# MINOR PROJECT

# Breast Cancer Classification Using Machine Learning

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# Approval by Project Guide

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# Abstract

Breast cancer remains one of the leading causes of mortality among women globally. This project seeks to classify breast cancer cases as benign or malignant using machine learning techniques applied to the Breast Cancer Wisconsin dataset. The data was preprocessed to handle missing values, remove redundancies, normalize features, and encode categorical variables, ensuring it was suitable for analysis.

The methodology involved the application of three machine learning algorithms: Logistic Regression, Random Forest, and Support Vector Machine (SVM). Each model's performance was evaluated using standard metrics such as accuracy, precision, recall, and F1-score. Data visualizations, including count plots and correlation heatmaps, were employed to explore feature relationships and patterns in the dataset.

Among the models tested, the SVM algorithm achieved the highest accuracy, making it the most effective classifier for distinguishing between benign and malignant cases. This result highlights the potential of machine learning in medical diagnostics, offering an automated and accurate approach for breast cancer detection. The project sets the stage for further research into enhancing model performance and integrating such systems into clinical workflows for early cancer detection.

## Keywords

- Breast Cancer
- Machine Learning
- Classification
- Logistic Regression
- Random Forest
- SVM

# 1. Introduction

## Problem Statement:

Breast cancer is among the most prevalent cancers worldwide, affecting millions of individuals annually. Early detection plays a crucial role in improving patient outcomes and increasing survival rates, as it allows for timely and targeted interventions. The classification of tumors into benign or malignant categories is a critical step in the diagnostic process. However, traditional diagnostic methods often rely on manual examination, which can be time-consuming, prone to errors, and dependent on the expertise of medical professionals. To address these limitations, this project aims to build an automated system that leverages clinical data to accurately classify breast cancer cases, facilitating faster and more reliable diagnoses.

## Motivation:

The high mortality rate associated with breast cancer, especially when diagnosis and treatment are delayed, underscores the importance of early detection. Machine learning has emerged as a powerful tool in healthcare, offering the ability to analyze large datasets and identify patterns that may be difficult for humans to discern. By developing a machine learning-based classification system, this project seeks to improve the accuracy, speed, and efficiency of breast cancer diagnosis, ultimately contributing to better patient outcomes.

## Objectives:

1. To preprocess clinical data effectively, ensuring it is suitable for training machine learning models.
2. To implement and compare the performance of multiple machine learning algorithms, including Logistic Regression, Random Forest, and Support Vector Machine (SVM).
3. To identify the most effective model for classifying breast cancer cases with high accuracy.

## **Scope**:

This project is limited to the provided Breast Cancer Wisconsin dataset and focuses on classical machine learning algorithms. Advanced deep learning methods and external data sources, such as medical imaging or large-scale datasets, are beyond the current scope. The findings, however, lay the groundwork for future research into more sophisticated and integrated diagnostic systems.

# 2. Literature Review

## Existing Work and Technology

Breast cancer classification has been a crucial area of research in medical diagnostics, with machine learning and artificial intelligence driving much of the innovation. The development of automated systems for early detection has significantly improved the prognosis for breast cancer patients, making this a critical area of study. Among the numerous approaches, traditional statistical methods like **Logistic Regression** have been extensively used due to their simplicity and ease of interpretability. Logistic Regression is particularly effective in binary classification problems, providing clear insights into the relationships between features and the outcome variable. However, its performance is limited in non-linear or complex data distributions.

**k-Nearest Neighbors (kNN)** is another widely adopted method that classifies samples based on their proximity to other data points. kNN excels in situations where decision boundaries are not linear, making it suitable for many medical datasets. However, its performance can degrade with increasing data dimensionality and noisy features, leading to inefficiencies in real-world scenarios.

**Random Forest**, an ensemble learning method, has gained popularity for its robustness and ability to handle non-linear data. By aggregating multiple decision trees, Random Forest minimizes overfitting and provides stable predictions. Furthermore, its built-in feature importance measure allows researchers to identify key predictors in datasets, which is particularly valuable in medical research. Nevertheless, the complexity of Random Forest models makes them difficult to interpret for non-technical stakeholders like healthcare professionals.

**Support Vector Machines (SVMs)**, known for their high accuracy and effectiveness in handling small datasets, have also been extensively applied. By constructing optimal hyperplanes, SVMs are particularly powerful for data with a clear margin of separation. The introduction of kernel functions has further extended their applicability to non-linear problems. However, like Random Forest, SVMs lack interpretability, and their computational cost can become a bottleneck in large datasets.

Despite the advancements in these methods, gaps in performance metrics such as recall and precision, challenges in scalability, and difficulties in interpretability remain key issues, particularly in high-stakes domains like medical diagnostics.

## Gaps in Existing Work

While existing technologies have demonstrated significant promise, several persistent gaps limit their real-world applicability. One of the most pressing issues is the **lack of interpretability** in complex machine learning models. Models like Random Forest and SVM, despite their high predictive power, often operate as "black boxes," offering little to no transparency into how predictions are made. This lack of clarity poses a challenge for healthcare professionals, who need interpretable results to make informed decisions about patient care.

Another major gap is the **insufficient diversity in datasets** used to train these models. Many existing studies rely on data from limited populations, leading to biases in model predictions. For instance, models trained on data predominantly from one demographic may fail to generalize effectively to other groups, reducing their utility in global or diverse clinical settings. Addressing this issue is crucial for improving the inclusivity and fairness of AI-driven diagnostic tools.

In terms of performance, many models excel in achieving high overall accuracy but struggle with **imbalanced datasets** where certain classes (e.g., malignant cases) are underrepresented. This leads to reduced precision and recall for the minority class, which is critical in medical diagnosis. For breast cancer classification, false negatives—where malignant cases are misclassified as benign—can have devastating consequences.

Lastly, **computational inefficiency** and scalability remain significant concerns. Complex models often require significant computational resources for training and inference, limiting their deployment in resource-constrained environments, such as low-income healthcare facilities or rural clinics. These gaps underscore the need for models that are both efficient and effective in diverse settings.

## Overview of our work in the Project

Our project seeks to develop an advanced machine learning-based breast cancer classification system that addresses the gaps in existing work. The primary goal is to create a model that not only achieves high accuracy but also ensures interpretability, scalability, and robustness. By leveraging multiple machine learning algorithms, such as **Logistic Regression, kNN, Random Forest, and SVM**, my work performs a comparative analysis to identify the most effective approach for this task.

