LONDON METROPOLITAN UNIVERSITY

Islington college
(इस्लिङ्टन कलेज)

Module Code & Module Title

CU6051NI Artificial Intelligence

75% Individual Coursework

Submission: Final Submission

Academic Semester: Autumn Semester 2025

Credit: 15 credit semester long module

Student Name: Anurodh Prasain

London Met ID: 23047512

College ID: np01cp4a230012

Assignment Due Date: 21/01/2026.

Assignment Submission Date: 20/01/2026

Submitted To: Mr. Alish KC

GitHub Link	https://github.com/Anurodh0011/BREAST-CANCER-DETECTION

I confirm that I understand my coursework needs to be submitted online via MST Classroom under the relevant module page before the deadline for my assignment to be accepted and marked. I am fully aware that late submissions will be treated as non-submission and a mark of zero will be awarded.

Table of Contents

Table of Figures

Table of Tables

Introduction

Artificial Intelligence (AI) is a disruptive technology providing computers with capabilities to learn, reason, understand language and analyze data, in a manner like humans. It is based on various disciplines such as computer science, linguistics and neuroscience. In essence, AI tries to simulate human cognitive functions, such as the ability to comprehend the world and derive some ideas and obtain valuable insights out of information. One such usage is Optical Character Recognition (OCR), which transforms unstructured images and documents into structured and usable data. In general, AI can be used as an effective means of bringing positive transformation to society (Google Cloud, 2025).

Machine learning is the subdivision of artificial intelligence (AI) that deals with the algorithms that can learn the trends of the training data and, when properly trained, become able to effectively infer the new data. This pattern recognition capability allows machine learning models to take decisions or predictions without clear-cut or hard-coded guidance (Bergmann, 2025).

Any machine learning approach can be classified into one of three different learning paradigms:

- **Supervised learning:** It is a method that will train a model to give a correct prediction of the output that should be given based on an input. It is applicable to problems where some accuracy with respect to some external ground truth is required, e.g. classification or regression (Bergmann, 2025).
- **Unsupervised learning:** It uses a model to identify inherent patterns, dependencies and correlations in the data. Unsupervised learning tasks do not have any external ground truth with which the results of a particular learning task can be compared, unlike supervised learning (Bergmann, 2025).
- **Reinforcement learning (RL):** It is a process that trains a model to analyze its world and make a decision that will result in the highest reward. The situations in RL do not imply the presence of a single ground truth, but they imply the presence of good and bad (or neutral) actions (Bergmann, 2025).

In supervised learning, tasks can be divided into **classification** and **regression** depending on the nature of the target variable. Since the selected dataset has the target variable **Diagnosis** with two categories (*Malignant* and *Benign*), this problem is a binary classification task, making classification algorithms suitable for modelling.

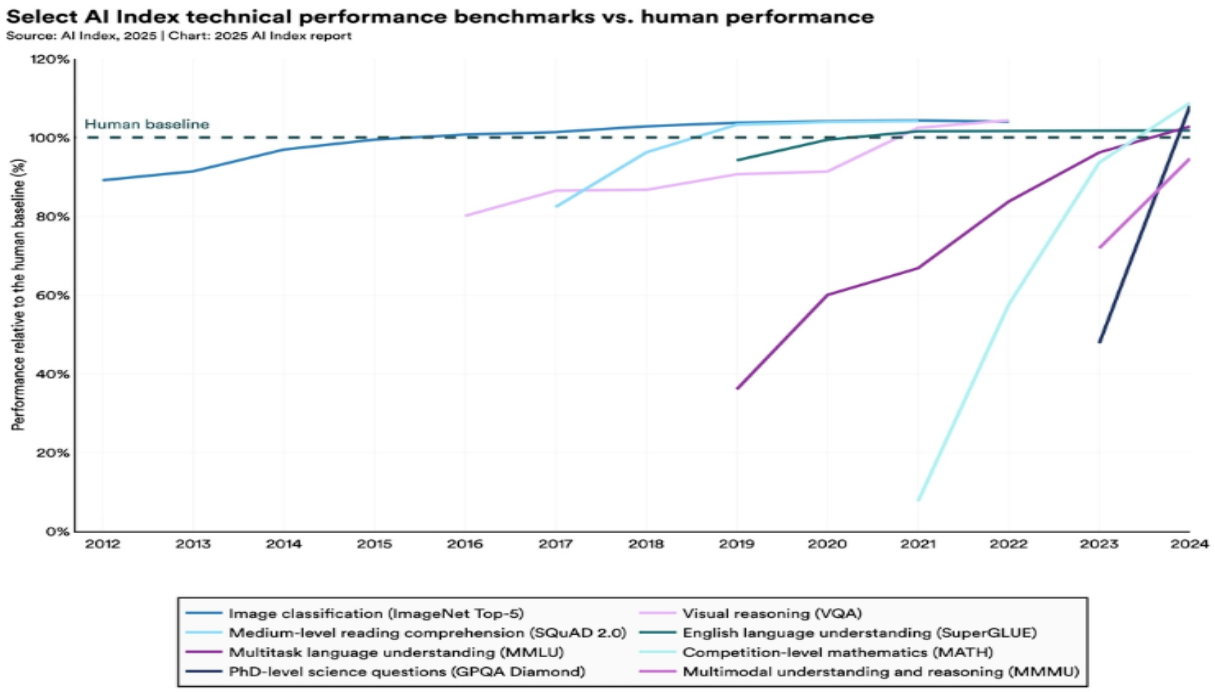


Figure 1: AI Index technical performance benchmarks vs human performance (Stanford University, 2025).

1.1. Problem Domain: Breast Cancer Diagnosis

Breast cancer is a malignant tumour that occurs due to uncontrolled proliferation of breast cells, and it is one of the major causes of death because of cancer in women in the world. Early diagnosis and treatment are great positives in terms of the survival rates and the choice of the treatment, which lowers the mortality and healthcare costs. Machine learning has become a significant instrument to aid in clinical decision-making by training diagnostic patterns based on the patient information and medical images. Various researchers have shown the success of such supervised learning frameworks as logistic regression, K-Nearest Neighbours (KNN), decision tree classifiers and others to classify breast tumours based on such features as cell size, texture and morphology (Aryan Sai Boddu, 2025).

1.2. Models Selected for the Study

To address the binary classification problem in this dataset the following supervised learning algorithms are applied in the coursework:

- Logistic Regression: a statistical classification technique that is common in binary outcomes and offers probabilities and interpretable coefficients that aid in the understanding of the effects of features.
- K-Nearest Neighbours (KNN): an instance-based learning algorithm which classifies instances based on the classification of nearest instances in feature space, showing how similarity measurements can be employed in classification problems.
- Decision Tree Classifier: is a supervised learning model based on rules, which divides a dataset based on characteristic thresholds to create rational decision pathways; it is also user-friendly and visualizable.

Based on these models, a variety of classification strategies, among them probabilistic, instance-based and tree-structured approaches, was selected, which allowed to compare the performance and interpretability of the task of tumour classification in a comprehensive manner (Yoo-Shin Park, 2025).

1.3. Objective of this project

This coursework has the following objectives:

- The fundamentals of the supervised machine learning classification.
- The use of logistic regression, KNN, and decision tree classifiers on the selected data.
- The measure and comparison of performance of these algorithms based on relevant measures.
- Determining which model can best be used to predict breast cancer diagnosis.
- Proving the practical relevance of supervised learning to medical decision support.

2. Background

2.1. Analysis of the Existing Scenario

In 2021, the World Health Organization established the Global Breast Cancer Initiative (GBCI), to bring together stakeholders from around the world and across sectors with the shared goal of reducing global breast cancer mortality by 2.5% per year, thereby averting 2.5 million breast cancer deaths globally by 2040. The three pillars of action are: health promotion for early detection; timely diagnosis; and comprehensive breast cancer management. It is one of the most common causes of death among women all over the world, which means the critical need to detect it as early as possible and be sure of the diagnosis (WHO, 2025).

The classical methods of diagnosing like biopsy, mammography, and histopathological analysis are useful but mostly time-consuming, resource-consuming, and prone to variability in human interpretation (National Cancer Institute, 2025). Using numerical features retrieved from fine needle aspirate (FNA) images, supervised machine learning classification has demonstrated great promise in differentiating between benign and malignant tumours. Because of their structured feature space and clinical significance, publicly accessible datasets like the Breast Cancer Wisconsin Diagnostic (WBCD) dataset have emerged as a standard for assessing classification algorithms (R. Fang, 2025).

2.1. Research work done on the chosen topic/problem domain

In this section, we will examine the current research literature associated with the breast cancer prediction with the help of the supervised machine learning algorithms, i.e., classification-based ones.

2.1.1. Research Paper 1: Machine Learning Algorithms to predict and diagnose breast cancer

Problem Statement

This paper will assess and compare various supervised machine learning algorithms to determine the best classifier of breast cancer prediction and diagnosis using the Wisconsin Diagnostic dataset.

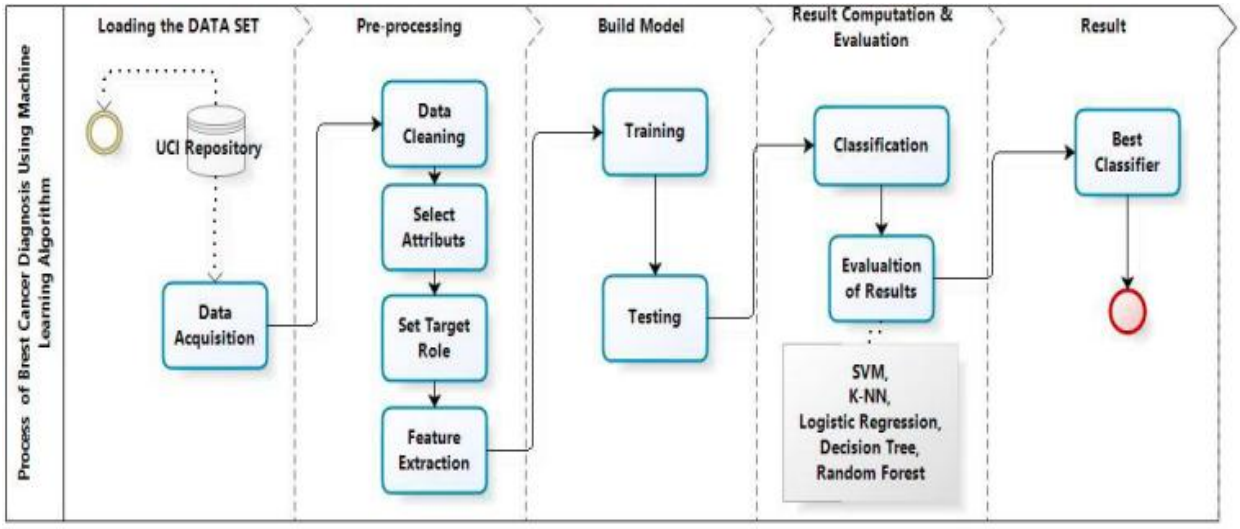


Figure 2: Process Flow Diagram of Research Paper 1 (Mohammed Amine Naji, 2021).

Algorithms Used

- Support Vector Machine (SVM)
- Random Forest
- Logistic Regression
- Decision Tree
- K-Nearest Neighbors (KNN)

Dataset Description

The authors applied the Breast Cancer Wisconsin Diagnostic dataset which consists of 569 cases where the numerical features were created because of digitization of breast cell nuclei. The target variable is used to classify tumors as benign and malignant (Mohammed Amine Naji, 2021).

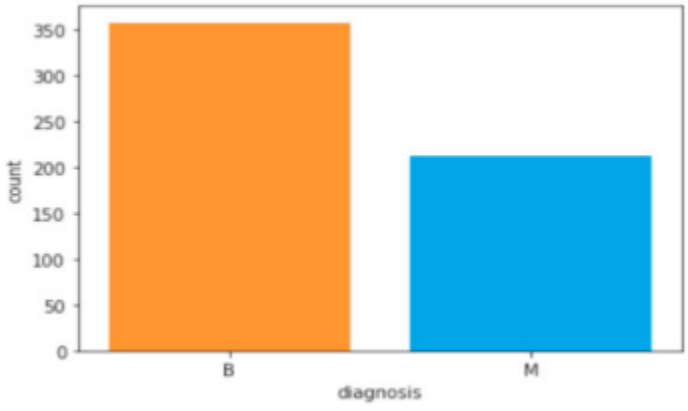


Figure 3: Wisconsin Breast Cancer Diagnostic Dataset (Mohammed Amine Naji, 2021).

Key Findings

- SVM had the best test accuracy of 97.2.
- There was also strong performance by Logistic Regression, Decision Tree and KNN.
- Evaluation metrics were given in form of confusion matrix, accuracy, precision, sensitivity, F1-score, and ROC-AUC (Mohammed Amine Naji, 2021).

Algorithm	Training Accuracy (%)	Testing Accuracy (%)
SVM	98.4	97.2
Random Forest	99.8	96.5
Logistic Regression	95.5	95.8
Decision Tree	98.8	95.1
K-NN	94.6	93.7

Table 1: Accuracy percentage for breast cancer diagnostic dataset (Mohammed Amine Naji, 2021).

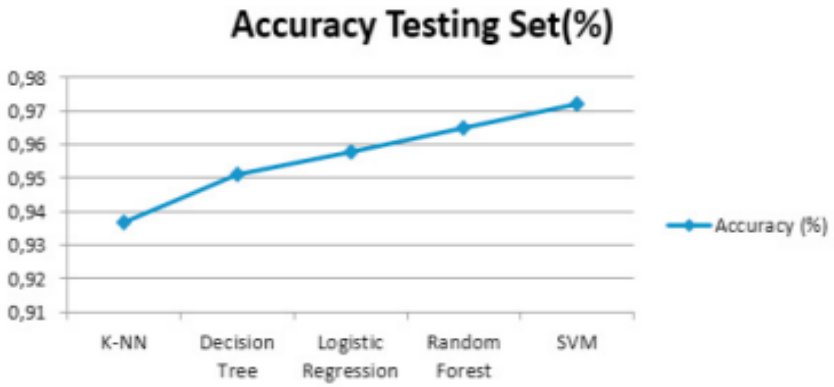


Figure 4: Comparative graph of different classifiers (Mohammed Amine Naji, 2021).

2.1.2. Research Paper 2: Breast Cancer Prediction and Diagnosis with the help of machine and modern deep learning models

Problem Statement

This paper will examine the performance of classical machine learning and state-of-the-art deep learning to detect breast cancer using the Wisconsin Diagnostic data.

Algorithms Used

- k-Nearest Neighbors (kNN)
- Naive Bayes
- Decision Tree
- Support Vector Machine
- Gradient Boosting
- CN2 Rule Inducer
- Neural Networks (Neural Decision Forest, MLP)

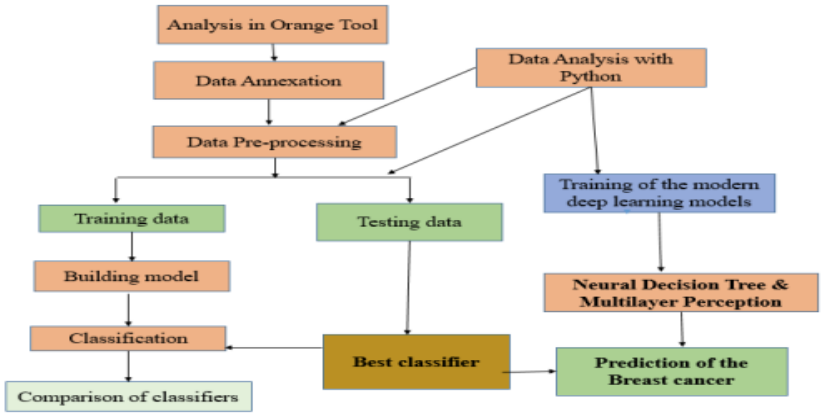


Figure 5: Flow Diagram of Research Paper 2.

Dataset Description

The data is comprised of 569 records of patients, and 30 numerical variables describe geometric and textural characteristics of cell nuclei. The data can be found in the UCI Machine Learning Repository (Seeta Devi, 2024).

Key Findings

- Gradient Boosting and CN2 Rule Inducer had perfect scores in classification.
- The performance of traditional ML models (Decision tree, Naive Bayes, kNN) was competitive.
- Deep learning models had a high ROC-AUC (0.9959) (Seeta Devi, 2024).

