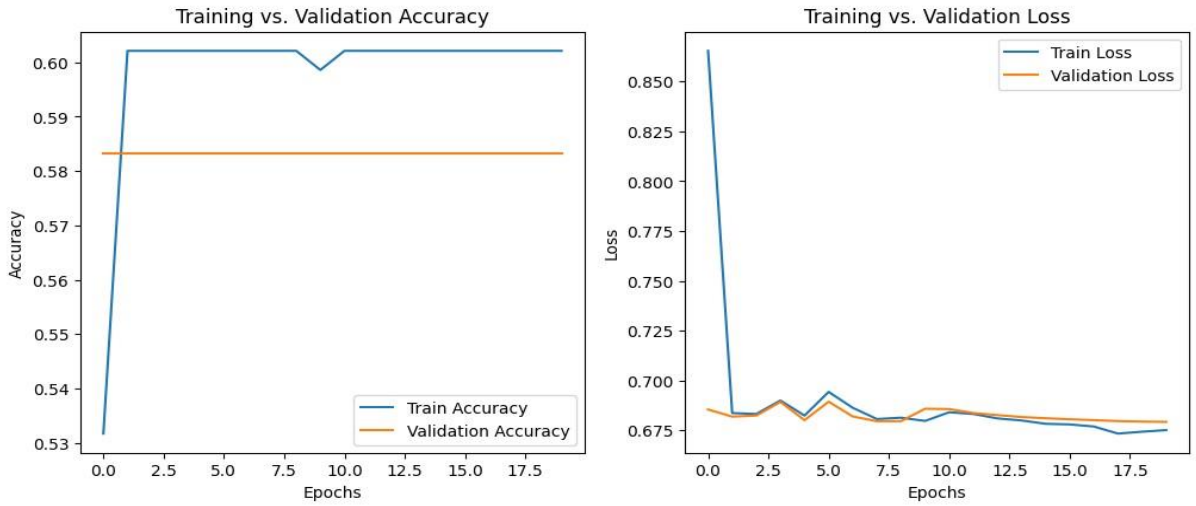

Figure 12: Training vs. Validation Accuracy and Loss

The Training vs. Validation Loss plot (right) shows that the training loss starts at a high value but drops significantly within the first few epochs, indicating that the model is quickly adapting to the training data. A similar trend is observed for validation loss, but it stabilizes at a higher value compared to training loss, reinforcing the concern of overfitting. The persistent gap between training and validation loss suggests that the model performs well on the training dataset but struggles to maintain low loss on validation data. This issue can be addressed using techniques such as Dropout that helps to prevent overfitting by randomly deactivating neurons during training, Batch Normalization that stabilizes learning by normalizing activations, improving generalization, and Early Stopping that monitors validation loss and stops training when overfitting is detected. By incorporating these strategies, the model's ability to generalize to unseen data can be improved, leading to better classification performance in breast cancer detection.

5.3 Survival analysis to estimate survival probabilities

Kaplan-Meier Survival Curve

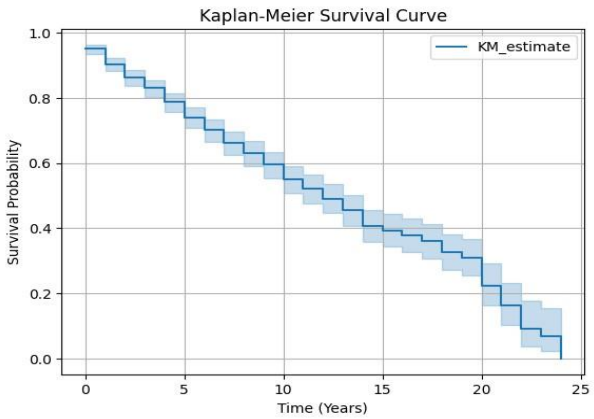

Figure 13: Kaplan-Meier Survival Curve

The survival analysis conducted in this study provides valuable insights into breast cancer prognosis and factors influencing patient survival. The Kaplan-Meier survival curve was used

to estimate survival probabilities over time, revealing a gradual decline in survival rates across 25 years. This confirms the expected trend that as time progresses, the probability of survival decreases.