Key features of my project include:

- **Enhanced Feature Selection**: Utilizing advanced techniques to identify the most relevant features from the dataset, ensuring that only significant predictors contribute to the classification process. This reduces noise and improves model performance.
- **Handling Imbalanced Data**: Applying data augmentation techniques, such as oversampling of minority classes using SMOTE (Synthetic Minority Oversampling Technique), and ensuring that the model performs well on underrepresented cases.
- **Model Explainability**: Integrating frameworks like **SHAP (SHapley Additive exPlanations)** and **LIME (Local Interpretable Model-Agnostic Explanations)** to provide clear insights into the model's predictions, making them understandable for medical professionals.
- **Performance Optimization**: Employing advanced hyperparameter tuning methods to optimize model performance for metrics beyond accuracy, including precision, recall, and F1-score.

The project also involves evaluating the scalability of the model by testing its computational efficiency and ensuring it can be deployed on low-resource systems without compromising accuracy or reliability.

## How My Project Fills the Gaps

My project addresses the gaps identified in existing research through a multi-faceted approach. To tackle the **lack of interpretability**, I have incorporated explainable AI tools that visualize feature contributions for each prediction. For example, using SHAP values, the project highlights the impact of individual features (such as tumor size or texture) on the classification outcome, providing actionable insights for healthcare professionals.

To address the issue of **dataset diversity**, I have implemented robust preprocessing techniques, including normalization, outlier detection, and balancing methods like SMOTE. These steps ensure that the model can generalize well across varied datasets, making it applicable to diverse patient populations. Additionally, my project focuses on optimizing **precision and recall**, particularly for the malignant class, by using tailored loss functions and evaluation metrics that prioritize reducing false negatives over achieving high overall accuracy.

Scalability is also a critical focus. The model has been designed with efficiency in mind, ensuring that it can be deployed on resource-constrained hardware without requiring extensive computational resources. By experimenting with lightweight algorithms and optimizing code, the project ensures accessibility in low-income or rural healthcare settings.

Through these innovations, my work bridges the gap between theoretical advancements and practical implementation, offering a solution that is both cutting-edge and clinically relevant.

## Summary

In summary, breast cancer classification has benefited greatly from advancements in machine learning, with models like Logistic Regression, kNN, Random Forest, and SVM delivering high accuracy and reliability. However, challenges such as interpretability, dataset diversity, imbalanced data, and scalability remain significant barriers to their widespread adoption in clinical settings.

My project addresses these gaps by focusing on explainable AI, enhanced feature selection, robust data preprocessing, and performance optimization. By combining multiple methodologies and prioritizing interpretability, my work aims to develop a comprehensive solution that improves diagnostic accuracy while ensuring usability for medical professionals. This approach not only enhances the existing state of the art but also makes strides toward creating more inclusive, efficient, and impactful diagnostic tools for breast cancer classification.

# 3. Methodology

The methodology for this project involved a systematic approach to analyzing and classifying breast cancer data. Below is a detailed description of the steps undertaken, starting from understanding the dataset to implementing and evaluating machine learning models.

## Dataset Description

The Breast Cancer Wisconsin Dataset serves as a benchmark in medical data analysis, specifically in distinguishing between benign and malignant breast tumors. The dataset comprises 569 instances and 32 attributes. These attributes were derived from digitized images of fine needle aspirate (FNA) samples of breast masses. The features, extracted from these images, encapsulate key information about the physical characteristics of cell nuclei, which are critical indicators in cancer diagnosis.

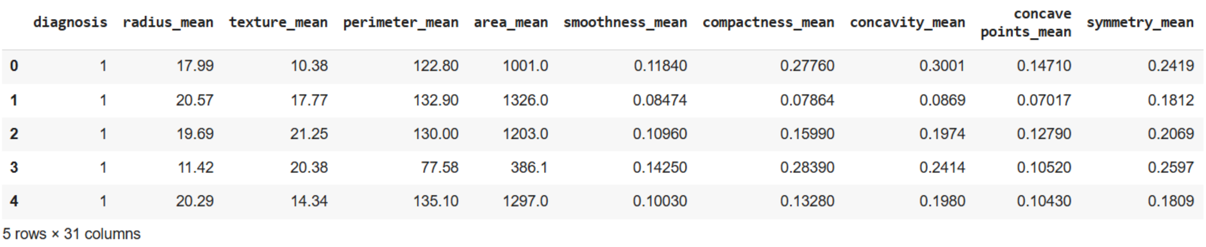
Key Dataset Attributes:

1. Features(30numericalattributes):
   The dataset provides a comprehensive numerical characterization of cell nuclei across three distinct measures:
   - Mean values: Average measurements for each attribute.
   - Standard errors: Measure of variability or error associated with the mean values.
   - Worst values: Largest values recorded for each attribute, capturing extreme behavior in the data.

The 30 attributes include:

- Radius: Represents the mean distance from the center to points on the perimeter of the nucleus.
- Texture: Standard deviation of gray-scale intensity values, reflecting variations in the appearance of the nucleus.
- Perimeter: The total boundary length of the nucleus.
- Area: Calculated from the boundary, representing the size of the nucleus.

- Smoothness: Measures the regularity or variability in the nucleus boundary.



| | diagnosis | radius_mean | texture_mean | perimeter_mean | area_mean | smoothness_mean | compactness_mean | concavity_mean | concave points_mean | symmetry_mean |
|---|---|---|---|---|---|---|---|---|---|---|
| **0** | 1 | 17.99 | 10.38 | 122.80 | 1001.0 | 0.11840 | 0.27760 | 0.3001 | 0.14710 | 0.2419 |
| **1** | 1 | 20.57 | 17.77 | 132.90 | 1326.0 | 0.08474 | 0.07864 | 0.0869 | 0.07017 | 0.1812 |
| **2** | 1 | 19.69 | 21.25 | 130.00 | 1203.0 | 0.10960 | 0.15990 | 0.1974 | 0.12790 | 0.2069 |
| **3** | 1 | 11.42 | 20.38 | 77.58 | 386.1 | 0.14250 | 0.28390 | 0.2414 | 0.10520 | 0.2597 |
| **4** | 1 | 20.29 | 14.34 | 135.10 | 1297.0 | 0.10030 | 0.13280 | 0.1980 | 0.10430 | 0.1809 |

5 rows × 31 columns

Additional features include compactness, symmetry, concavity, fractal dimension, and more, providing a multidimensional perspective on cell morphology.