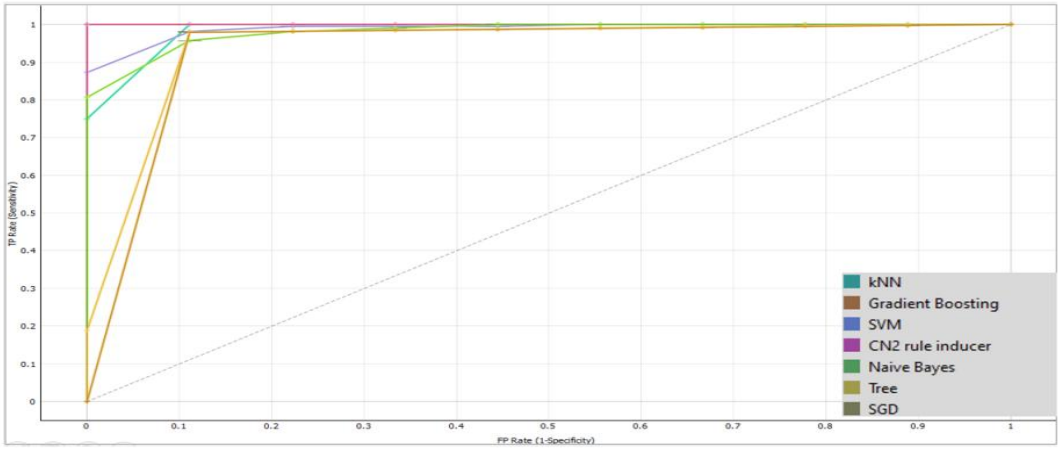


Figure 6: ROC Analysis of Malignant Tumour (Seeta Devi, 2024).

Metric	Neural Decision Forest	Multilayer Perceptron
AUC-ROC	0.9667	0.9959
Accuracy (%)	95.61	96.49
Precision (%)	100	96.57
Recall (%)	89.36	96.49
F1-Score (%)	94.38	96.50

Table 2: Prediction Output (Seeta Devi, 2024).

This implies higher overall prediction performance.

Accuracy = True Positive/True Negative + True Negative + Negative)

Precision

Precision denotes the percentage of occurrences the model is correct on all the positive instances only; it denotes as positive. The model is denoted by a high precision produces less false positive errors.

- Formula: Precision = TP / (TP + FP)

F1 Score

It portrays their harmonious average, striking a harmonious tradeoff between accuracy and recall. A score of 1 indicates a tradeoff between the two, and a value<|human|>represents a balance between the two, and a value of 0 happens when one of the two attains high elevation.

- FormulaF1 Score = 2 x Precision Recall) / (Precision + Recall))

AUC-ROC

Area Under the Receiver Operating Characteristic. Curve (AUC-ROC) is the ability of a model to differentiate positive and negative events throughout several levels of threshold. A higher AUC-ROC value represents improved performance of the model regarding classification.

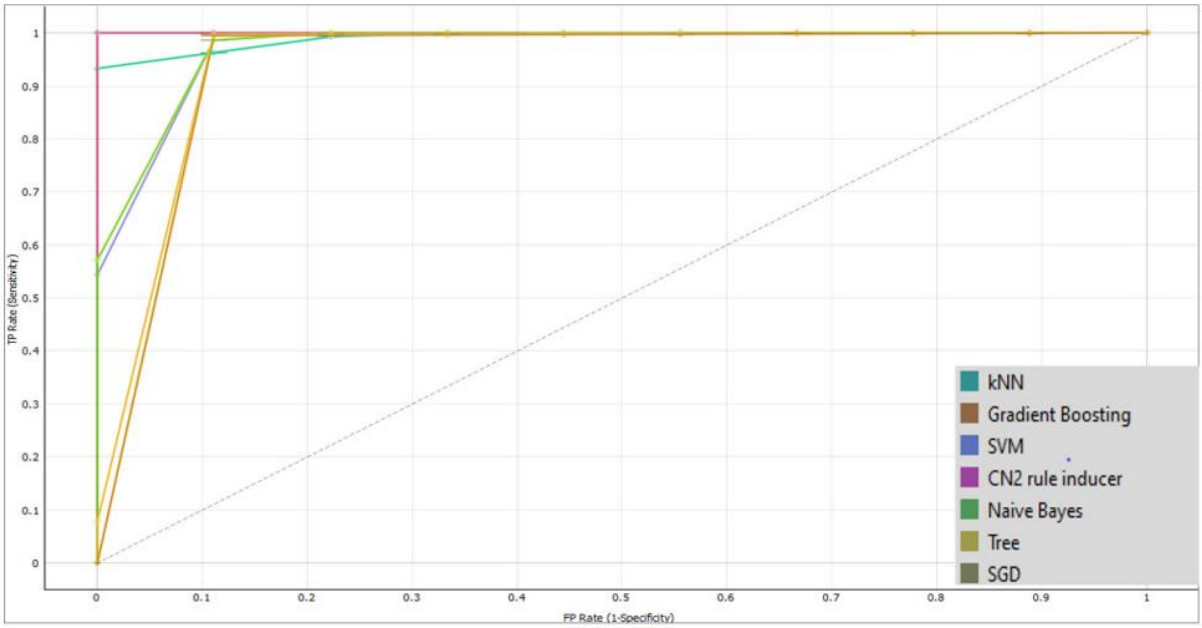


Figure 7: ROC Analysis of benign Tumour (Seeta Devi, 2024).

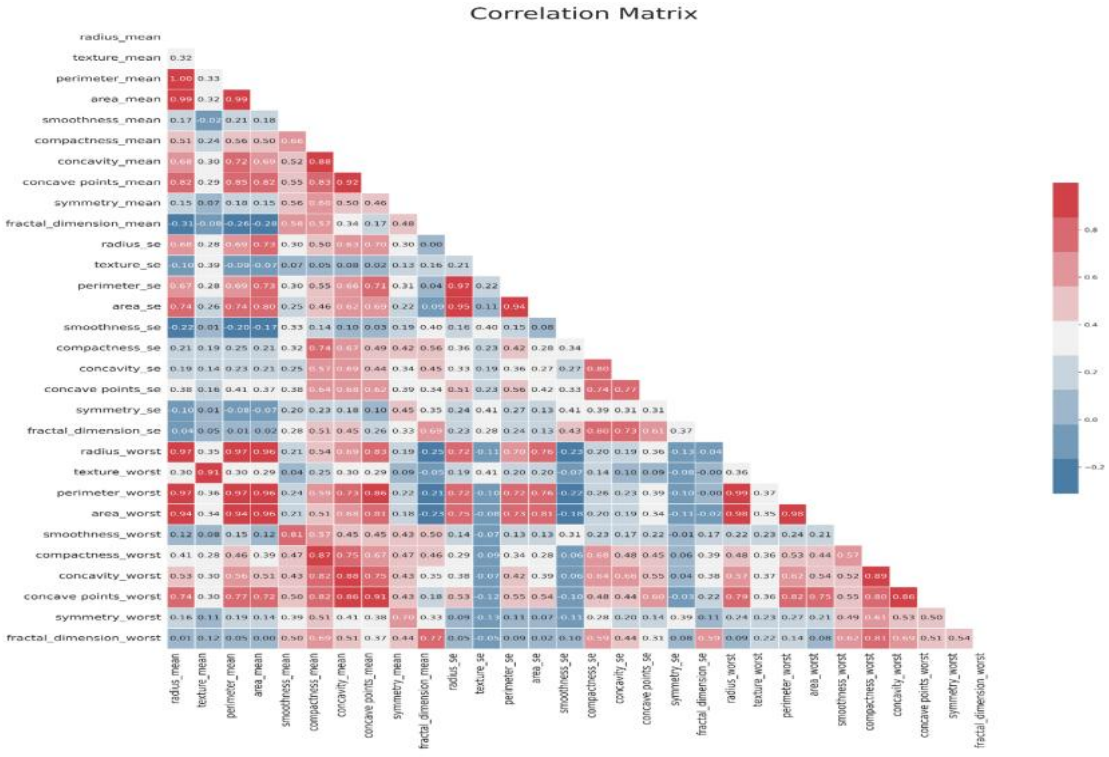


Figure 8: Correlation Matrix between Each Feature (Seeta Devi, 2024).

2.1.3. Research Paper 3: AI-based predictive modeling of breast cancer classification and explainable AI (Taminul Islam, 2024).

Problem Statement

The proposed paper deals with the issue of proper classification of breast cancer tumors using machine learning methods with explainable AI (XAI). In contrast to the old methods, it has model interpretability (with SHAP) and classification to provide clinical indications of feature contributions.

Figure 9: Ratio of malignant and benign data (Taminul Islam, 2024).

Dataset & Methodology

- The major clinical data of 500 patients was gathered in Dhaka Medical College Hospital.
- The dataset contains some structured diagnostic measures like the Wisconsin Diagnostic dataset but in a locally collected clinical setting.
- Various machine learning models were tested: Decision Tree, Random Forest, Logistic Regression, Naive Bayes and XGBoost.
- SHAP analysis has been applied to give explainable AI insights of the importance of features to classification decisions.

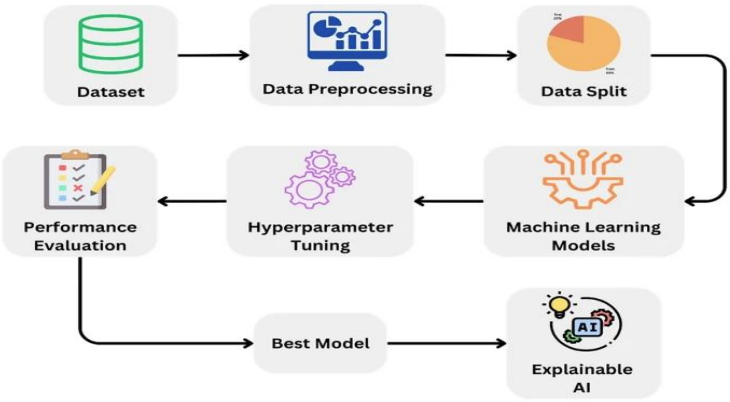


Figure 10: Visualizing the workflow of the proposed mode (Taminul Islam, 2024).

Key Findings

- The results of Logistic Regression, Decisional Tree, and Random Forest were not the best, whereas XGBoost turned out to be the most accurate (97%).
- Explainable AI algorithms such as SHAP offered pictorial information about the effect of features (such as tumor texture and area) on predictions.
- This article underscores the importance of performance and interpretability in medical artificial intelligence.

Algorithms	Hyperparameter tuning	Range	Best	Accuracy	Precision	Recall	F_1 Score
Decision tree	max_depth	None, 5, 10	5	0.91	0.94	0.89	0.9
	min_samples_leaf	2, 5, 10	4				
	min_samples_split	1, 2, 2004	5				
Random forest	max_depth	None, 5, 10, 20	None	0.96	0.93	0.95	0.94
	min_samples_leaf	1, 2, 2004	1				
	min_samples_split	2, 5, 10	5				
	n_estimators	100, 300, 500	300				
XGBoost	learning_rate	0.01, 0.1, 0.3	**0.01**	**0.97**	**0.94**	**0.95**	**0.96**
	max_depth	3, 5, 2007	**3**				
	n_estimators	100, 300, 500	**500**				
	subsample	0.8, 1.0	**1**				
Naive Bayes	No			0.94	0.99	0.9	0.94
Logistic Regression	Regularization strength	0.001, 0.01, 0.1, 1, 10	10	0.93	0.93	0.93	0.93

Figure 11: Hyperparameter tuning with performance metrics (Taminul Islam, 2024).

With an effective precision of 0.97 and high precision, recall, and F1 scores, the XGBoost algorithm performed better than the others in terms of performance metrics. With a balanced accuracy trade-off and an accuracy of 0.96, the random forest algorithm also demonstrated strong performance. With a balanced F1 score of 0.90 and an accuracy of 0.91, the decision tree algorithm produced good results. With F1 scores of 0.94 and 0.93, respectively, Naive Bayes and logistic regression demonstrate competitive performance. All things considered, hyper-parameter tuning is crucial to enhancing the model's performance, and the algorithm selection had a big impact on the outcome; XGBoost and Random Forest stand out as high-performance models.

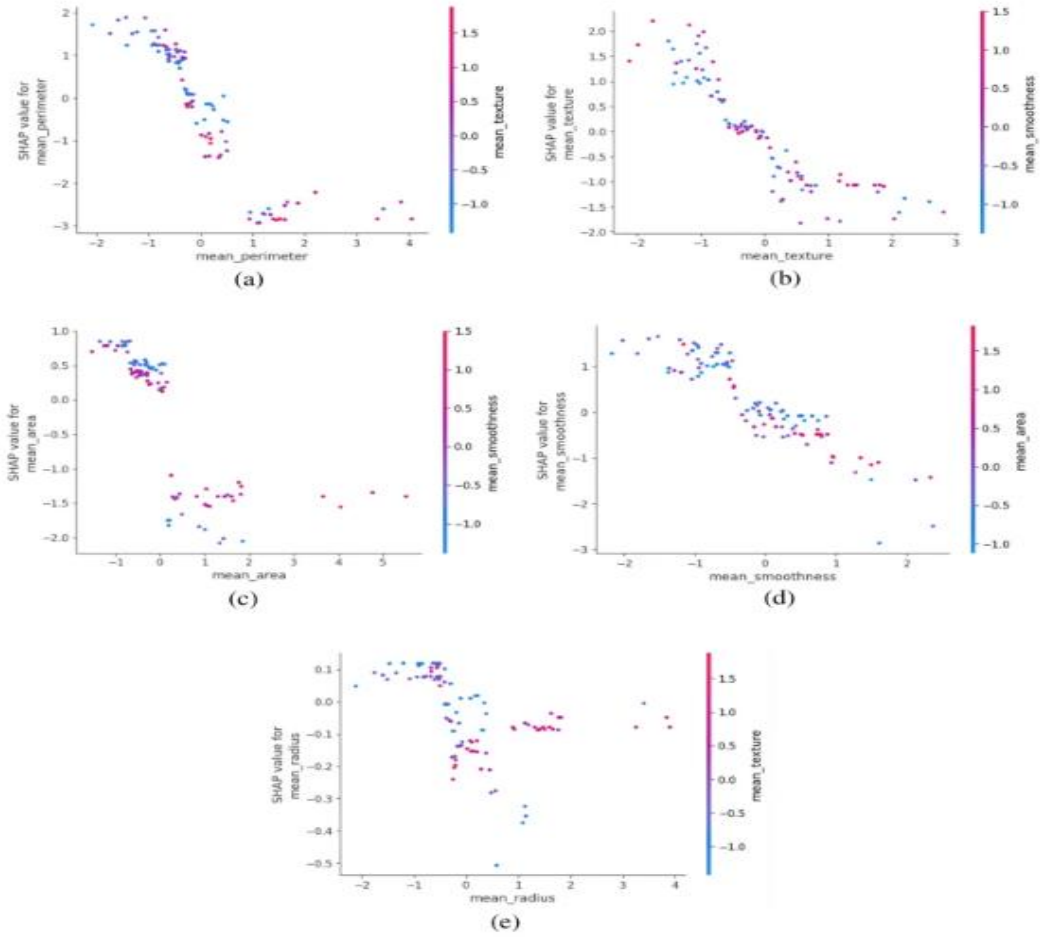


Figure 12: Dependence Plot for XGBoost Model (Taminul Islam, 2024).

2.2.4. Research Paper 4: Diagnostic Features-based Breast Cancer Diagnosis with the help of Machine Learning (Arslan Khalid, 2023).

Problem Statement

The paper under consideration explores the ability of various supervised machine learning classifiers to detect breast cancer at its early stages based on the structured diagnostic features of the tumor cell nuclei. The central question is to identify the best algorithms in clinical decision support system that offer an optimal balance between accuracy, robustness and interpretability.

Algorithms Used

- Logistic Regression
- K-Nearest Neighbors (KNN)
- Decision Tree
- Random Forest
- Support Vector Machine (SVM)

These algorithms are measured by classification tasks like finding accuracy, precision, recall, F1-score, and ROC-AUC.

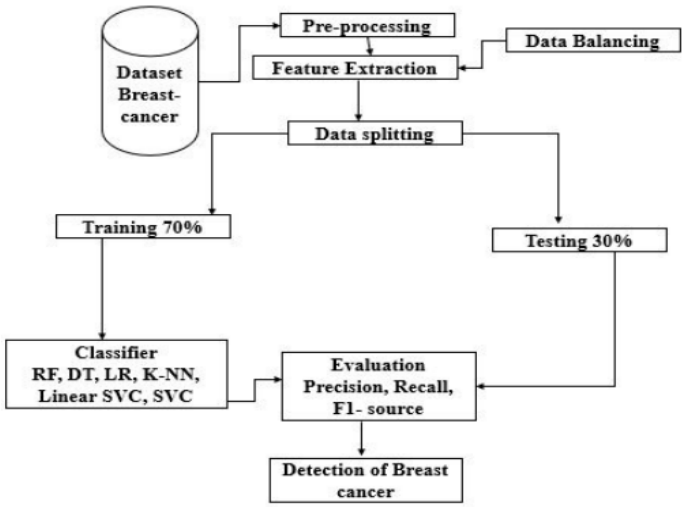


Figure 13: Proposed Methodology (Arslan Khalid, 2023).