Comparison of Survival by HER2 Status

A survival analysis was conducted to compare outcomes between HER2-positive and HER2-negative breast cancer patients. Kaplan-Meier survival curves for both groups revealed a clear difference in survival probabilities, with HER2-negative patients generally showing slightly better survival outcomes than those who were HER2-positive. This finding highlights the critical role of HER2 status in breast cancer prognosis and underscores the importance of targeted HER2 therapies in improving patient survival rates.

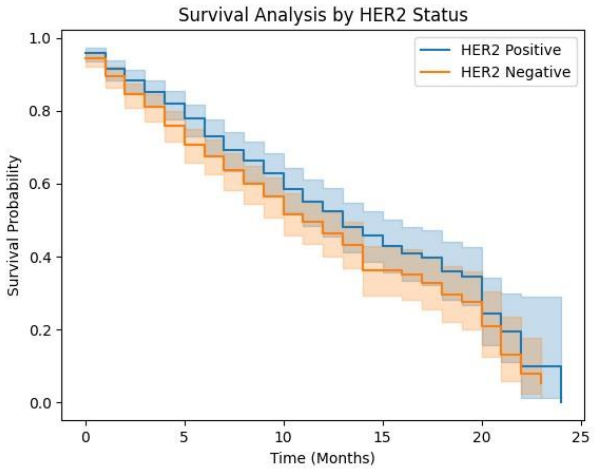

Figure 14: Comparison of Survival by HER2 Status

Correlation Analysis of Clinical Factors

To examine relationships among different clinical factors, a correlation heatmap was generated. The analysis revealed strong associations between tumor stage, patient status, and survival time, suggesting that these factors are closely linked to disease progression. Other variables, including tumor size, chemotherapy, radiation therapy, and HER2 status, also displayed varying levels of correlation with survival outcomes, emphasizing their impact on patient prognosis. These findings indicate that incorporating multiple clinical factors into personalized treatment

strategies could enhance survival predictions and guide more effective clinical decision-making. Since multiple variables influence patient outcomes, further analysis using Cox Proportional Hazards models could provide deeper insights into risk factors and improve predictive models for breast cancer survival.