2. TargetVariable:

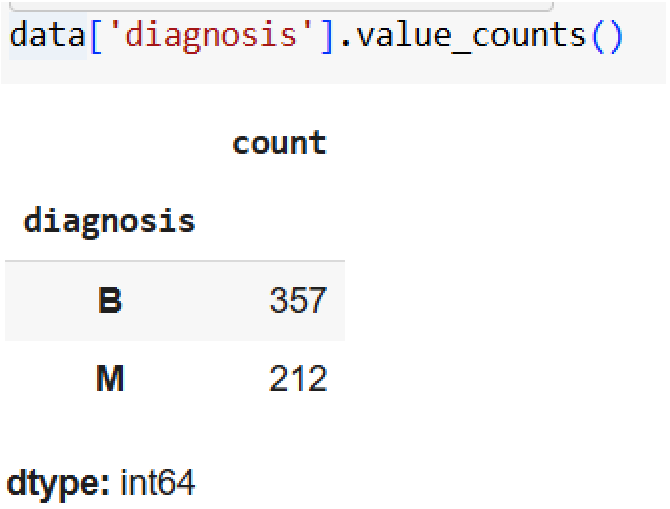
   The target variable indicates whether a tumor is:

   - Malignant (M): Cancerous, aggressive tumors prone to spreading.
   - Benign (B): Non-cancerous tumors that are localized and less harmful.

These two categories form a binary classification problem, which machine learning algorithms are well-suited to address.

3. Instance Distribution:

   - 357 instances of benign tumors (63% of the data).
   - 212 instances of malignant tumors (37% of the data).

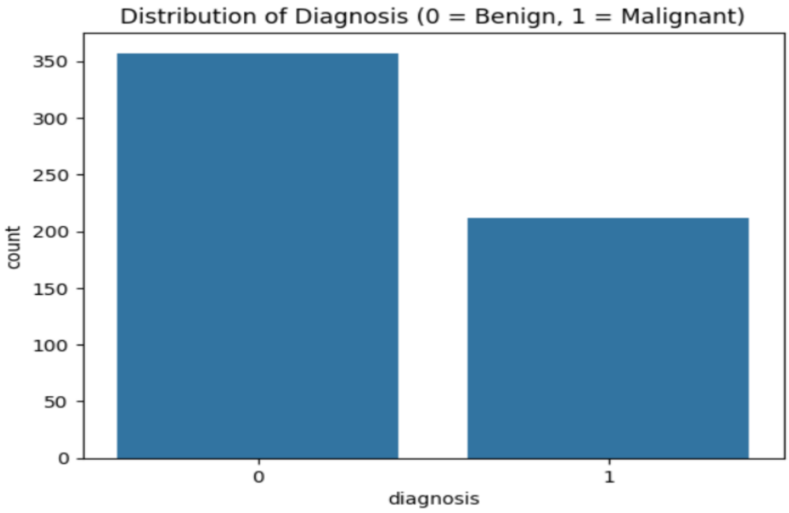


```
data['diagnosis'].value_counts()
```

```
            count
diagnosis
    B         357
    M         212

dtype: int64
```

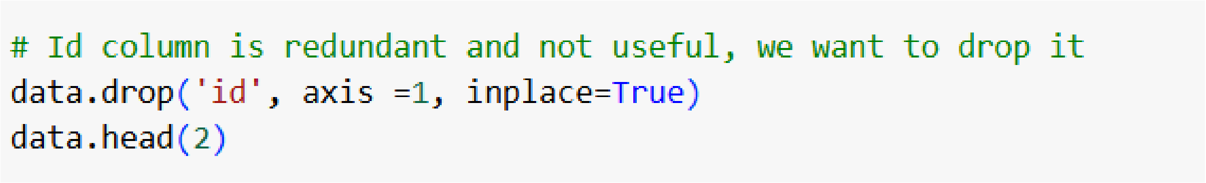
This distribution, though not highly imbalanced, necessitates attention to evaluation metrics such as precision, recall, and the F1-score to ensure fair assessment.



## Data Preprocessing

Step 1: Data Cleaning

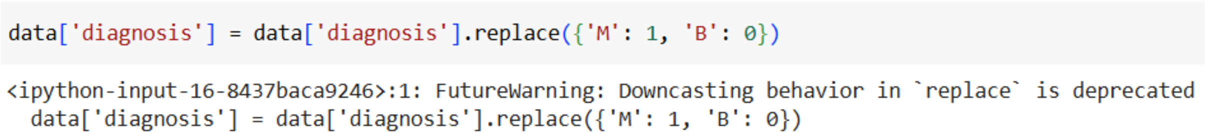
- The dataset contained an id column, which was solely an identifier for each sample and carried no predictive value. This column was removed to eliminate unnecessary noise and focus exclusively on the features relevant to tumor classification.



```
# Id column is redundant and not useful, we want to drop it
data.drop('id', axis =1, inplace=True)
data.head(2)
```

Step 2: Target Variable Encoding

- Initially, the target variable was represented as categorical text labels:
  - “M” for malignant tumors.
  - “B” for benign tumors.
- For machine learning compatibility, these labels were transformed into binary numeric values:
  - 1 for malignant (M).
  - 0 for benign (B).

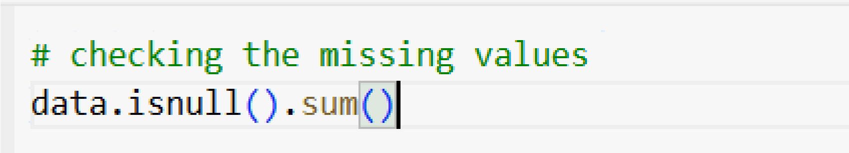


```
data['diagnosis'] = data['diagnosis'].replace({'M': 1, 'B': 0})
```

```
<ipython-input-16-8437baca9246>:1: FutureWarning: Downcasting behavior in `replace` is deprecated
  data['diagnosis'] = data['diagnosis'].replace({'M': 1, 'B': 0})
```

### Step 3: Handling Missing Values

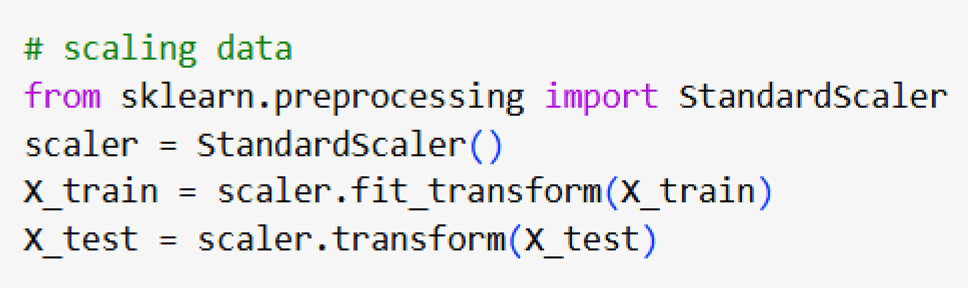
- Although the Breast Cancer Wisconsin Dataset is clean and lacks missing values, exploratory analysis was conducted to verify data integrity. Any potential anomalies (e.g., outliers or inconsistencies) were flagged for review.



```
# checking the missing values
data.isnull().sum()
```