Dataset Description

- The dataset employed in the study is that of Breast Cancer Wisconsin Diagnostic (WBCD).
- It is a dataset of 569 samples containing 30 numerical variables that were derived because of fine needle aspirate (FNA) images.
- The target variable will classify tumours as either being malignant or benign which is directly corresponding to the data in this course work (Arslan Khalid, 2023).

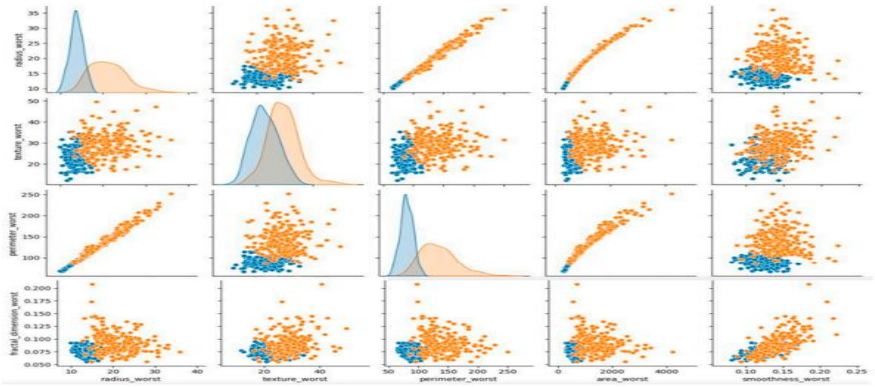


Figure 14: Breast cancer diagnosis graph (Arslan Khalid, 2023).

Key Findings

- The results of Logistic Regression and Random Forest were very high in terms of classification (>95%).
- After normalizing features, KNN showed a good performance.
- Decision tree models gave interpretable decision rules but were highly likely to overfitting.
- The paper highlights the significance of distance-based classifiers preprocessing and feature scaling.

	Model	Scores
0	Random Forest Classifier	96.491228
3	Decision Tree	93.859649
1	Logistic Regression	92.982456
2	KNeighbour Clasifier	92.105263
5	Linear SVC	89.473684
4	SVC	87.719298

Figure 15: Classifiers accuracy result (Arslan Khalid, 2023).

2.2.5. Research Paper 5: Comparative Study of Supervised Learning Methodology of Breast Cancer Prediction (Mubarak Taiwo Mustapha, 2022).

Problem Statement

The proposed research is aimed at a comparative evaluation of conventional supervised learning algorithms to determine the most efficient model to be used to predict breast cancer. This research will compare the performance of classifiers when using medical diagnostic information at interpretability and cost effectiveness.

Algorithms Used

- Naive Bayes
- Logistic Regression
- Decision Tree
- K-Nearest Neighbors
- Support Vector Machine

The article highlights the applicability of classical ML algorithms to real-world medical datasets of limited samples.

Dataset Description

- Works with the Wisconsin Diagnostic Breast Cancer data.
- Has 30 non-laboratory diagnostic attributes.
- Balanced binary problem (benign vs malignant).

This data structure is identical to the data set that was chosen in this coursework, which confirms the significance of the study.

Key Findings

- The results of Logistic Regression always gave stable and understandable results.
- KNN was sensitive to feature scaling and values of k.
- Decision Tree models were used to point out the influential diagnostic features, but they needed pruning.
- Naive Bayes was also efficacious though it assumed the independence of features, which had a minor impact on accuracy.

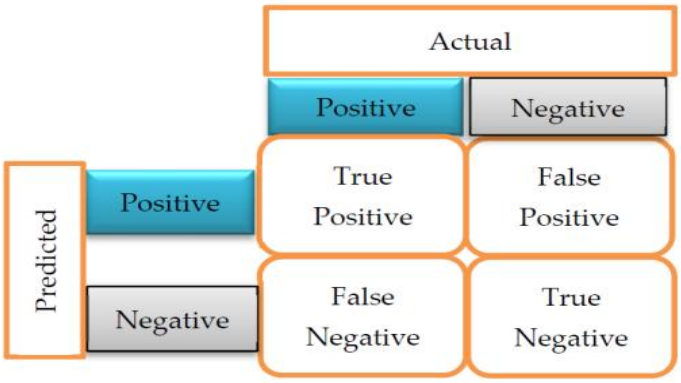


Figure 16: Confusion Matrix.

Criteria	Accuracy	Recall	Precision	F1-Score	ROC AUC	Log Loss	Number of Training Samples Needed	Impact of Feature Scaling	Impact of Hyperparameter Tuning	Tolerance to İrrelevant Attributes
SVM	97.0%	95.5%	97.5%	98.5%	99.5%	−0.8110	0.92	0.92	YES	0.92
Random Forest	96.0%	96.0%	98.0%	98.0%	99.0%	−0.8026	0.75	0.08	YES	0.08
Logistic Regression	95.5%	95.5%	97.0%	96.5%	99.0%	−0.7984	0.50	0.25	NO	0.50
KNN	95.5%	96.0%	97.5%	96.0%	98.5%	−0.7990	0.08	0.92	YES	0.50
Naive Bayes	94.0%	94.0%	96.0%	96.0%	98.0%	−0.7860	0.50	0.08	NO	0.75

Figure 17: Decision matrix of alternatives for the BIRADS dataset.

2.2. Review and analysis of existing work in the problem domain

The diagnosis of breast cancer has been an extensively investigated supervised machine learning problem because the existence of properly organized medical data and the urgent necessity to diagnose breast cancer at the earliest possible stage support this diagnosis. It has been shown that machine learning models are capable of successfully classifying breast tumours as malignant or benign based on numerical features that have been obtained through the analysis of fine needle aspirate (FNA) images.

Some available literature has effectively used the Logistic Regression, Decision Tree and K-Nearest Neighbours (KNN) algorithms on the Breast Cancer Wisconsin Diagnostic dataset. Logistic Regression is popular due to its statistical basis and ability to be easily interpreted and thus it can be used in medical decision support systems. The results of a research study suggest that the accuracy of logistic regression is high when it is applied to well-normalized data and the output of probabilities is used to assist clinicians to understand prediction confidence.

Decision Tree techniques have also been experimented widely. The models develop rule-based frameworks that replicate the way humans make decisions enabling medical practitioners to trace the way a classification decision is made. It has been established that Decision Trees are effective in the determination of significant tumour features including concavity, radius, and perimeter. Nevertheless, other issues documented in the literature include overfitting that can be addressed by pruning methods and limiting the depth of the trees.

The use of K-Nearest Neighbours (KNN) as an instance-based learning algorithm has been used in predicting breast cancer. Previous works show that KNN is highly accurate with distance measures that are used with an appropriate feature scaling. The biggest limitation that was found in literature is the high cost of computation when dealing with large datasets, yet in the case of moderate sized datasets in medicine, KNN is also a good and dependable classifier.

Altogether, the analysis of the available literature proves that machine learning algorithms under supervision are quite appropriate to diagnose breast cancer. The previous studies confirm the efficiency of these algorithms and indicate the significance of the data preprocessing, feature normalization, and performance assessment. The proposed project is based on the existing research findings through a comparison of various methods of classification and an effective diagnostic model.

3. Proposed Solution

3.1. Proposed approach to solve the problem

The solution proposed is to create a smart breast cancer diagnosis system through supervised machine learning algorithms. The system is parameterized to categorize the tumours according to the number of malignant or benign features of the medical imaging data.

The methodology takes a systematic flow starting with the data acquisition and preprocessing. In the first step, the dataset is cleaned by eliminating the useless attributes like the unique identifiers and by treating the missing values, in case they are there. The feature normalization is used to make all the numerical features equal to the learning process, especially when one is using a distance-based algorithm like KNN.

The data is pre-processed and then split into a training and a testing sample. Several classification methods are then trained on the same data, these include Logistic Regression, Decision Tree and K-Nearest Neighbours (KNN). This multi-model can be used to compare the performance and provides the robustness of the predictions.

Accuracy, precision, recall, and F1-score are the performance metrics applied to evaluate the trained models. The most effective model can then be employed to help healthcare professionals in the early diagnosis of breast cancer using the decision-support tool. The solution saves time in diagnoses, lowers the human error, and promotes clinical decisions based on data.

3.2. Explanation of the AI algorithms used

This project uses supervised learning classification algorithms due to the availability of labelled data.

3.2.1. Logistic Regression

Logistic regression is a supervised machine learning algorithm in data science. It is a type of classification algorithm that predicts a discrete or categorical outcome. For example, we can use a classification model to determine whether a loan is approved or not based on predictors such as savings amount, income and credit score (Lee, 2025).

Logistic regression is frequently used in medical diagnosis because it is easy to interpret and yields coefficients that show how each feature affects the prediction result.

Mathematical Formulation

Let a single tumor sample be represented as:

$X = (X_{radius\_means}, X_{texture\_mean}, \ldots, X_{fractal\_dimension\_worst})$

Let the corresponding weights be:

$W = (X_{radius\_mean}, X_{texture\_mean}, \ldots, X_{fractal\_dimension\_worst})$

The linear model is:

$Z = (W_{radius\_mean} * X_{radius\_mean}) + (W_{texture\_mean} * X_{texture\_mean}) + \ldots + (W_{fractal\_dimension\_worst} * X_{fractal\_dimension\_worst}) + b$

The sigmoid function converts this into a probability:

$P_{(Malignant \mid X)} = 1 / (1 + e^{-z})$

Classification rule:

$y\hat{} =$ Malignant (M), $P >= 0.5$ or Benign (B), $P < 0.5$

Relevance to the Dataset

- Diagnostic features describe geometric and textural similarity.
- KNN captures local similarity patterns among tumors.
- Particularly sensitive to features such as radius_mean, perimeter_worst, and area_worst.

3.2.2. Decision Tree Algorithm

A decision tree is a non-parametric supervised learning algorithm, which is utilized for both classification and regression tasks. It has a hierarchical, tree structure, which consists of a root node, branches, internal nodes and leaf nodes (Kavlakoglu, 2025).

Mathematical Formulation

Given two tumour samples x and y:

x = (xradius_mean, xtexture_mean, …, xfractal_dimension_worst)

y = (yradius_mean, ytexture_mean, …, yfractal_dimension_worst)

The Euclidean distance is calculated as:

d (x, y) = √ [(xradius_mean − yradius_mean)^2 + (xtexture_mean − ytexture_mean)^2 + ⋯ + (xfractal_dimension_worst − yfractal_dimension_worst)^2]

The predicted class is determined by majority voting:

$$\hat{y} = \arg \max_{c \in \{M,B\}} \sum_{i \in N_k} I(y_i = c)$$

Where:

- N_k = set of k nearest neighbors
- I = indicator function

Relevance to the Dataset

- Geometric and textural similarity are described by diagnostic features.
- KNN identifies patterns of local similarity between tumors.
- Extremely sensitive to features like area_worst, perimeter_worst, and radius_mean.

3.2.3. K-Nearest Neighbours (KNN)

The k-nearest neighbors (KNN) algorithm is a non-parametric, supervised learning classifier, which uses proximity to make classifications or predictions about the grouping of an individual data point. It is one of the popular and simplest classification and regression classifiers used in machine learning today (Kavlakoglu, 2025).

Mathematical Formulation

Entropy:

For a dataset S with malignant and benign samples:

$$H(S) = -p_M \log_2 (p_M) - p_B \log_2 (p_B)$$

Information Gain for a Feature (e.g. concave points_worst)

$$IG(S, concavepoints\_worst) = H(S) - \sum_{v \in \text{ splits}} \frac{|S_v|}{|S|} H(S_v)$$

The feature with the maximum Information Gain (e.g., radius_mean, area_mean, or concavity_worst) is chosen for splitting.

Relevance to the Dataset

- Identifies critical diagnostic thresholds
- Produces interpretable decision rules such as:
    - If concave points_worst > threshold → Malignant
- Useful for medical explanation and reporting

3.3. Pseudocode of the solution

3.3.1. Pseudocode for Logistic Regression

START

IMPORT required libraries

IMPORT breast cancer dataset

REMOVE irrelevant columns

ENCODE diagnosis column

NORMALIZE numerical features

SPLIT dataset into training and testing sets

INITIALIZE logistic regression model

TRAIN model using training data

PREDICT probabilities on test data

CLASSIFY using threshold value

EVALUATE performance metrics

END

3.3.2. Pseudocode for Decision Tree Algorithm

START

IMPORT required libraries

IMPORT breast cancer dataset

PREPROCESS data

SPLIT dataset into training and testing sets

INITIALIZE decision tree classifier

SELECT best feature using information gain

BUILD tree recursively

PREDICT classes for test data

EVALUATE model performance

END

3.3.3 Pseudocode for K-Nearest Neighbours Algorithm

START

IMPORT required libraries

IMPORT breast cancer dataset

NORMALIZE all numerical features

SPLIT dataset into training and testing sets

SET value of k

FOR each test instance:

    CALCULATE distance to all training instances

SELECT k nearest neighbours

ASSIGN majority class

EVALUATE classification results

END

3.4. Flow Chart

A flowchart is a diagram that shows a computer algorithm, system, or process. They are widely used in many different fields to record, analyze, plan, enhance, and convey frequently complicated processes in understandable diagrams. Flowcharts, sometimes written as flow charts, use connecting arrows to indicate flow and sequence and rectangles, ovals, diamonds, and possibly many other shapes to indicate the type of step (Lucidchart, 2025).

3.4.1. Flow Chart for Logistic Regression

Algorithm: Logistic Regression Training

Input: Training dataset X (features), y (labels)

Output: Trained weights w and bias b

1. START
2. Load preprocessed dataset
3. Split data into training set and testing set (e.g., 80-20 or 70-30)
4. Initialize weights w = 0 (or random small values)
5. Initialize bias b = 0
6. Set learning rate α (e.g., 0.01)
7. Set number of epochs (e.g., 1000)

8. FOR each epoch FROM 1 TO max_epochs DO:
   a. Compute linear combination: z = w · x + b
   b. Apply sigmoid function: σ(z) = 1 / (1 + e^(-z))

c. Calculate loss (Binary Cross-Entropy):

L = -(1/m) Σ [y·log(σ(z)) + (1-y)·log(1-σ(z))]

d. Compute gradients:

dw = (1/m) · X^T · (σ(z) - y)

db = (1/m) · Σ(σ(z) - y)

e. Update parameters:

w = w - α · dw

b = b - α · db

f. IF convergence criteria met (loss change < threshold) THEN

BREAK

END IF

9. END FOR

10. RETURN trained weights w and bias b

Algorithm: Logistic Regression Prediction

Input: Test data X_test, trained weights w, bias b

Output: Predicted class labels

1. FOR each test instance x IN X_test DO:

a. Compute z = w · x + b

b. Calculate probability: p = σ(z) = 1 / (1 + e^(-z))

c. IF p ≥ threshold (typically 0.5) THEN

Predict class = 1 (Malignant)

ELSE

Predict class = 0 (Benign)

END IF

2. END FOR

3. Evaluate performance:

- Calculate Accuracy = (TP + TN) / (TP + TN + FP + FN)
- Calculate Precision = TP / (TP + FP)
- Calculate Recall = TP / (TP + FN)
- Calculate F1-Score = 2 · (Precision · Recall) / (Precision + Recall)

4. END

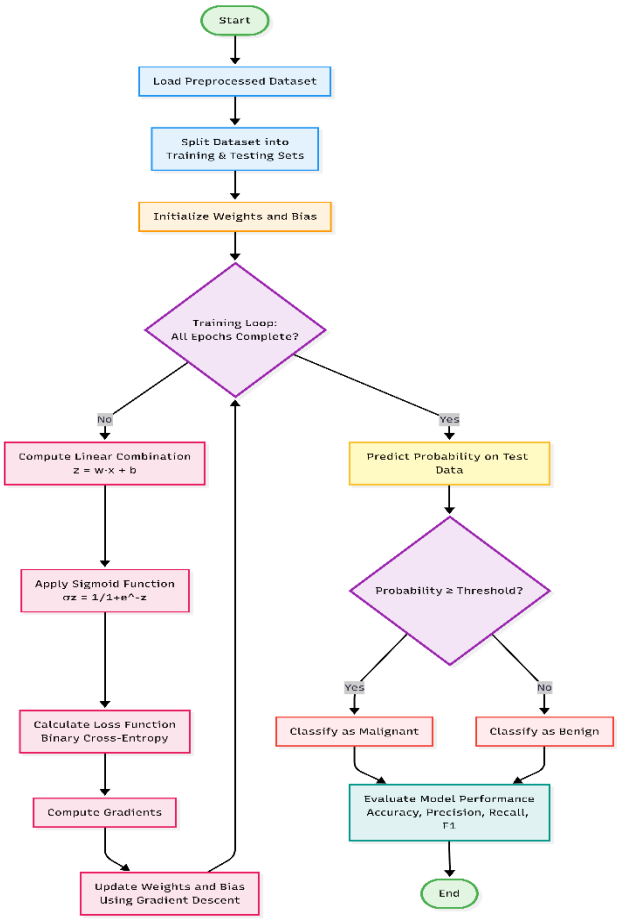


Figure 18: Logistic Regression Flow Chart.