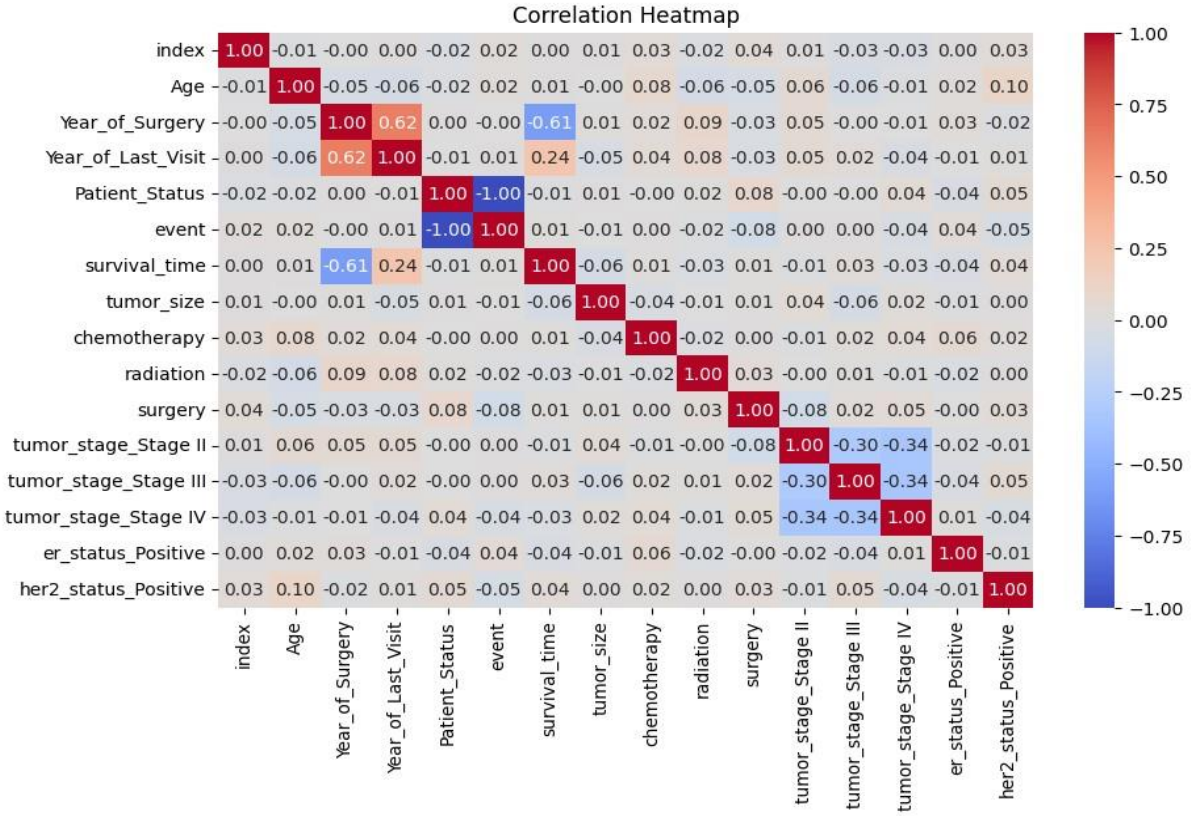

Figure 15: correlation heatmap

Cox Proportional Hazards (CoxPH) model

The Cox Proportional Hazards model was applied to identify key clinical factors influencing breast cancer survival. The results showed that tumor size, radiation therapy, and estrogen receptor status had a weak positive association with increased hazard (higher risk), while surgical intervention and HER2-positive status appeared to be linked to improved survival outcomes. However, the model's predictive accuracy, as indicated by a C-index of 0.57, suggests that additional variables or refined modeling techniques may be needed to improve performance. Techniques such as regularization, feature selection, or incorporating additional

patient data could enhance both interpretability and predictive reliability, leading to more effective survival analysis in breast cancer research.

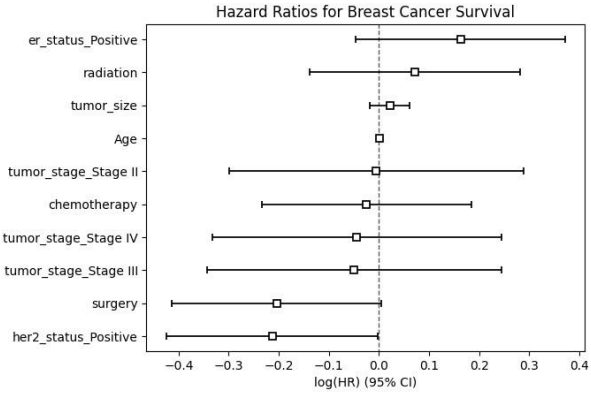

Figure 16: Cox Proportional Hazards model

Log-Rank Test

The log-rank test is a statistical method commonly used in survival analysis to compare the survival distributions between two groups. In this study, the test was applied to evaluate whether different treatment types led to significant differences in survival outcomes. The results showed that all pairwise comparisons yielded high p-values (greater than 0.05), indicating no statistically significant differences in survival between the treatment groups. The lowest p-value observed was 0.2787 for the comparison between radiation therapy and no treatment, suggesting that patients who underwent radiation did not experience a significantly different survival time compared to those who received no treatment. These findings suggest that treatment type alone may not be a strong predictor of survival outcomes within this dataset. However, this does not necessarily imply that these treatments are ineffective. Instead, it may point to limitations in the dataset, such as sample size or the need for more detailed categorization of treatments and clinical factors. A more comprehensive analysis incorporating a larger dataset, additional patient characteristics, and more granular treatment classifications may provide better insights into the factors influencing survival rates.

Conclusion

This study applied machine learning and deep learning to breast cancer detection and survival analysis using mammography data. The XGBoost model achieved 98% accuracy, demonstrating strong tumor classification performance. Deep learning models further reinforced the potential for automated mammography-based detection. The performance of these models suggests that deep learning can be a powerful tool for automated tumor detection, potentially aiding radiologists in early diagnosis. Survival analysis using the Kaplan-Meier estimator and log-rank tests showed no statistically significant differences ($p > 0.05$) between treatment groups. However, the Cox model indicated that surgical intervention and HER2-positive status were associated with better survival outcomes. The Kaplan-Meier curves highlighted the need for personalized treatment strategies, as survival probabilities did not vary significantly across treatments. These findings emphasize the potential of AI in early diagnosis while underscoring the complexity of survival prediction. Future work should integrate genomic, imaging, and clinical data to improve predictive accuracy and guide personalized treatment approaches.

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