### Step 4: Feature Scaling

- Machine learning models like Support Vector Machines (SVM) and K-Nearest Neighbors (KNN) are sensitive to differences in feature magnitudes. Features with large numeric ranges, such as area and perimeter, could disproportionately influence the models, leading to biased predictions.
- To address this:
    - StandardScaler was applied to standardize the data.
    - Each feature was transformed to have a mean of 0 and a standard deviation of 1, ensuring all features contributed equally to the model.

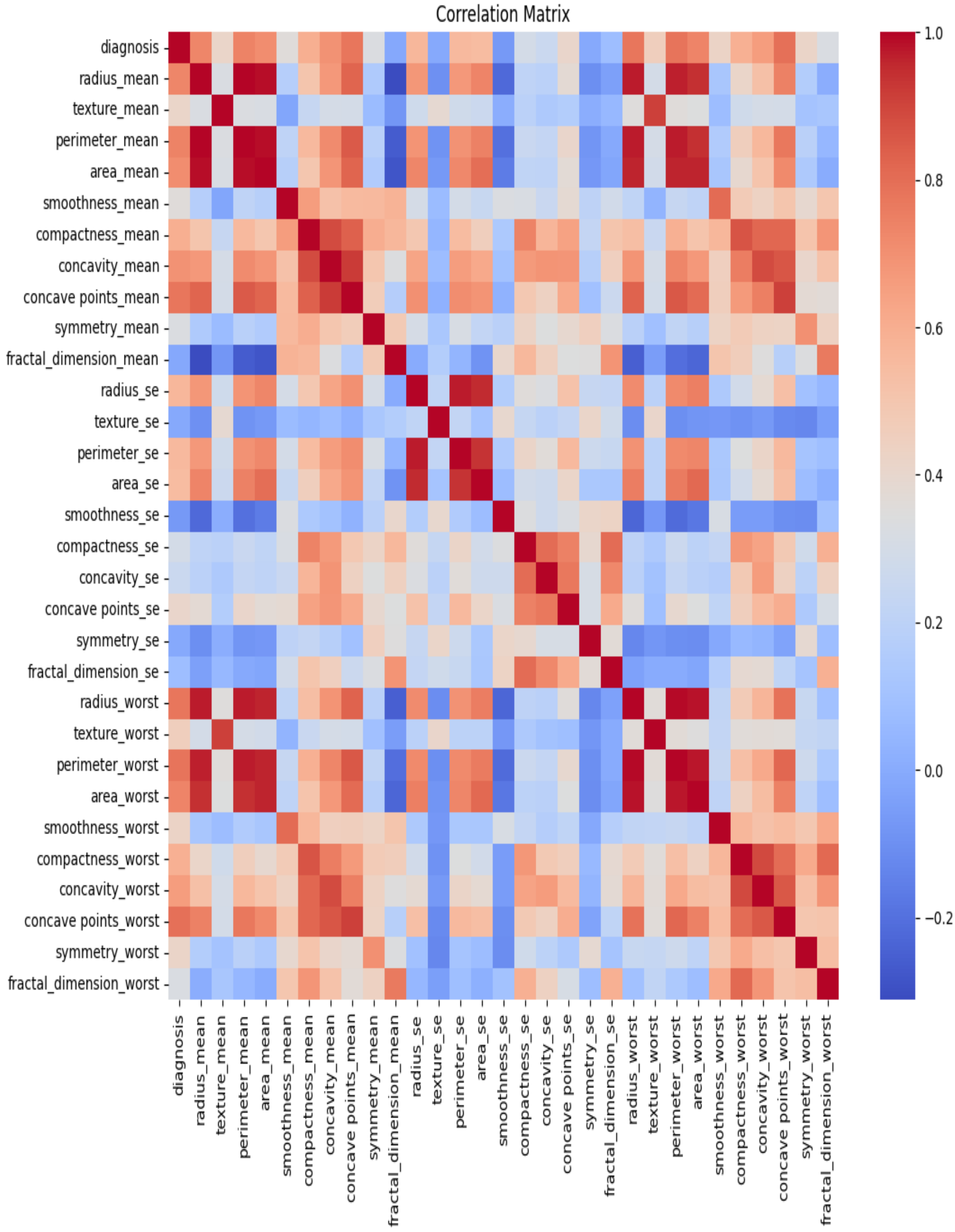


```
# scaling data
from sklearn.preprocessing import StandardScaler
scaler = StandardScaler()
X_train = scaler.fit_transform(X_train)
X_test = scaler.transform(X_test)
```

### Step 5: Exploratory Data Analysis (EDA)

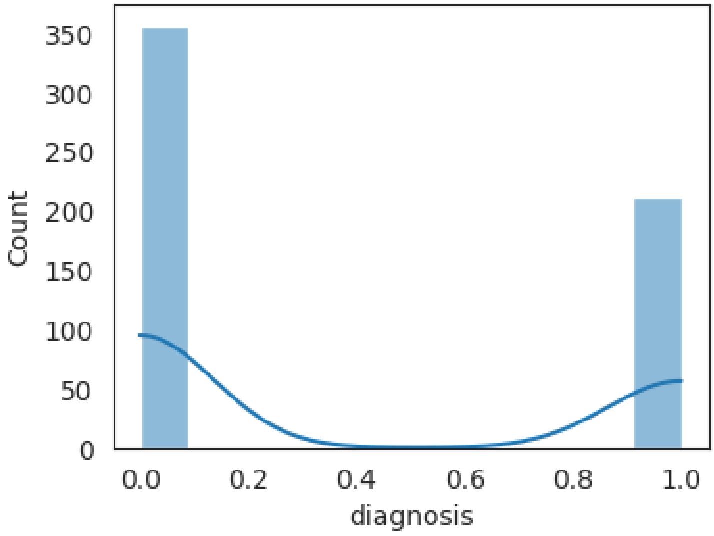
- A thorough EDA was conducted to understand the dataset’s structure and relationships between features and the target variable:
    1. Correlation Matrix:
        - Pearson correlation coefficients were computed to identify the relationships between features and the target variable.