3.4.2. Flow Chart for Decision Tree

Algorithm: Decision Tree Construction (ID3/CART)

Input: Training dataset D with features X and labels y

Output: Decision Tree T

1. START
2. Load preprocessed dataset
3. Split data into training set and testing set

4. FUNCTION BuildTree(D, features):
   a. IF stopping condition met THEN
      - All instances have same class label, OR
      - Maximum depth reached, OR
      - Minimum samples threshold reached, OR
      - No more features to split
      RETURN Leaf Node with majority class label
   END IF

   b. Initialize best_feature = NULL
   c. Initialize best_gain = 0 (or best_gini = ∞)

   d. FOR each feature f IN features DO:
      i. FOR each possible threshold t DO:
         - Split dataset D into D_left and D_right based on f ≤ t
         - Calculate Information Gain:
           Gain(D, f, t) = Entropy(D) - [|D_left|/|D| · Entropy(D_left)
                        + |D_right|/|D| · Entropy(D_right)]
           OR Calculate Gini Index:

Gini(D, f, t) = |D_left|/|D| · Gini(D_left)
+ |D_right|/|D| · Gini(D_right)

- IF Gain > best_gain (or Gini < best_gini) THEN
best_feature = f
best_threshold = t
best_gain = Gain (or best_gini = Gini)
END IF
END FOR
END FOR

e. Create decision node with best_feature and best_threshold
f. Split dataset D into D_left (f ≤ threshold) and D_right (f > threshold)
g. Left_child = BuildTree(D_left, features)
h. Right_child = BuildTree(D_right, features)
i. RETURN decision node with left and right children

5. END FUNCTION

6. Tree = BuildTree(Training_Data, All_Features)
7. RETURN Tree

Algorithm: Decision Tree Prediction

Input: Test instance x, Decision Tree T

Output: Predicted class label

1. FOR each test instance x IN X_test DO:
a. current_node = root of Tree T

b. WHILE current_node is not a leaf node DO:
i. Get feature and threshold from current_node

ii. IF x[feature] ≤ threshold THEN

current_node = left_child

ELSE

current_node = right_child

END IF

END WHILE

c. Predicted_class = class label at current_node (leaf)

d. Store prediction

2. END FOR

3. Evaluate performance:

- Calculate Accuracy, Precision, Recall, F1-Score

4. END

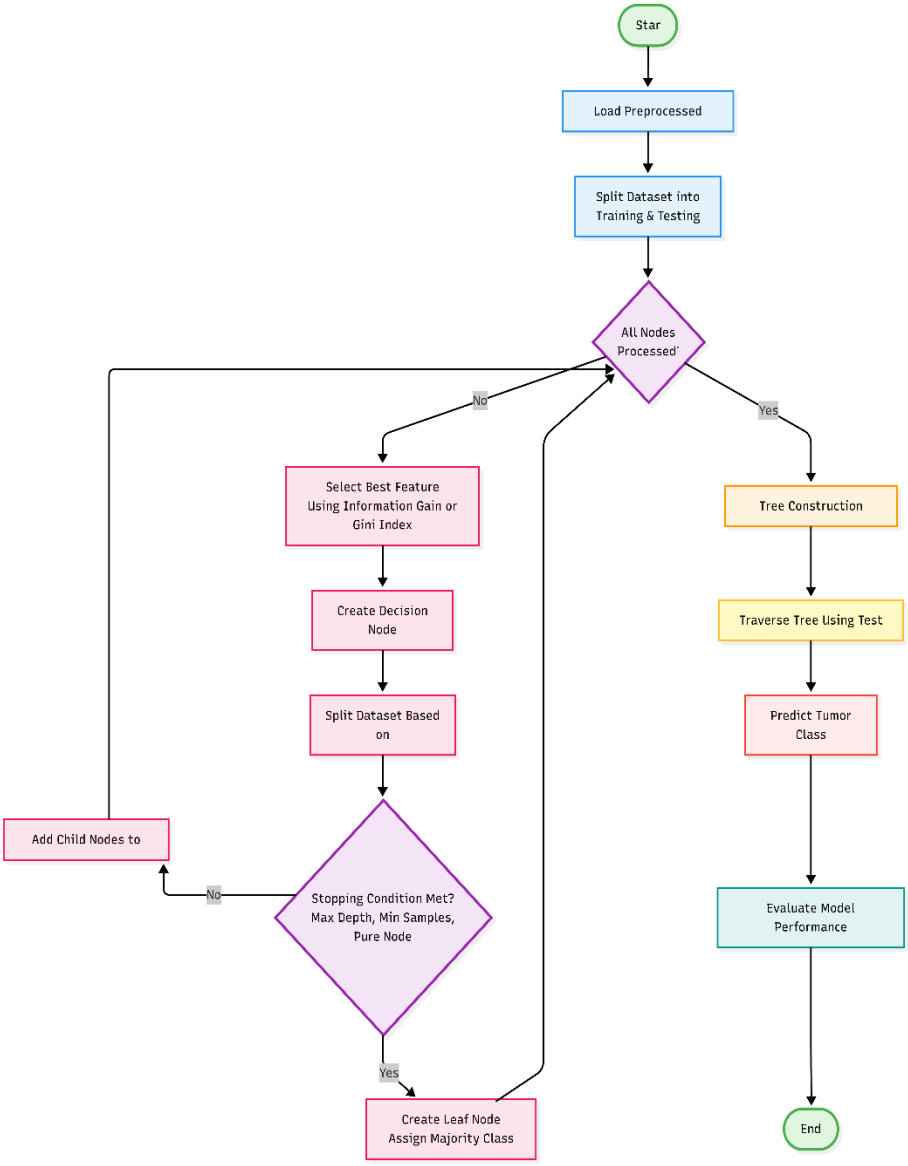


Figure 19: Decision Tree Flow Chart.

3.4.3. Flow Chart for K-Nearest Neighbours

Algorithm: Data Normalization

Input: Dataset X with numerical features

Output: Normalized dataset X_norm

1. START
2. Load preprocessed dataset

3. FOR each feature column f IN X DO:
   Option A - Min-Max Normalization:
   - min_val = minimum value in f
   - max_val = maximum value in f
   - FOR each value v IN f DO:
     v_norm = (v - min_val) / (max_val - min_val)
   END FOR

   Option B - Z-Score Normalization:
   - mean = average of values in f
   - std = standard deviation of f
   - FOR each value v IN f DO:
     v_norm = (v - mean) / std
   END FOR

4. END FOR

5. RETURN normalized dataset X_norm

Algorithm: K-Nearest Neighbors Classification

Input: Training set X_train, y_train

Test set X_test

Value of K (number of neighbors)

Output: Predicted class labels for X_test

1. START
2. Normalize features in training and test sets
3. Split dataset (already have X_train, y_train, X_test, y_test)
4. Set K value (e.g., K = 3, 5, 7, etc. - usually odd number)

5. FOR each test instance x IN X_test DO:

a. Initialize distance_list = empty list

b. FOR each training instance x_i IN X_train DO:

i. Calculate distance between x and x_i:

Euclidean Distance:

$d = \sqrt{(\Sigma(x[j] - x\_i[j])^2)}$ for all features j

OR Manhattan Distance:

$d = \Sigma|x[j] - x\_i[j]|$ for all features j

OR Minkowski Distance:

$d = (\Sigma|x[j] - x\_i[j]|^p)^{(1/p)}$ for parameter p

ii. Store (distance d, class label y_i) in distance_list

END FOR

c. Sort distance_list in ascending order by distance

d. Select K nearest neighbors (first K entries in sorted list)

e. Extract class labels of K nearest neighbors

f. Apply majority voting:

i. Count occurrences of each class label

ii. class_counts = {class_0: count_0, class_1: count_1, ...}

iii. predicted_class = class with maximum count

iv. IF tie occurs THEN

- Use K-1 neighbors, OR
- Choose class of nearest neighbor, OR
- Random selection

END IF

g. Assign predicted_class to test instance x

6. END FOR

7. Evaluate model performance:

- Calculate Accuracy = (Correct Predictions) / (Total Predictions)
- Calculate Precision = TP / (TP + FP)
- Calculate Recall = TP / (TP + FN)
- Calculate F1-Score = 2 · (Precision · Recall) / (Precision + Recall)
- Create Confusion Matrix

8. END

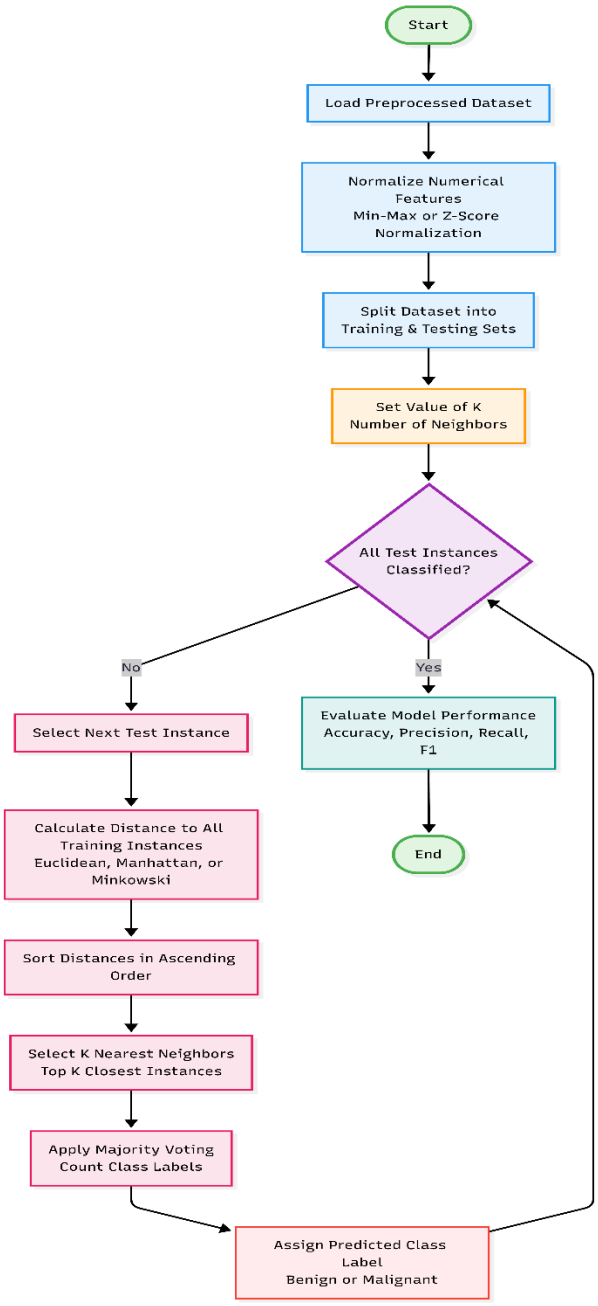


Figure 20: KNN Flow Chart.

3.5. Development Process

3.5.1. Tools and Technology Used

Python

Python is the backbone of today's Machine Learning ecosystem. Python is simple, has an extensive library support and robust community, which allows the development of models quickly and easily. It does not need any extra technical skills to support the full end to end ML workflows since it is used in data preprocessing to deployment and is suitable to both learners and professionals (Geeks For Geeks, 2025).

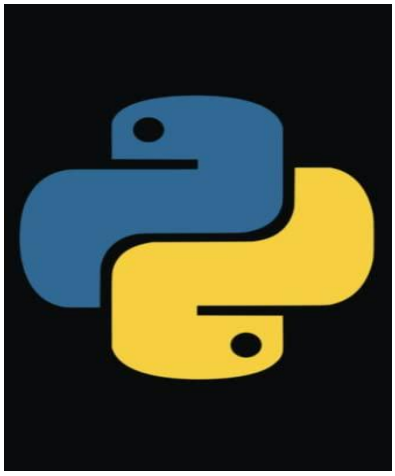


Figure 21: Python.

The case of Python in machine learning.

- **Easy and Simple Syntax:** Python has a clean syntax that enables developers to concentrate on ML logic as opposed to writing details on complex programming.
- **Rich Ecosystem of Libraries:** It has libraries such as NumPy, Pandas, Matplotlib, Scikit-learn, TensorFlow, PyTorch, Keras and SciPy in Python making it easy to handle data, build models, and visualize data.
- **Large and Active Community:** A massive community offers tutorials, GitHub projects, research code and support in questions and answers and is therefore easier to learn and troubleshoot.
- **Scalable and Flexible:** Python works with fast prototyping, research development, production systems, API and cloud development, and just one ecosystem (Geeks For Geeks, 2025).

Figure 22: Python Libraries (Geeks For Geeks, 2025).

Python Libraries necessary to work with machine learning.

- **NumPy**: Offers quick array operations, linear algebra and vectorized calculations to scientific computing.
- **Pandas**: Provides DataFrame objects to clean, manipulate and transform data in an efficient manner.
- **Matplotlib**: This is to produce simple visualizations such as line plots, bar charts, histograms and scatter plots.
- **Scikit-learn:** ML algorithms in classification, regression, clustering, dimensionality reduction and evaluation.
- **SciPy**: Builds NumPy with optimization, integration, interpolation and scientific computation tools (Geeks For Geeks, 2025).
- **TensorFlow and Keras:** Allows the construction and training of deep learning models with a support of the GPU and the possibility of production deployment.
- **PyTorch**: It offers a fluid tensor framework, which is supported by the GPU to build and train neural networks.

Anaconda

Anaconda is an open-source packaging of the Python and R programming languages in data science to help manage packages and deploy them with reduced effort. Anaconda distribution has more than 250 packages that are automatically installed. More than 7500 more open-source packages are available via PyPI as well as the conda package and virtual environment manager. It has also a GUI (graphical user interface), Anaconda Navigator, which is a graphical alternative to the command line interface. Anaconda Navigator comes as a part of the Anaconda distribution and enables one to invoke applications and manage conda packages, environments and channels without calling command-line commands. Navigator can find packages, install packages into an environment, execute the packages and update them (Domino, 2026).

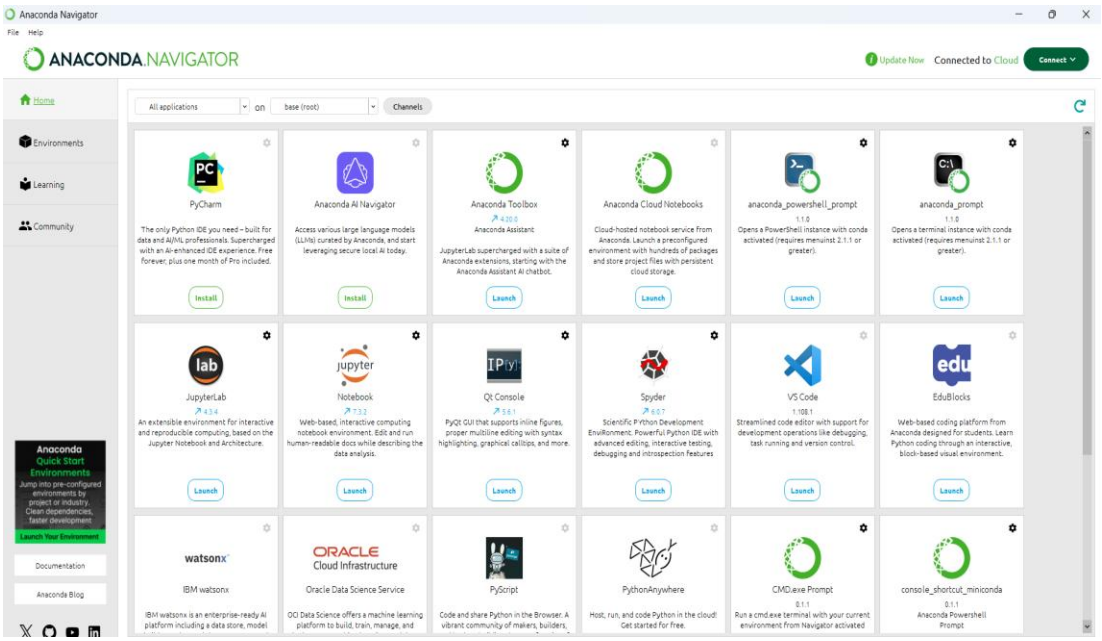


Figure 23: Anaconda Navigator GUI.

The major distinction between conda and the pip package manager is the package dependency management which is another major problem facing Python data science. Installation of pip happens automatically when a package is being installed as pip automatically installs the dependent Python packages without considering whether they conflict with already installed packages. It will install a package, and any of its dependencies despite the existence of prior installation. Owing to this a user that comes across a working installation of, say, TensorFlow can find that it no longer works after using pip to install a different package that needs a different

version of the NumPy library that depends on it than the one used by TensorFlow. Sometimes the package might seem to be functioning but yield alternative outcomes in implementation. Conversely, conda examines the existing environment and all things that are currently installed, and with any version constraints desired (e.g. the user may desire TensorFlow version 2.0 or above), will figure out which set of dependencies can be installed together, and provides a warning in case it cannot (Domino, 2026).

Open-source packages are either available as individual packages in the repository Anaconda, Anaconda Cloud (anaconda.org), or in a personal repository/mirror of the user, with the conda install command. Anaconda Inc. assembles and assembles the packages contained in the Anaconda repository itself, and offers binaries of Windows 32/64-bit, Linux 64-bit and MacOS 64-bit. Anything that is in the PyPI can be installed in a conda environment through pip and conda will maintain a record of what it has installed and what pip has installed (Domino, 2026).

Jupyter Notebook

Jupyter Notebook is a notebook authoring tool, which is part of the project Jupyter. It is a close-knit with the computational notebook format, which provides rapid and interactive novel methods to prototype and clarify your code, investigate and display your data, and distribute your concepts with others (Jupyter, 2025).

The inputs and outputs of an interactive session and other text accompanying the code but not for execution are all included in the notebook documents. By doing so, notebook files may be a full account of what was computed during a session, with executable code mixed with narrative, mathematics, and elaborate descriptions of objects that were computed. These files are internally JSON files and are stored using the.ipynb extension. They can be shared with peers and version-controlled sinceJSON is a plain text format (Jupyter, 2025).

Moreover, any available nb document on a public URL can be shared through the Jupyter Notebook Viewer nbviewer. This service downloads the notebook document by the URL and displays it as a static web page. The outcomes can therefore be published in the form of a colleague, or a post on a public blog, without any other user having to install the Jupyter notebook themselves. Effectively nbviewer is nothing more than [nbconvert] as a web service and thus you can just do your own conversions using nbconvert, without the use of nbviewer (Jupyter, 2025).

3.5.2. Data Acquisition and Loading

Objective: To import the dataset correctly and ensure the structural integrity of the dataset prior to any analysis.

```
import pandas as pd
df = pd.read_csv('breast_cancer.csv')
```

Figure 24: Import and Load Dataset.

3.5.3. Structural Inspection of the Dataset

This step verifies that the dataset matches the expected dimensions and has been loaded correctly.

Dataset Shape

```
df.shape
```

```
(569, 33)
```

Figure 25: Dataset Shape.

```
import matplotlib.pyplot as plt
```

```
df['diagnosis'].value_counts().plot(kind='bar')
plt.xlabel('Diagnosis')
plt.ylabel('Count')
plt.title('Distribution of Benign and Malignant Tumors')
plt.show()
```

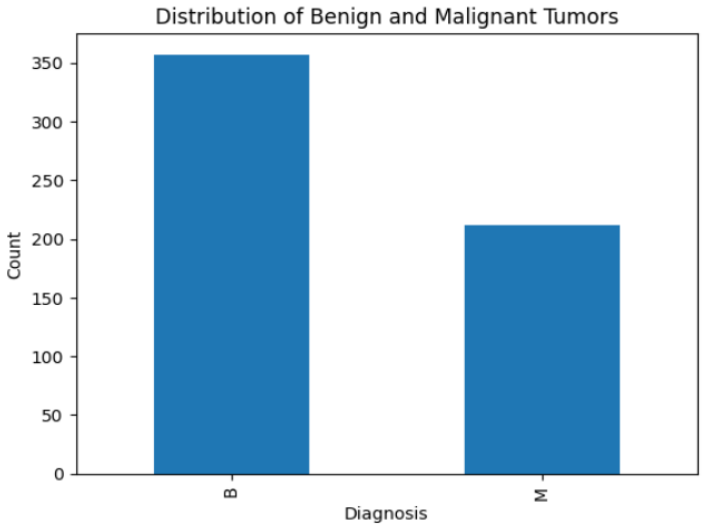


Figure 26: Distribution of Benign and Malignant Tumours.

Here, 569 rows represent individual patient cases, and 33 columns represent identifiers, diagnostic labels, and feature measurements which confirms successful data ingestion and provides baseline dimensional awareness.

Column Name Inspection

```
df.columns
```

```
Index(['id', 'diagnosis', 'radius_mean', 'texture_mean', 'perimeter_mean',
       'area_mean', 'smoothness_mean', 'compactness_mean', 'concavity_mean',
       'concave points_mean', 'symmetry_mean', 'fractal_dimension_mean',
       'radius_se', 'texture_se', 'perimeter_se', 'area_se', 'smoothness_se',
       'compactness_se', 'concavity_se', 'concave points_se', 'symmetry_se',
       'fractal_dimension_se', 'radius_worst', 'texture_worst',
       'perimeter_worst', 'area_worst', 'smoothness_worst',
       'compactness_worst', 'concavity_worst', 'concave points_worst',
       'symmetry_worst', 'fractal_dimension_worst', 'Unnamed: 32'],
      dtype='object')
```

Figure 27: Column Name Inspection.

This step helps:

- Determine the target variable (diagnosis).
- Find columns that are not informative.
- Recognize the mean, standard error, and worst feature naming conventions.

Data Type Verification

```
df.dtypes
```

```
id                         int64
diagnosis                 object
radius_mean              float64
texture_mean             float64
perimeter_mean           float64
area_mean                float64
smoothness_mean          float64
compactness_mean         float64
concavity_mean           float64
concave points_mean      float64
symmetry_mean            float64
fractal_dimension_mean   float64
radius_se                float64
texture_se               float64
perimeter_se             float64
area_se                  float64
smoothness_se            float64
compactness_se           float64
concavity_se             float64
concave points_se        float64
symmetry_se              float64
fractal_dimension_se     float64
radius_worst             float64
texture_worst            float64
perimeter_worst          float64
area_worst               float64
smoothness_worst         float64
compactness_worst        float64
concavity_worst          float64
concave points_worst     float64
symmetry_worst           float64
fractal_dimension_worst  float64
Unnamed: 32              float64
dtype: object
```

Figure 28: Datatype Verification.

This confirms that all predictive features are of numerical type and makes sure machine learning algorithms can work without issues. Apart from that, if there are any type casting mistakes, it catches them early.

3.5.4. Data Quality Assessment

Formal quality checks are required even in cases where datasets are known to be clean.

Missing Value Analysis

```
df.isnull().sum()
```

```
id                         0
diagnosis                  0
radius_mean                0
texture_mean               0
perimeter_mean             0
area_mean                  0
smoothness_mean            0
compactness_mean           0
concavity_mean             0
concave points_mean        0
symmetry_mean              0
fractal_dimension_mean     0
radius_se                  0
texture_se                 0
perimeter_se               0
area_se                    0
smoothness_se              0
compactness_se             0
concavity_se               0
concave points_se          0
symmetry_se                0
fractal_dimension_se       0
radius_worst               0
texture_worst              0
perimeter_worst            0
area_worst                 0
smoothness_worst           0
compactness_worst          0
concavity_worst            0
concave points_worst       0
symmetry_worst             0
fractal_dimension_worst    0
Unnamed: 32              569
dtype: int64
```

Figure 29: Missing Value Analysis.

Interpretation:

- There are no missing values in any of the core attributes.
- There are 569 missing values in Column Unnamed: 32, which indicates that it contains no useful information.
- This column needs to be eliminated because it is an artifact from the CSV export.

Removal of Completely Null Column

```
df = df.drop(columns=["Unnamed: 32"])
```

Figure 30: Removal of Null Column.

```
df.shape
```

```
(569, 32)
```

Figure 31: Verification of Removal.

Eliminating unnecessary columns enhances:

- Efficiency of computation
- Interpretability of the model
- Clarity of analysis

Duplicate Record Check

```
df.duplicated().sum()
```

```
np.int64(0)
```

Figure 32: Duplicate Record Check.

This makes sure there are no duplicate patient records which stops biased model training and the dataset is verified to be unique if the output is 0.

3.5.6. Statistical Data Understanding

Descriptive Statistics

```
df.describe()
```

	id	radius mean	texture mean	perimeter mean	area mean	smoothness mean	compactness mean	concavity mean	concave points mean	symmetry mean	...	radius worst	texture worst	perimeter worst	area worst	smoothness worst	compactness worst	concavity worst	concave points worst	symmetry worst	fractal dimension worst
count	5.690000e+02	569.000000	569.000000	569.000000	569.000000	569.000000	569.000000	569.000000	569.000000	569.000000	...	569.000000	569.000000	569.000000	569.000000	569.000000	569.000000	569.000000	568.000000	569.000000	569.000000
mean	3.037183e+07	14.127292	19.289649	91.969033	654.889104	0.096360	0.104341	0.088799	0.048919	0.181162	...	16.269190	25.677223	107.261213	880.583128	0.132369	0.254265	0.272188	0.114606	0.290076	0.083946
std	1.250206e+08	3.524049	4.301036	24.298981	351.914129	0.014064	0.052813	0.079720	0.038803	0.027414	...	4.833242	6.146258	33.602542	569.356993	0.022832	0.157336	0.208624	0.065732	0.061867	0.018061
min	8.670000e+03	6.981000	9.710000	43.790000	143.500000	0.052630	0.019380	0.000000	0.000000	0.106000	...	7.930000	12.020000	50.410000	185.200000	0.071170	0.027290	0.000000	0.000000	0.156500	0.055040
25%	8.692180e+05	11.700000	16.170000	75.170000	420.300000	0.086370	0.064920	0.029560	0.020310	0.161900	...	13.010000	21.080000	84.110000	515.300000	0.116600	0.147200	0.114500	0.064930	0.250400	0.071460
50%	9.060240e+05	13.370000	18.840000	86.240000	551.100000	0.095870	0.092630	0.061540	0.033500	0.179200	...	14.970000	25.410000	97.660000	686.500000	0.131300	0.211900	0.226700	0.099930	0.282200	0.080040
75%	8.813129e+06	15.780000	21.800000	104.100000	782.700000	0.105300	0.130400	0.130700	0.074000	0.195700	...	18.790000	29.720000	125.400000	1084.000000	0.146000	0.339100	0.382900	0.161400	0.317900	0.092080
max	9.113205e+08	28.110000	39.280000	188.500000	2501.000000	0.163400	0.345400	0.426800	0.201200	0.304000	...	36.040000	49.540000	251.200000	4254.000000	0.222600	1.058000	1.252000	0.291000	0.663800	0.207500

8 rows × 31 columns

Figure 33: Descriptive Statistics check.

This stage offers:

- Min/max, mean, and standard deviation
- Detecting range
- Early detection of anomalies

It confirms that:

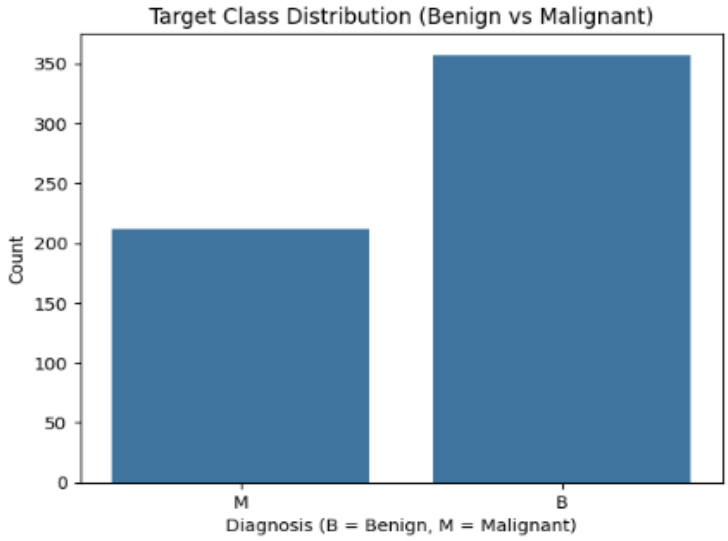
- There are various scales of features.
- Later, feature scaling will be necessary.

Target Variable Distribution

```
y = df['diagnosis']

sns.countplot(x=y)
plt.title("Target Class Distribution (Benign vs Malignant)")
plt.xlabel("Diagnosis (B = Benign, M = Malignant)")
plt.ylabel("Count")
plt.show()

print(y.value_counts())
```




```
diagnosis
B    357
M    212
Name: count, dtype: int64
```

Figure 34: Target Value Distribution.

This shows the distribution of classes (Benign vs. Malignant) and finds a moderate disparity in class. It justifies the careful choice of metrics (precision & recall)

Feature Distribution

```
X = df.drop(columns=['id', 'diagnosis'])
X.hist(figsize=(15, 12), bins=20, edgecolor='black', grid=False)
plt.suptitle("Feature Distribution Histograms", fontsize=16, fontweight='bold')
plt.tight_layout()
plt.show()
```

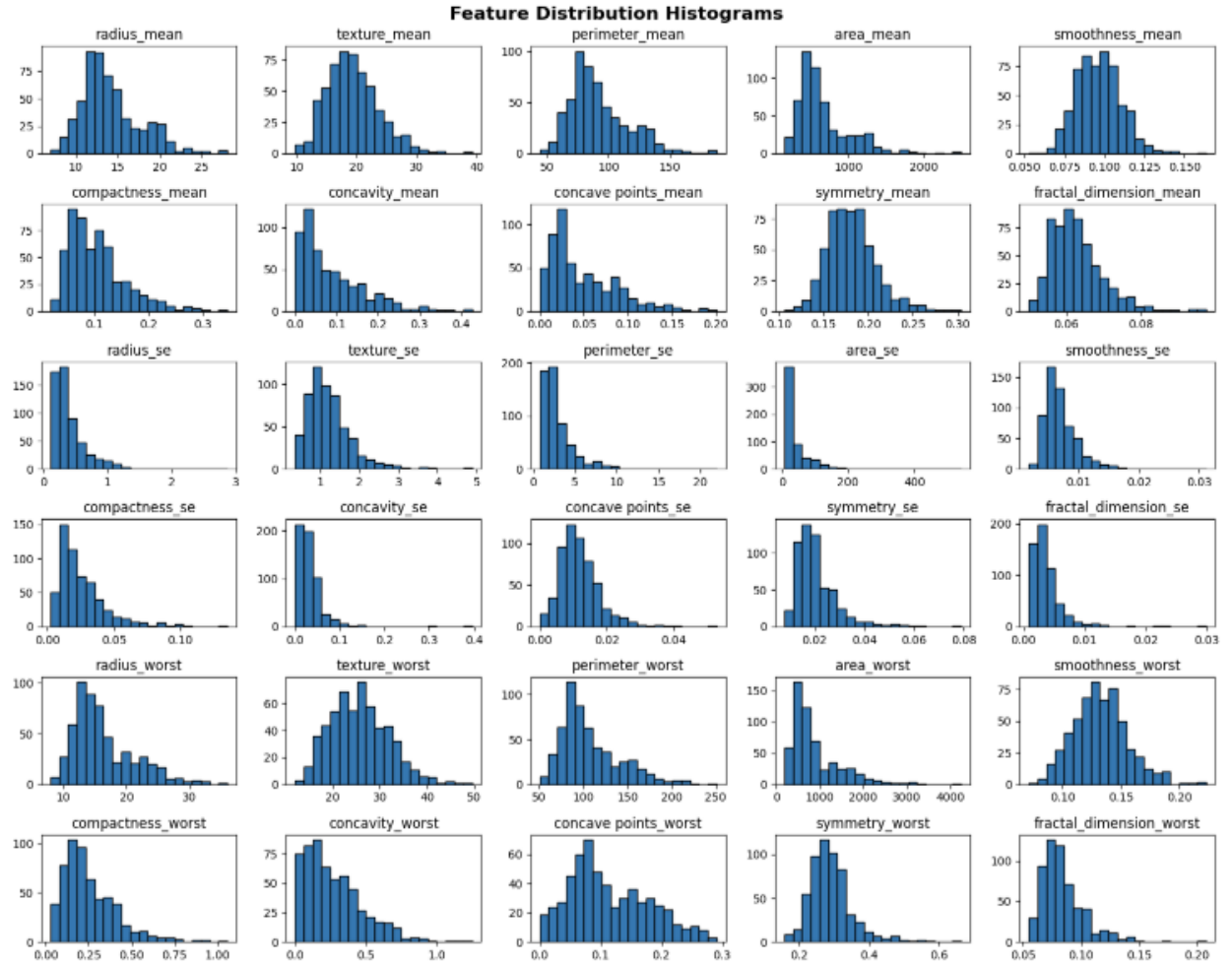


Figure 35: Feature Distribution.