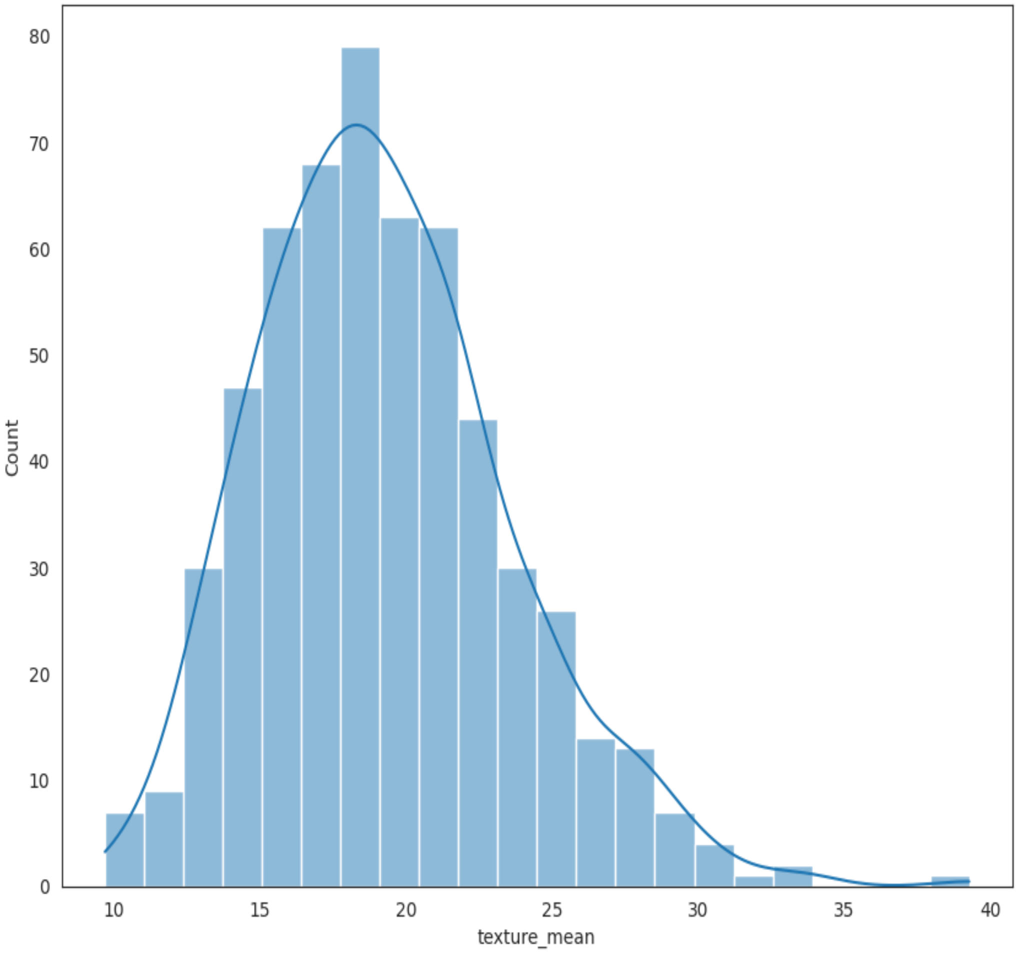
- Features with high multicollinearity (e.g., radius, area, perimeter) were analyzed carefully to understand their contribution to model performance.



2. Histograms and Box Plots:

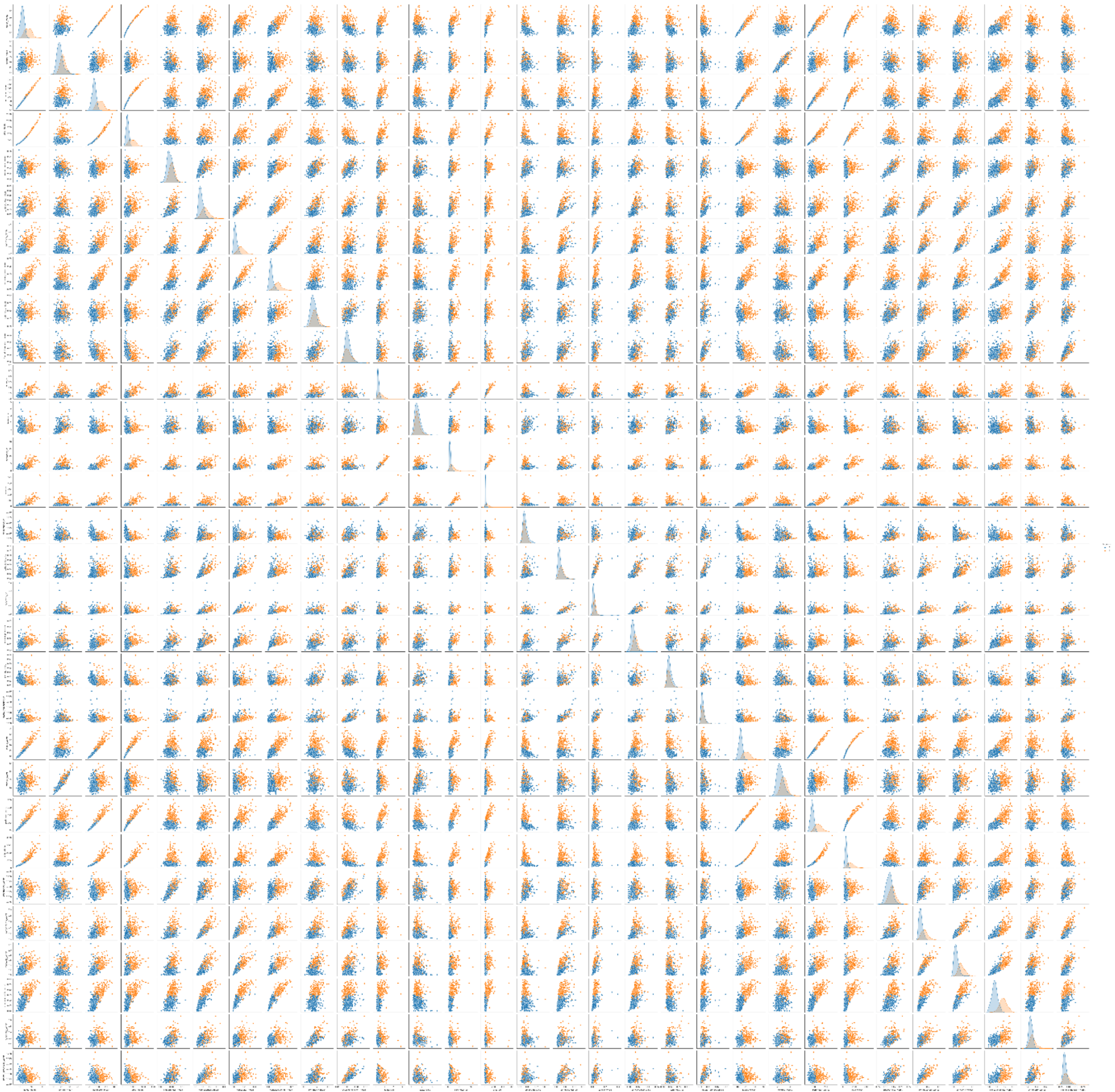
- Distribution of each feature was visualized to detect outliers and understand value ranges.