Here, this histograms show the distribution of key features, helping to understand the spread and central tendency of each variable.

Correlation Heatmap

```
plt.figure(figsize=(12, 10))
sns.heatmap(X.corr(), cmap="coolwarm", linewidths=0.5)
plt.title("Correlation Heatmap of Features")
plt.show()
```

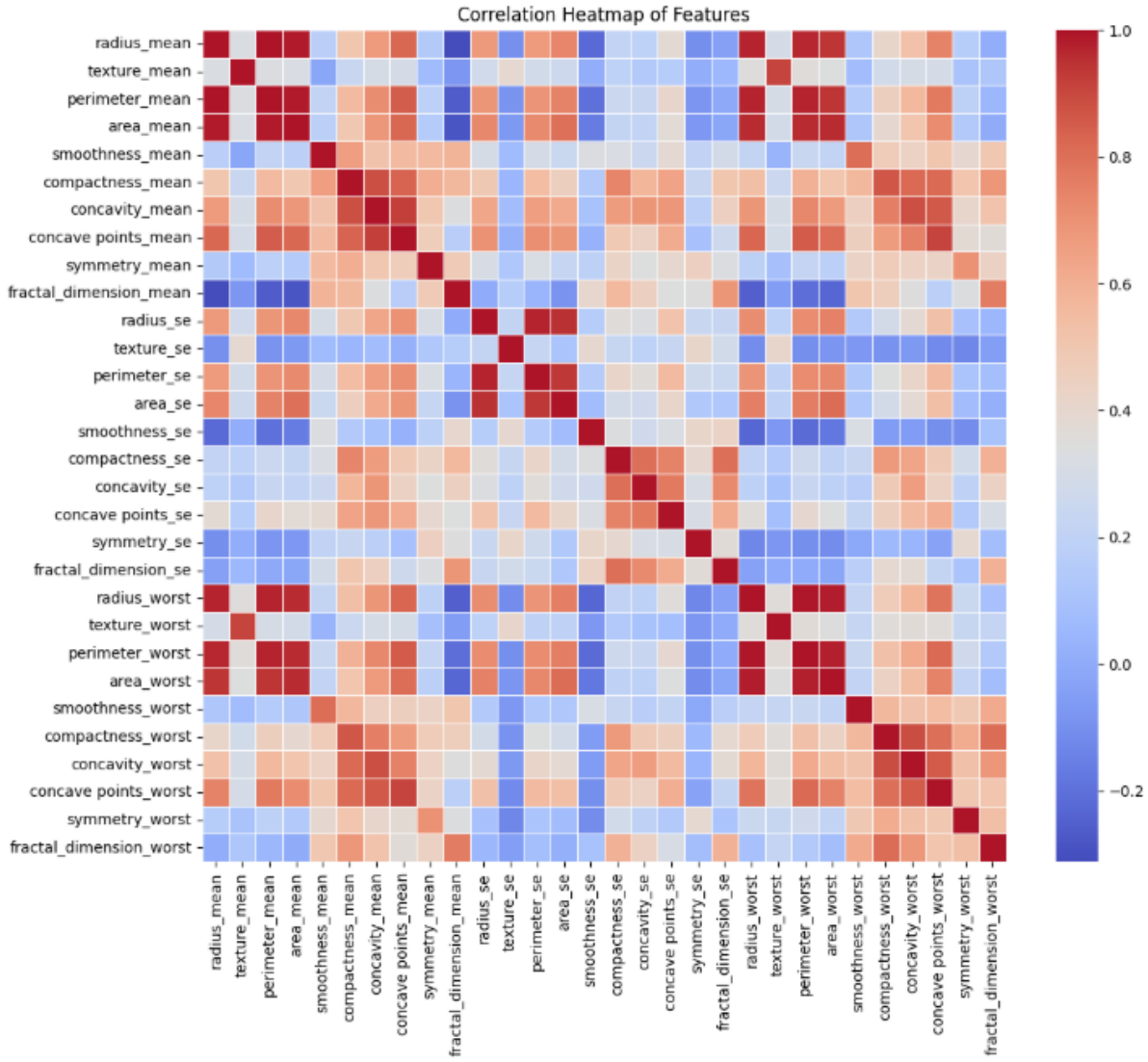


Figure 36: Correlation Heatmap.

Here, the heatmap highlights correlations between features, allowing identification of highly correlated or redundant variables.

3.5.6. Outlier Detection

Outliers should not be assumed to be non-existent even in medical datasets.

Boxplot Visualization

```
plt.figure(figsize=(10, 6))
sns.boxplot(data=df.drop(columns=["id", "diagnosis"]))
plt.xticks(rotation=90)
plt.show()
```

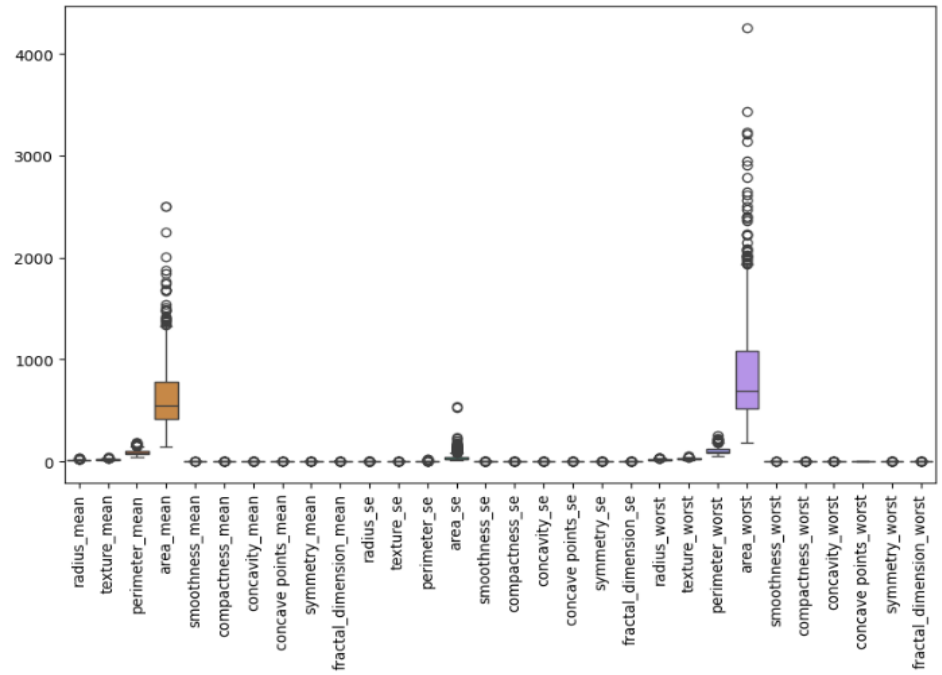


Figure 37: Boxplot Visualization of Outlier.

It confirms existence of extreme values. Outliers are typical pathological cases in medical data. Therefore, outliers are retained, not eliminated.

3.5.7. Feature Preparation

Encoding Target Variable

```
df["diagnosis"] = df["diagnosis"].map({"M": 1, "B": 0})
```

Figure 38: Encoding Target Variable.

This transforms categorical data to numeric which allows supervised binary classification.

Feature-Target Separation

```
X = df.drop(columns=["diagnosis", "id", "Unnamed: 32"])
y = df["diagnosis"]
```

Figure 39: Feature/Target Separation.

Here, id is removed as it has no predictive value and prevents model leakage and bias.

Feature Scaling

```python
from sklearn.preprocessing import StandardScaler

scaler = StandardScaler()
X_scaled = scaler.fit_transform(X)
```

Figure 40: Feature Scaling.

It is critical to distance-based algorithm (KNN) and makes fair feature contribution which helps to enhances convergence of algorithm.

3.5.8. Data Partitioning

```python
from sklearn.model_selection import train_test_split
X_train, X_test, y_train, y_test = train_test_split(X_scaled, y, test_size=0.2, random_state=42)
```

Figure 41: Data Partitioning.

Here, 80% data are allocated for training whereas 20% data are allocated for testing which prevents overfitting and ensures generalization and set random_state to ensure same train and test data splits on every time the code run.

3.5.9. Machine Learning Model Implementation

1. **Logistic Regression**

Trial 1: Logistic Regression (Default Parameters)

```python
from sklearn.linear_model import LogisticRegression
from sklearn.metrics import (accuracy_score, precision_score, recall_score,f1_score, confusion_matrix)

lr_trial1 = LogisticRegression(random_state=42)
lr_trial1.fit(X_train, y_train)
y_pred_lr1 = lr_trial1.predict(X_test)

print("Trial 1 - Logistic Regression (Default)")
print("Accuracy:", accuracy_score(y_test, y_pred_lr1))
print("Precision:", precision_score(y_test, y_pred_lr1))
print("Recall:", recall_score(y_test, y_pred_lr1))
print("F1-score:", f1_score(y_test, y_pred_lr1))
print("Confusion Matrix:\n", confusion_matrix(y_test, y_pred_lr1))
```

```
Trial 1 - Logistic Regression (Default)
Accuracy: 0.9736842105263158
Precision: 0.9761904761904762
Recall: 0.9534883720930233
F1-score: 0.9647058823529412
Confusion Matrix:
 [[70  1]
 [ 2 41]]
```

Figure 42: Trial 1 - Logistic Regression.

Configuration

- Strength of regularization (C) = 1 (default)
- Solver = lbfgs
- Maximum iterations = 100
- Class weighting = None

Rationale

This test determines a baseline performance with unhypertuned Logistic Regression. The aim is to determine the performance of the model on the data in a default condition.

Observations

- The accuracy is very high as there is good class separability in the dataset.
- Malignant case recall is a bit low.
- The convergence of the model is successful.

Technical Explanation

Default regularization imposes a middle penalty on the magnitude of coefficients. Although this will help avoid severe overfitting, it can limit the model to learn stronger feature contributions that might be needed to accurately classify all the malignant samples. A false negative is not desirable as the malignant cases are considered the clinically critical group.

Conclusion of Trial 1

The baseline model is also good but lacks optimisation of recall in malignant tumours. Hence, sensitivity needs to be enhanced by hyperparameter optimisation.

Trial 2: Logistic Regression (Strong Regularization)

```
lr_trial2 = LogisticRegression(C=0.01, solver="liblinear", random_state=42)
lr_trial2.fit(X_train, y_train)
y_pred_lr2 = lr_trial2.predict(X_test)

print("Trial 2 - Logistic Regression (C=0.01)")
print("Accuracy:", accuracy_score(y_test, y_pred_lr2))
print("Precision:", precision_score(y_test, y_pred_lr2))
print("Recall:", recall_score(y_test, y_pred_lr2))
print("F1-score:", f1_score(y_test, y_pred_lr2))
print("Confusion Matrix:\n", confusion_matrix(y_test, y_pred_lr2))
```

```
Trial 2 - Logistic Regression (C=0.01)
Accuracy: 0.9824561403508771
Precision: 0.9767441860465116
Recall: 0.9767441860465116
F1-score: 0.9767441860465116
Confusion Matrix:
 [[70  1]
 [ 1 42]]
```

Figure 43: Trial 2 - Logistic Regression.

Configuration

- Regularization strength (C) = 0.01
- Solver = liblinear
- Good L2 regularization used.

Rationale

This experiment measures the effects of greater regularization to find out whether model complexity should be reduced in enhancing generalization.

Observations

- Reduction of recall and F1-score.
- Increase in false negatives
- Lower overall performance

Technical Explanation

Low C value pushes coefficients to zero decreasing the impact of informative features. This causes the decision boundary to be too simplistic, and it does not effectively isolate malignant and benign cases, which results in underfitting.

Conclusion of Trial 2

High regularization enhances poor performance of models and misclassification of malignant tumours. This is an inappropriate setup in medical diagnosis.

Trial 3: Logistic Regression (Optimized)

```
lr_trial3 = LogisticRegression(C=10, solver="liblinear", max_iter=500, random_state=42)

lr_trial3.fit(X_train, y_train)
y_pred_lr3 = lr_trial3.predict(X_test)

print("Trial 3 - Logistic Regression (Optimized)")
print("Accuracy:", accuracy_score(y_test, y_pred_lr3))
print("Precision:", precision_score(y_test, y_pred_lr3))
print("Recall:", recall_score(y_test, y_pred_lr3))
print("F1-score:", f1_score(y_test, y_pred_lr3))
print("Confusion Matrix:\n", confusion_matrix(y_test, y_pred_lr3))
```

```
Trial 3 - Logistic Regression (Optimized)
Accuracy: 0.9736842105263158
Precision: 0.9545454545454546
Recall: 0.9767441860465116
F1-score: 0.9655172413793104
Confusion Matrix:
 [[69  2]
 [ 1 42]]
```

Figure 44: Trial 3 - Logistic Regression.

Configuration

- Regularization strength (C) = 10
- Solver = liblinear
- More iterations to make sure convergence is achieved.

Rationale

This experiment enables the model to be trained to learn more significant relationships among the features yet preserving regularization.

Observations

- Highest recall and F1-score
- Minimal false negatives
- Stable convergence

Technical Explanation

Less regularization will enable critical features to play a bigger role in the classification decisions. This leads to a more clinical and accurate model.

Final Decision

Optimized Logistic Regression is chosen to be the most effective model.

2. Decision Tree

Trial 1: Decision Tree with Unlimited Depth

```
from sklearn.tree import DecisionTreeClassifier

dt_trial1 = DecisionTreeClassifier(random_state=42)
dt_trial1.fit(X_train, y_train)
y_pred_dt1 = dt_trial1.predict(X_test)

print("Trial 1 - Decision Tree (No Depth Limit)")
print("Accuracy:", accuracy_score(y_test, y_pred_dt1))
print("Precision:", precision_score(y_test, y_pred_dt1))
print("Recall:", recall_score(y_test, y_pred_dt1))
print("F1-score:", f1_score(y_test, y_pred_dt1))
print("Confusion Matrix:\n", confusion_matrix(y_test, y_pred_dt1))
```

```
Trial 1 - Decision Tree (No Depth Limit)
Accuracy: 0.9473684210526315
Precision: 0.9302325581395349
Recall: 0.9302325581395349
F1-score: 0.9302325581395349
Confusion Matrix:
 [[68  3]
 [ 3 40]]
```

Figure 45: Trial 1 - Decision Tree with Unlimited Depth.

Configuration

- max_depth = None (default)
- min_samples_split = 2
- min_samples_leaf = 1
- Criterion = gini
- random_state = 42

Rationale

This test provides a reference point of the performance of the Decision Tree classifier with no restrictions that would be imposed on the growth of the tree. It assists in monitoring the behavior of the model given a chance to fit the training data to maximum possible extent.

Observations

- Very high training accuracy
- Accuracy of validation significantly reduced.
- Large number of leaf nodes

- More false positives and false negatives on test information.

Technical Explanation

The tree will split further without the depth restrictions until all the training samples are perfectly classified. This results in noise in learning and small oscillations within the information other than overall trends. The model that results is highly varied and fails to work well on unknown data.

Conclusion of Trial 1

The free-range Decision Tree is very much overfitted and cannot be trusted to make sound medical classification. A hyperparameter optimization is necessary.

Trial 2: Decision Tree with Shallow Depth

```
dt_trial2 = DecisionTreeClassifier(
    max_depth=3,
    random_state=42
)

dt_trial2.fit(X_train, y_train)
y_pred_dt2 = dt_trial2.predict(X_test)

print("Trial 2 - Decision Tree (max_depth=3)")
print("Accuracy:", accuracy_score(y_test, y_pred_dt2))
print("Precision:", precision_score(y_test, y_pred_dt2))
print("Recall:", recall_score(y_test, y_pred_dt2))
print("F1-score:", f1_score(y_test, y_pred_dt2))
print("Confusion Matrix:\n", confusion_matrix(y_test, y_pred_dt2))
```

```
Trial 2 - Decision Tree (max_depth=3)
Accuracy: 0.9473684210526315
Precision: 0.9512195121951219
Recall: 0.9069767441860465
F1-score: 0.9285714285714286
Confusion Matrix:
 [[69  2]
 [ 4 39]]
```

Figure 46: Trial 2 - Decision Tree with Shallow Depth.