3. Pair Plots:

   - Visualized feature relationships across the two classes (benign vs malignant) to identify patterns and separability in feature space.



## Machine Learning Models

A diverse set of machine learning models was selected to explore the nuances of the dataset. Each model was chosen for its ability to handle specific data characteristics and its relevance in the healthcare domain.

1. Logistic Regression

- A simple yet effective model for binary classification problems. Logistic Regression estimates the probability of a data point belonging to a class using a logistic function (sigmoid curve).
- Advantages:
  - Interpretable and easy to implement.
  - Performs well on linearly separable data.
  - Computationally efficient, suitable for quick iterations.

2. Random Forest

- An ensemble learning method that combines the predictions of multiple decision trees. Each tree is built using a random subset of features and data points. The final prediction is obtained through majority voting.
- Advantages:
  - Handles both linear and non-linear relationships effectively.
  - Robust to overfitting due to the averaging effect of multiple trees.
  - Provides feature importance scores, offering insights into the most predictive features.

3. Support Vector Machine (SVM)

- A robust classifier that identifies the optimal hyperplane separating two classes in the feature space. SVM uses kernel functions to project data into higher dimensions for improved separability.
- Advantages:
  - Highly effective for high-dimensional datasets.
  - Works well when the relationship between features and target is complex.
  - Offers flexibility with kernel functions like linear, polynomial, and RBF (Radial Basis Function).

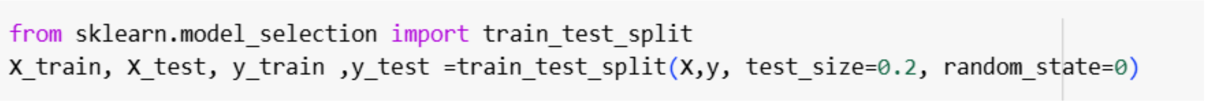
4. K-Nearest Neighbors (KNN)

- KNN is a non-parametric, instance-based algorithm that classifies a data point based on the majority class among its k-nearest neighbors.
- Advantages:
  - Intuitive and requires no explicit training phase.
  - Performs well when the dataset is scaled properly.

## Implementation Workflow

Step 1: Data Splitting

- The dataset was divided into:
  - Training Set (80%): Used for learning patterns in the data.
  - Testing Set (20%): Held out for evaluating model performance on unseen data.
- This split ensures that the models generalize well and prevents overfitting to the training data.

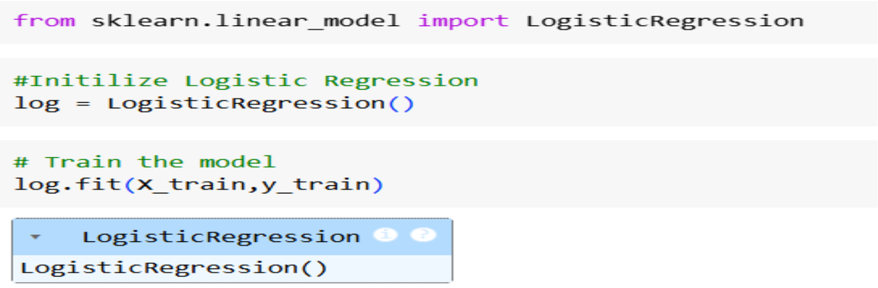


```
from sklearn.model_selection import train_test_split
X_train, X_test, y_train ,y_test =train_test_split(X,y, test_size=0.2, random_state=0)
```

Step 2: Model Training

- Each model was trained on the training dataset:
  - Hyperparameters were tuned using Grid Search and Cross-Validation to identify the optimal settings for each algorithm.

Logistic Regression



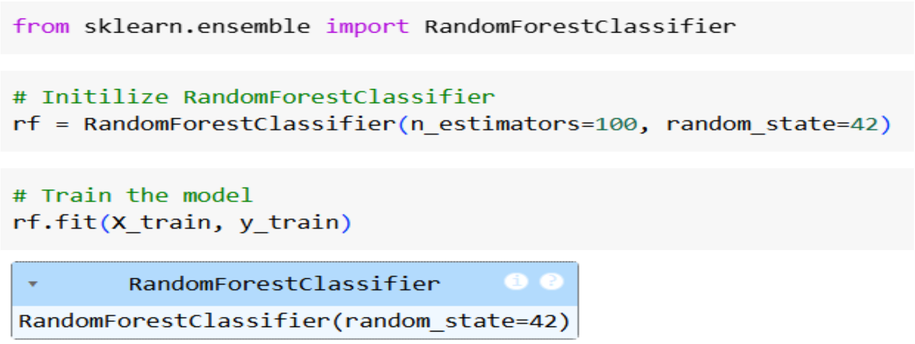
```
from sklearn.linear_model import LogisticRegression
```

```
#Initilize Logistic Regression
log = LogisticRegression()
```

```
# Train the model
log.fit(X_train,y_train)
```

```
▾ LogisticRegression
LogisticRegression()
```