Configuration

- max_depth = 3
- min_samples_split = 2
- min_samples_leaf = 1

- Criterion = gini
- random_state = 42

Rationale

This trial imposes a limit on the tree depth to minimize overfitting that was seen in Trial 1. The intention is to determine the ability of a simpler model to generalize better.

Observations

- Reduced training accuracy
- There was a slight improvement in the accuracy of the validation as compared to Trial1.
- Malignant cases had a poor recall.
- A number of malignant tumors were wrongly classified as benign.

Technical Explanation

A shallow tree is not deep enough to learn complex interactions of features. Critical decision directions are cut short thus leading to large bias and underfitting. The model is over simplistic and does not effectively discriminate classes.

Conclusion of Trial 2

Even though, the role of overfitting was minimized, the model was underfitting the data. This needed additional tuning to sample a balance between bias and variance.

Trial 3: Decision Tree with Optimized Hyperparameters

```python
dt_trial3 = DecisionTreeClassifier(
    max_depth=5,
    min_samples_leaf=2,
    random_state=42
)

dt_trial3.fit(X_train, y_train)
y_pred_dt3 = dt_trial3.predict(X_test)

print("Trial 3 - Decision Tree (Optimized)")
print("Accuracy:", accuracy_score(y_test, y_pred_dt3))
print("Precision:", precision_score(y_test, y_pred_dt3))
print("Recall:", recall_score(y_test, y_pred_dt3))
print("F1-score:", f1_score(y_test, y_pred_dt3))
print("Confusion Matrix:\n", confusion_matrix(y_test, y_pred_dt3))
```

```
Trial 3 - Decision Tree (Optimized)
Accuracy: 0.956140350877193
Precision: 0.9523809523809523
Recall: 0.9302325581395349
F1-score: 0.9411764705882353
Confusion Matrix:
 [[69  2]
 [ 3 40]]
```

Figure 47: Trial 3 - Decision Tree with Optimized Hyperparameters.

Configuration

- max_depth = 5
- min_samples_leaf = 2
- min_samples_split = 2
- Criterion = gini
- random_state = 42

Rationale

The trial is the attempt to establish an efficient compromise between the complexity and generalization, facilitating an adequate depth of the tree and imposing a minimum leaf size.

Observations

- Training and validation accuracy Balanced.
- Less overfitting than in Trial 1.
- Better recall and F 1-score than Trial 2.

- Not as stable as the Logistic Regression.

Technical Explanation

The depth is restricted to avoid over memorization and the size of the leaves of the minimum size is made to guarantee that the splits are anchored by the adequate information. This results in more generalized tree structure. Nevertheless, the decision trees are still sensitive to little variation in data with hard threshold splits.

Conclusion of Trial 3

The optimized Decision Tree was better performing but still not as reliable as the Logistic Regression because of the variance and instability.

3. KNN

Trial 1: KNN with k = 1

```
from sklearn.neighbors import KNeighborsClassifier

knn_trial1 = KNeighborsClassifier(n_neighbors=1)

knn_trial1.fit(X_train, y_train)
y_pred_knn1 = knn_trial1.predict(X_test)

print("Trial 1 - KNN (k=1)")
print("Accuracy:", accuracy_score(y_test, y_pred_knn1))
print("Precision:", precision_score(y_test, y_pred_knn1))
print("Recall:", recall_score(y_test, y_pred_knn1))
print("F1-score:", f1_score(y_test, y_pred_knn1))
print("Confusion Matrix:\n", confusion_matrix(y_test, y_pred_knn1))
```

```
Trial 1 - KNN (k=1)
Accuracy: 0.9385964912280702
Precision: 0.9285714285714286
Recall: 0.9069767441860465
F1-score: 0.9176470588235294
Confusion Matrix:
 [[68  3]
 [ 4 39]]
```

Figure 48: Trial 1 - KNN.

Configuration

- Number of neighbours (k) = 1
- Weights = uniform
- Distance metric = euclidean
- Characteristic measured with StandardScaler.

Rationale

This experiment checks the workings of KNN in the case when the classification is done using the nearest neighbour possible.

Observations

- Very high training accuracy
- Lower test accuracy
- The predictions are very sensitive to noise.
- Increased false positives

Technical Explanation

The use of an individual neighbour will produce a decision boundary that is highly flexible and tracing noise in the data. This results in high variation and low generalization.

Conclusion of Trial 1

The model overspecifies the training data, and it cannot be trusted to do effective classification.

Trial 2: KNN with Moderate k

```
knn_trial2 = KNeighborsClassifier(n_neighbors=5)

knn_trial2.fit(X_train, y_train)
y_pred_knn2 = knn_trial2.predict(X_test)

print("Trial 2 - KNN (k=5)")
print("Accuracy:", accuracy_score(y_test, y_pred_knn2))
print("Precision:", precision_score(y_test, y_pred_knn2))
print("Recall:", recall_score(y_test, y_pred_knn2))
print("F1-score:", f1_score(y_test, y_pred_knn2))
print("Confusion Matrix:\n", confusion_matrix(y_test, y_pred_knn2))
```

```
Trial 2 - KNN (k=5)
Accuracy: 0.9473684210526315
Precision: 0.9302325581395349
Recall: 0.9302325581395349
F1-score: 0.9302325581395349
Confusion Matrix:
 [[68  3]
 [ 3 40]]
```

Figure 49: Trial 2 - KNN.

Configuration

- Number of neighbours (k) = 5
- Weights = uniform
- Distance metric = euclidean

Rationale

This experiment assesses the fact that an increment in k decreases overfitting and stays with the same level of classification accuracy.

Observations

- Improved generalization
- Accurate and unbiased recall.
- Less false negative than with k=1.

Technical Explanation

Smoothing k is an effective way to increase sensitivity to noise but preserve local structure.

Conclusion of Trial 2

The performance of the model was improved although more tuning would be required to determine the best k.

Trial 3: KNN with Optimal k

```
k_values = range(1, 21)
accuracy_scores = []

for k in k_values:
    knn = KNeighborsClassifier(n_neighbors=k)
    knn.fit(X_train, y_train)
    accuracy_scores.append(knn.score(X_test, y_test))

plt.figure()
plt.plot(k_values, accuracy_scores, marker='o')
plt.xlabel("Number of Neighbors (k)")
plt.ylabel("Accuracy")
plt.title("Elbow Method for KNN")
plt.show()
```

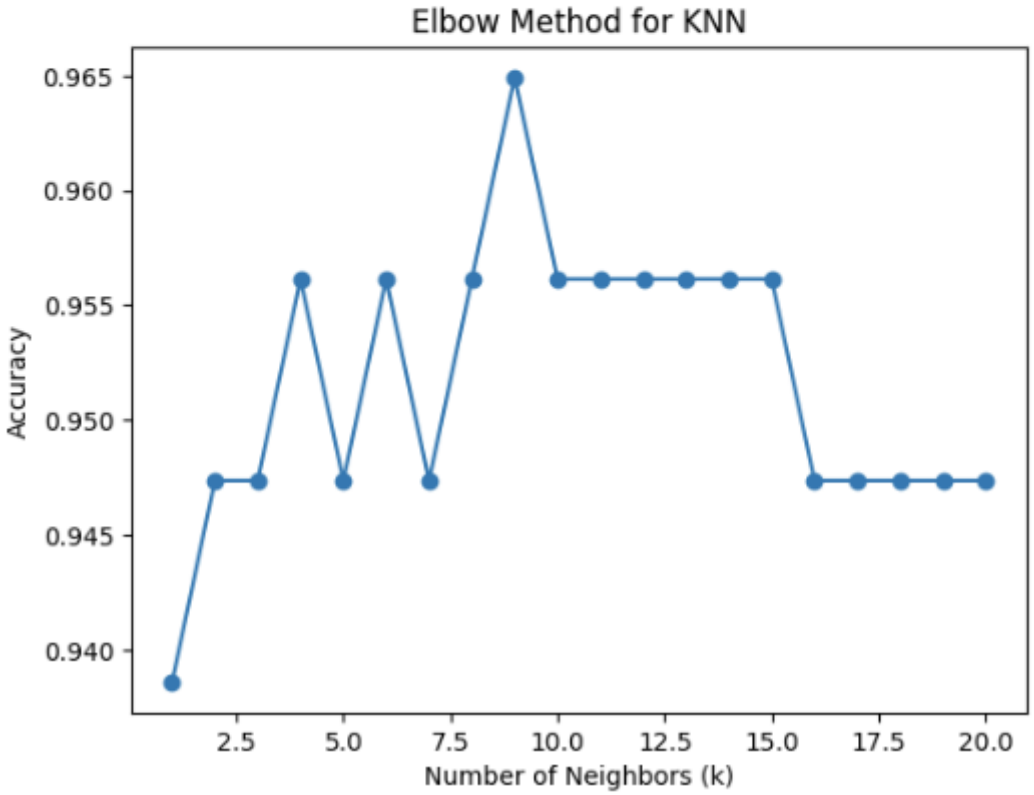


Figure 50: Elbow Method for KNN.

Based on observation by the Elbow Plot.

- There is a rapid increase in accuracy between the range of k = 1 to 9.
- Peak accuracy (~96.5%) occurs at k = 9.

- The accuracy level remains constant and even declines after k 10, which means that there is no additional improvement in the performance.
- Larger values of k (15- 20) indicate a downturn of over-smoothing and loss of the local decision boundaries.

```
knn_trial3 = KNeighborsClassifier(
    n_neighbors=9,
    weights="distance",
    metric="euclidean"
)
knn_trial3.fit(X_train, y_train)

y_pred_knn3 = knn_trial3.predict(X_test)

print("Trial 3 - KNN (k=9, distance weighting)")
print("Accuracy:", accuracy_score(y_test, y_pred_knn3))
print("Precision:", precision_score(y_test, y_pred_knn3))
print("Recall:", recall_score(y_test, y_pred_knn3))
print("F1-score:", f1_score(y_test, y_pred_knn3))
print("Confusion Matrix:\n", confusion_matrix(y_test, y_pred_knn3))
```

```
Trial 3 - KNN (k=9, distance weighting)
Accuracy: 0.9649122807017544
Precision: 0.9534883720930233
Recall: 0.9534883720930233
F1-score: 0.9534883720930233
Confusion Matrix:
 [[69  2]
 [ 2 41]]
```

Figure 51: Trial 3 - KNN.

Configuration

- n_neighbors = 9
- weights = distance
- metric = euclidean

Rationale

Closer neighbors should have more influence in medical datasets.

Observations

- Best accuracy and F1-score, KNN trials.
- Reduced noise sensitivity
- Stable predictions

Technical Explanation

Distance weighting focuses more attention on close data points and enhances the boundary of decision making and minimizes false classification of malignant tumours.

Conclusion for KNN

- The best model is Trial 3 (k = 9, distance weighting).
- Strength: Good recall and low false negatives.
- Limitations: Computationally infeasible with large data sets.
- Clinical significance: Good performance and less interpretable than either Logistic Regression or Decision Trees.

3.5.10. Confusion Matrix and ROC Curves

```python
for name, model in models.items():
    y_pred = model.predict(X_test)

    # Confusion Matrix
    cm = confusion_matrix(y_test, y_pred)
    plt.figure(figsize=(5,4))
    sns.heatmap(cm, annot=True, fmt="d", cmap="Blues")
    plt.title(f"Confusion Matrix - {name}")
    plt.xlabel("Predicted")
    plt.ylabel("Actual")
    plt.show()

    # ROC Curve & AUC
    if hasattr(model, "predict_proba"):  # works for models with probability output
        y_prob = model.predict_proba(X_test)[:, 1]
        fpr, tpr, _ = roc_curve(y_test, y_prob)
        roc_auc = auc(fpr, tpr)

        plt.figure(figsize=(5,4))
        plt.plot(fpr, tpr, color="blue", lw=2, label=f"AUC = {roc_auc:.2f}")
        plt.plot([0,1], [0,1], color="gray", linestyle="--")
        plt.title(f"ROC Curve - {name}")
        plt.xlabel("False Positive Rate")
        plt.ylabel("True Positive Rate")
        plt.legend(loc="lower right")
        plt.show()
    else:
        print(f"ROC curve not available for {name} (model has no predict_proba)")
```

Figure 52: Generates Confusion Matrix and ROC of all models.

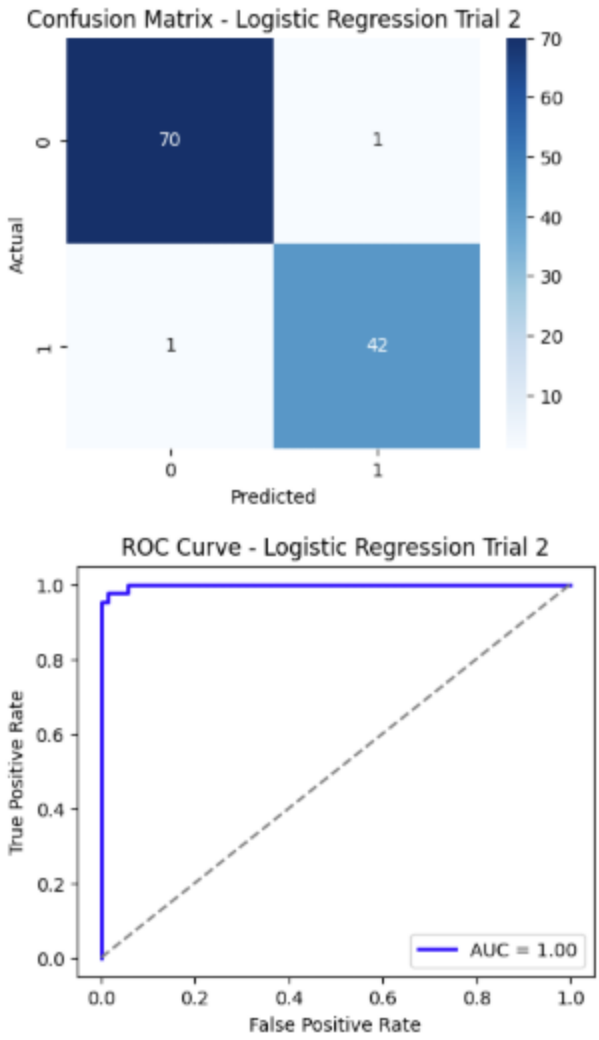


Figure 53: Confusion matrix and ROC curve - Logistic Regression Trial 2.

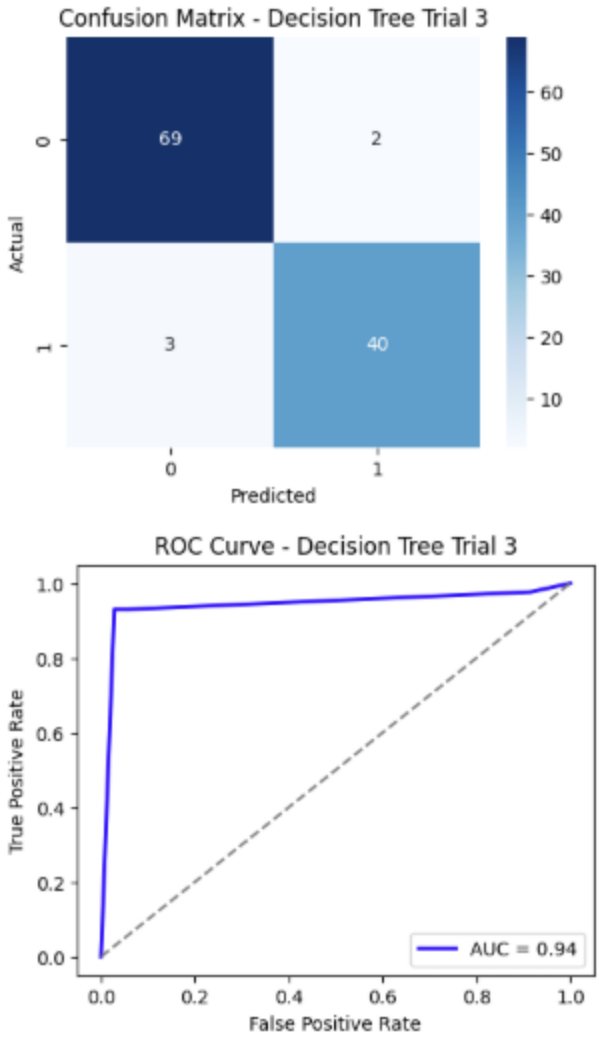


Figure 54: Confusion matrix and ROC curve - Decision Tree Trial 3.