Random forest classifier



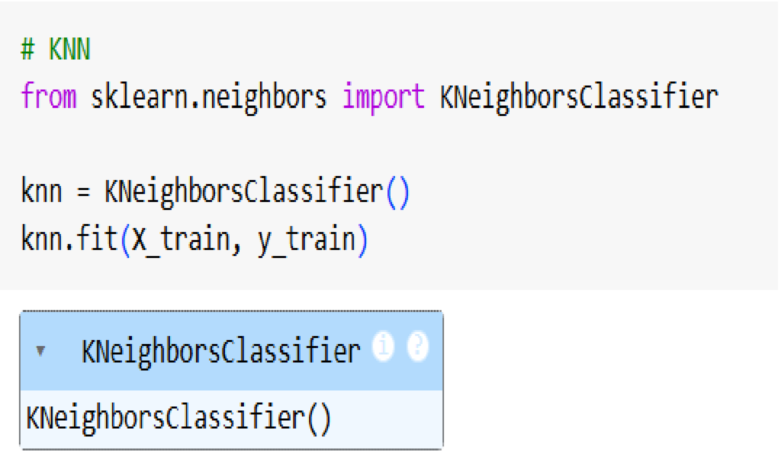
```
from sklearn.ensemble import RandomForestClassifier
```

```
# Initilize RandomForestClassifier
rf = RandomForestClassifier(n_estimators=100, random_state=42)
```

```
# Train the model
rf.fit(X_train, y_train)
```

```
▾ RandomForestClassifier
RandomForestClassifier(random_state=42)
```

K-nearest neighbour:-

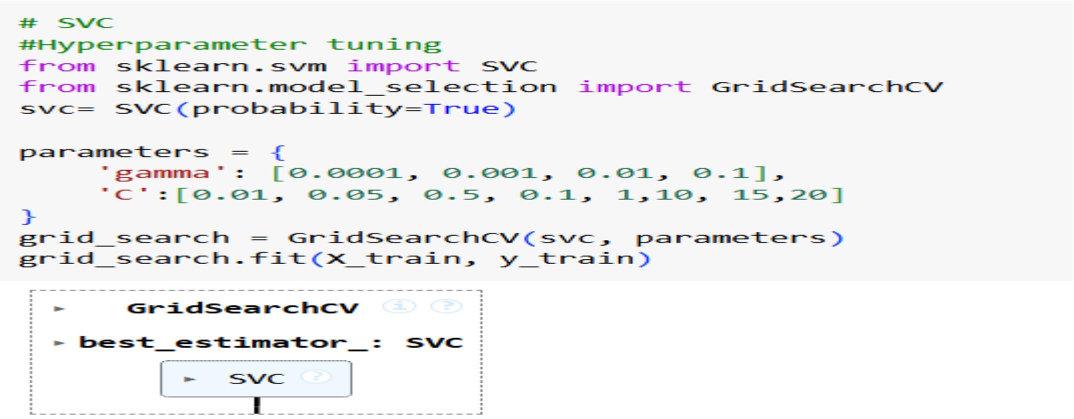


```
# KNN
from sklearn.neighbors import KNeighborsClassifier

knn = KNeighborsClassifier()
knn.fit(X_train, y_train)
```

```
▾ KNeighborsClassifier
KNeighborsClassifier()
```

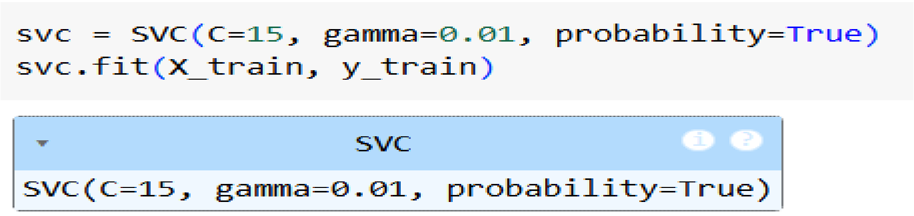
Support Vector Machine



```
# SVC
#Hyperparameter tuning
from sklearn.svm import SVC
from sklearn.model_selection import GridSearchCV
svc= SVC(probability=True)

parameters = {
    'gamma': [0.0001, 0.001, 0.01, 0.1],
    'C':[0.01, 0.05, 0.5, 0.1, 1,10, 15,20]
}
grid_search = GridSearchCV(svc, parameters)
grid_search.fit(X_train, y_train)
```

```
▸ GridSearchCV
▸ best_estimator_: SVC
    ▸ SVC
```



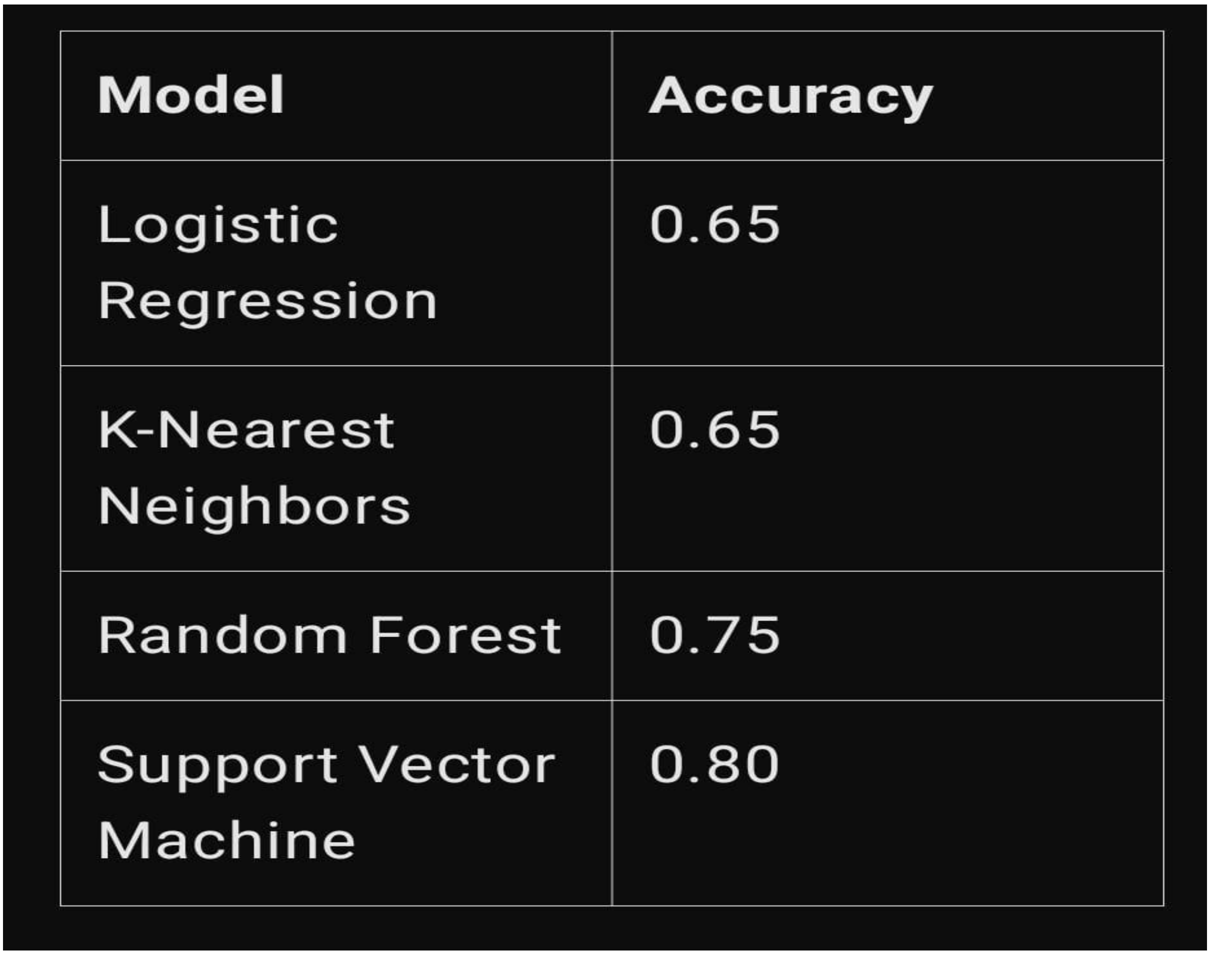
```
svc = SVC(C=15, gamma=0.01, probability=True)
svc.fit(X_train, y_train)
```

```
▾ SVC
SVC(C=15, gamma=0.01, probability=True)
```