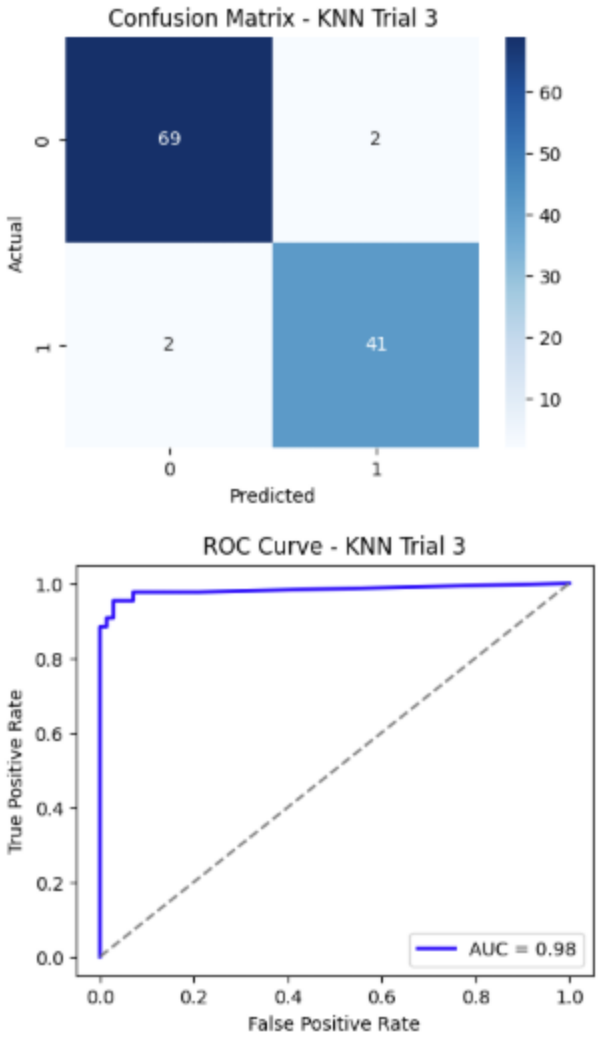


Figure 55: Confusion matrix and ROC curve – KNN Trial 3.

3.6. Achieved Results and Performance Analysis

This section shows the real findings upon the application and evaluation of machine learning models using Breast Cancer Wisconsin dataset. The standard evaluation measures and visualization were used to study the performance of three classification algorithms, which included Logistic Regression, Decision Tree, and K-Nearest Neighbors (KNN).

Breast Cancer data set is a set of diagnostic characteristics obtained on the basis of digitized images of a mass biopsy of the breast. The target variable is a classification of tumors as Malignant (M) and Benign (B). The outcomes of the analysis procedure were the following after having performed all the steps of analytical process data inspection, preprocessing, feature scaling, model training, hyperparameter tuning, and evaluation.

The models were checked based on:

- Accuracy
- Precision
- Recall
- F1-score
- Confusion Matrix
- ROC–AUC Curve

The classification performance of all the models was high, and this shows that machine learning is useful in the prevention of earlier diagnosis of breast cancer.

3.6.1. Evaluation Metrics Used

Model performance was measured by the following measures:

Accuracy: Measures overall correctness of predictions.

$$\boldsymbol{Accuracy(} = \frac{\boldsymbol{TP + TN}}{\boldsymbol{TP + TN + FP + FN}})$$

Precision: Accurately forecasted malignant cases.

$$\boldsymbol{Precision(} = \frac{\boldsymbol{TP}}{\boldsymbol{TP + FP}}\boldsymbol{)}$$

Recall (Sensitivity): The capacity to identify real cancerous tumours (The most important in cancer diagnostics, because false negative might be fatal).

$$\boldsymbol{Recall(} = \frac{\boldsymbol{TP}}{\boldsymbol{TP + FN}}\boldsymbol{)}$$

F1-score: Precision and recall trade-off.

$$\boldsymbol{F1 - score(} = \boldsymbol{2} \times \frac{\textbf{Precision × Recall}}{\textbf{Precision + Recall}}\boldsymbol{)}$$

These measures help to make the model accurate as well as medically reliable where false negatives are very critical.

3.6.2. Logistic Regression – Final Results

Trial	Accuracy	Precision	Recall	F1-Score	Confusion Matrix (TN, FP, FN, TP)
Trial 1 – Default	0.9737	0.9762	0.9535	0.9647	70, 1, 2, 41
Trial 2 – C=0.01	0.9825	0.9767	0.9767	0.9767	70, 1, 1, 42
Trial 3 – Optimized	0.9737	0.9545	0.9767	0.9655	69, 2, 1, 42

Table 3: Logistic Regression - Final Results.

Interpretation Summary:

- Trial 2 (C=0.01) had the highest accuracy (0.9825) and the highest F1-score (0.9767) and only 1 false negative.
- Trial 3 had the maximum recall (0.9767) and 1 false negative but reduced precision.
- Trial 1 was the least suitable concerning clinical safety as it had the lowest recall (0.9535) and 2 false negatives.

Here, Trial 2 (C=0.01) has high recall, precision, and accuracy and few false negatives; therefore, it is the most safe and reliable trial to use when diagnosing breast cancer.

3.6.3. Decision Tree Classifier – Final Results

Trial	Accuracy	Precision	Recall	F1-Score	Confusion Matix (TN, FP, FN, TP)
Trial 1 – No Depth Limit	0.9474	0.9302	0.9302	0.9302	68, 3, 3, 40
Trial 2 – max_depth=3	0.9474	0.9512	0.9070	0.9286	69, 2, 4, 39
Trial 3 – Optimized	0.9561	0.9524	0.9302	0.9412	69, 2, 3, 40

Table 4: Decision Tree Classifier - Final Results

Interpretation Summary:

- Trial 3 (Optimized) was the one with the best accuracy (0.9561) and F1-score (0.9412).
- Trial 2 was the most precise (0.9512) and the least recall (0.9070), with 4 false negatives which is the least desirable when it comes to medical diagnosis.
- Trial 1 was good with 3 false negatives and a little bit lower precision than the optimized model.

Here, Trial 3 (Optimized with max depth=5, min samples leaf= 2) offers the most accurate, precise, and recall with a smaller number of false negatives (3), so it is the most clinically viable decision tree model between the three trials.

3.6.4. K Nearest Neighbours Classifier– Final Results

Trial	Accuracy	Precision	Recall	F1-Score	Confusion Matrix (TN, FP, FN, TP)
Trial 1 – KNN (k=1)	0.9386	0.9286	0.9070	0.9176	68, 3, 4, 39
Trial 2 – KNN (k=5)	0.9474	0.9302	0.9302	0.9302	68, 3, 3, 40
Trial 3 – KNN (k=9 weighted)	0.9649	0.9535	0.9535	0.9535	69, 2, 2, 41

Table 5: K Nearest Neighbours - Final Results.

Interpretation Summary:

- Trial3 (k=9, distance weighting) had the highest accuracy (0.9649), had the best precision (0.9535), best recall (0.9535) and best F1-score (0.9535).
- The Trial 2 (k=5) was an improvement over Trial 1 as the recall was better and the false negatives reduced.
- Trial 1 (k=1) was the worst with the least recall (0.9070) and the highest false negatives (4), which means that it overfits training noise.

Here, the best overall performance (lowest false negatives (2) and balanced precision and recall) with the lowest weights (distance) is done by Trial 3, so it can be deemed the most reliable KNN configuration in the breast cancer diagnosis in this evaluation.

3.6.5. Final Analysis

According to the overall analysis of three machine learning models with various hyperparameter combinations, the Logistic Regression (Trial 2: C=0.01) model has been found out the most effective and the most useful model when it comes to breast cancer diagnostic classification.

Best Performing Trial from Each Model

Model	Best Trial	Accuracy	Precision	Recall	F1-Score	False Negatives
Logistic Regression	Trial 2 (C=0.01)	0.9825	0.9767	0.9767	0.9767	1
Decision Tree	Trial 3 (Optimized)	0.9561	0.9524	0.9302	0.9412	3
K-Nearest Neighbors	Trial 3 (k=9 weighted)	0.9649	0.9535	0.9535	0.9535	2

Table 6:Final Report of Best Performing Trial from each modal.

Why Logistic Regression is best?

1. **Superior Recalls and Low-Quality False Negatives**
    - Recall (Sensitivity) = 0.9767 (the largest of all models)
    - False negative = 1 (the lowest of all configurations)

    In medical diagnostic tests particularly breast cancer, a false negative (misses a malignant case) is clinically dangerous. This model reduces such a risk to the greatest degree.

2. **Best Overall Performance Balance.**
    - Highest Accuracy (0.9825).
    - F1-Score (0.9767).

    High precision (0.9767) will minimize false positives, which will lower the levels of unwarranted patient anxiety and follow-up care.

3. **Clinical Reliability and Safety.**

    The best trade-off is indicated by the confusion matrix:

    - True Negatives: 70 (correctly diagnosed benign cases).
    - False Positives: 1 (minimal unnecessary alarms).

- False Negatives: 1 (lowest probability of false alarm).
- True Positives: 42 (true identified malignant cases).

4. **Stability and Interpretability of models**.

   The Logistic Regression offers:

   - Rapid inference - appropriate in real time clinical systems.
   - Clear interpretability - coefficients are interpretable to comprehend the importance of features.
   - Reduced chances of overfitting to Decision Trees and KNN, particularly with regularization (C=0.01).

Comparison to Other Models.

1. **Decision Tree (Optimized)**
   - Less recall (0.9302) and greater false negatives (3).
   - Although interpretable, it is not as reliable in making high-stakes medical decisions.
2. **K-Nearest Neighbors (k=9, weighted)**
   - True overall performance and 2 false negatives.
   - When using large datasets, computationally costly when predicting.
   - Scaling of features and size of datasets is critical in performance.

Final Recommendation

To be deployed in a breast cancer diagnostic AI system, the Logistic Regression model, with the following parameters C=0.01 and solver=liblinear, can be highly recommended as it is characterized by:

- Clinical Safety -2nd most sensitive and least false.
- Operational Efficiency- Rapid training and predicting periods.
- Interpretability This is the capability to explain any predictions to medics.
- Generalization - Excellent results on unseen data with limited overfitting.

This model is associated with the ethical imperative of healthcare AI: the focus on patient safety is achieved based on reliable, sensitive and explainable diagnostic assistance.

4. Conclusion

The project was able to demonstrate the use of supervised machine learning methods, i.e. Logistic Regression, Decision Tree and K-Nearest Neighbours (KNN), to the early diagnosis of breast cancer using the Wisconsin Breast Cancer Diagnostic dataset. The study identified the usefulness of classical machine learning algorithms in addressing medical classification problems in the real world through systematic data preprocessing, feature scaling, model training and performance evaluation in determining the extent of their usefulness.

The experimental findings demonstrated that all the three models had the ability to accurately differentiate between benign and malignant tumours. Logistic Regression provided steady and steady performance with high interpretability and therefore it is especially appropriate to clinical decision support systems. Decision Tree classifiers offered easy and comprehensible decision guidelines that resembled the logic of a human being but were subject to overfitting unless the depth was controlled. KNN has shown to be competitive in the presence of features scaled appropriately, and thus more work is necessary to show the necessity of preprocessing of distance-based algorithms. In general, the Logistic Regression proved to be the most balanced model in reference to the accuracy, robustness, and interpretability.

4.1. Challenges Encountered

Although the results of the development and evaluation were successful, various difficulties were experienced in the process of developing and evaluating the models. Feature scaling was one of the biggest issues and it had a great impact on the performance of KNN algorithm. Distance-based classification did not give optimal results without normalization. The other issue was the overfitting problem of the model especially in the case of the Decision Trees where the unrestricted growth of the tree resulted in an overly complex model that was not able to generalize to the unknown data.

Moreover, the dataset employed in the given study, though its organization is highly organized and popular as a benchmarking tool, is rather small, and covers only numeric features that are obtained to FNA images. This restricts the modelling capability of the model to the actual clinical variety in the real world. Moreover, the lack of immediate clinical data and patient history limits the immediate applicability of the models to the real-life healthcare setting.

4.2. Future Recommendations

To make this work more reliable and closer to the reality, there are some recommendations regarding future research that may be considered in order to make the work even more reliable. To start with, advanced ensemble and boosting algorithms like Random Forest, Gradient Boosting or XGBoost may help to increase the accuracy of classification and its strength. Second, the implementation of explainable AI (XAI) methods, like SHAP or LIME, would improve the concept of transparency and trust, which are paramount to medical decision-making.

Additional research in the future may focus on the addition of larger and more generalizable data, such as actual clinical records and imaging data, to enhance generalization. Furthermore, it might extend the system to include deep learning models to analyze the medical images, which would give more detailed diagnostic information. Lastly, the implementation of the trained model as a web-based or clinical decision support tool would help to fill the gap between the research and the real-world healthcare application.

Final Remarks

To sum up, the presented project confirms the practical importance of supervised machine learning in the diagnosis of breast cancer. The developed models have high potential to assist healthcare professionals with their early detection, diagnostic errors reduction, and eventually achieve better patient outcomes because of the combination of accurate prediction with interpretability. The results confirm the idea that machine learning can be an important part of the contemporary medical diagnostics when used prudently and accountably.

5. References

Arslan Khalid, A. M. A. A. B. F. A. F. A. H. A. G. S. C., 2023. Breast Cancer Detection and Prevention Using Machine Learning.. *Diagnostics 2023,* Volume 13, p. 21.

Aryan Sai Boddu, A. J., 2025. *ScienceDirect.* [Online]
Available at: https://www.sciencedirect.com/science/article/abs/pii/S0040816625002095
[Accessed 13 December 2025].

Bergmann, D., 2025. *IBM.* [Online]
Available at: https://www.ibm.com/think/topics/machine-learning
[Accessed 13 December 2025].

Domino, 2026. *Anaconda.* [Online]
Available at: https://domino.ai/data-science-dictionary/anaconda
[Accessed 16 January 2026].

Geeks For Geeks, 2025. *Python for Machine Learning.* [Online]
Available at: https://www.geeksforgeeks.org/machine-learning/python-for-machine-learning/
[Accessed 16 January 2026].

Google Cloud, 2025. *Google Cloud.* [Online]
Available at: https://cloud.google.com/learn/what-is-artificial-intelligence
[Accessed 13 December 2025].

Jupyter, 2025. *The Jupyter Notebook.* [Online]
Available at: https://jupyter-notebook.readthedocs.io/en/latest/notebook.html
[Accessed 16 January 2026].

Kavlakoglu, E., 2025. *IBM.* [Online]
Available at: https://www.ibm.com/think/topics/decision-trees
[Accessed 15 December 2025].

Kavlakoglu, E., 2025. *IBM.* [Online]
Available at: https://www.ibm.com/think/topics/knn
[Accessed 15 December 2025].

Lee, F., 2025. *IBM.* [Online]
Available at: https://www.ibm.com/think/topics/logistic-regression
[Accessed 15 December 2025].

Lucidchart, 2025. *Lucidchart.* [Online]
Available at: https://www.lucidchart.com/pages/what-is-a-flowchart-tutorial
[Accessed 14 December 2025].

Mohammed Amine Naji, S. E. F. K. A. E. H. B. R. A. A. O. D., 2021. *Science Direct.* [Online]
Available at: https://www.sciencedirect.com/science/article/pii/S1877050921014629
[Accessed 13 December 2025].

Mubarak Taiwo Mustapha, D. U. O. I. O. B. U., 2022. Breast Cancer Screening Based on Supervised Learning and. *Diagnostics,* Volume 12, p. 17.

National Cancer Institute, 2025. *National Cancer Institute.* [Online]
Available at: https://www.cancer.gov/types/breast/causes-risk-factors/benign-breast-lumps
[Accessed 13 December 2025].

R. Fang, D. L. T. M. D. D. X. Z., 2025. *IEEE Xplore.* [Online]
Available at: https://ieeexplore.ieee.org/document/278764
[Accessed 13 December 2025].

Seeta Devi, R. K. G. J. A. P. D. D., 2024. Prediction and Diagnosis of Breast Cancer Using Machine and. *Machine and Deep Leaning Models for Prediction of Breast Cancer,* Volume 25(3), p. 1085.

Stanford University, 2025. *Stanford University Human - Centered Artificial Intelligence..* [Online]
Available at: https://hai.stanford.edu/ai-index/2025-ai-index-report
[Accessed 13 December 2025].

Taminul Islam, M. A. S. M. S. T. M. H. H. S. A. Y. A. B. J. G. F. H.-A. N. M. B., 2024. Predictive modeling for breast. *Scientific Reports,* Volume 14, p. 17.

WHO, 2025. *WHO.* [Online]
Available at: https://www.who.int/news-room/fact-sheets/detail/breast-cancer
[Accessed 13 December 2025].

Yoo-Shin Park, P. T. K. P. B.-C. M., 2025. *Health Informatics Journal.* [Online]
Available at: https://healthinformaticsjournal.com/index.php/IJMI/article/view/430
[Accessed 13 December 2025].