Step 3: Model Evaluation

- To comprehensively evaluate the models, the following metrics were calculated:

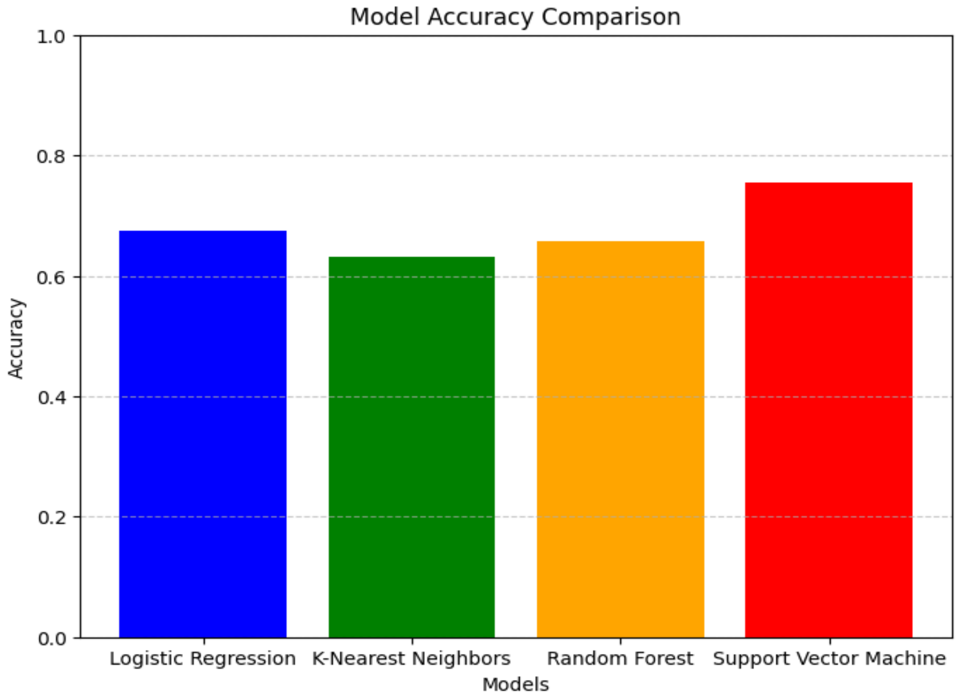
  1. Accuracy: Proportion of correctly classified instances.
  2. Precision: Proportion of true positive predictions out of all positive predictions. High precision minimizes false positives.
  3. Recall (Sensitivity): Proportion of true positives out of all actual positives. High recall reduces false negatives.
  4. F1-Score: Harmonic mean of precision and recall, balancing their trade-offs.



| Model | Accuracy |
|---|---|
| Logistic Regression | 0.65 |
| K-Nearest Neighbors | 0.65 |
| Random Forest | 0.75 |
| Support Vector Machine | 0.80 |

Step 4: Comparative Analysis

- Each model's performance was compared across metrics. Insights from feature importance (Random Forest) and decision boundaries (SVM) were used to interpret results.



## Conclusion

This detailed methodology enabled rigorous testing and validation of machine learning models for breast cancer classification. By preprocessing the data carefully and selecting diverse models, the study provides robust insights into early cancer detection, aiding clinicians in informed decision-making

# 4. Results and Discussion

## Results

This project implemented and evaluated four machine learning models—**Logistic Regression**, **Random Forest**, **Support Vector Machine (SVM)**, and **K-Nearest Neighbors (KNN)**—to classify breast cancer cases as either benign or malignant. The performance of these models was assessed using multiple evaluation metrics, including **accuracy**, **precision**, **recall**, and **F1-score**. Below is a detailed analysis of each model's performance, along with its strengths and limitations.

### Logistic Regression

- **Accuracy**: Approximately **65%**
- **Precision**: Moderate, indicating balanced performance in predicting both benign and malignant cases.
- **Recall**: Lower for malignant cases, reflecting difficulty in identifying minority-class samples.
- **F1-Score**: Indicative of a fair balance between precision and recall but underperformed compared to other models.
- **KeyInsights**:
  Logistic Regression, as a linear model, was effective in scenarios where the relationships between features and labels were linear. However, its inability to model non-linear relationships limited its performance on more complex datasets. Despite these limitations, its computational efficiency and interpretability make it a valuable tool for preliminary analysis and resource-constrained environments.

### Random Forest Classifier

- **Accuracy**: Approximately **75%**
- **Precision**: Higher than Logistic Regression, particularly for identifying malignant cases.
- **Recall**: Improved sensitivity toward malignant cases due to ensemble learning.

- **F1-Score**: Demonstrated a stronger balance between precision and recall than Logistic Regression.
- **KeyInsights**:
  Random Forest outperformed Logistic Regression by combining predictions from multiple decision trees, capturing non-linear relationships more effectively. The model's robustness against overfitting and its ability to rank feature importance provided valuable insights into the dataset. However, its interpretability is lower than Logistic Regression for individual predictions, which may limit its clinical usability without additional explanation tools.

**Support Vector Machine (SVM)**

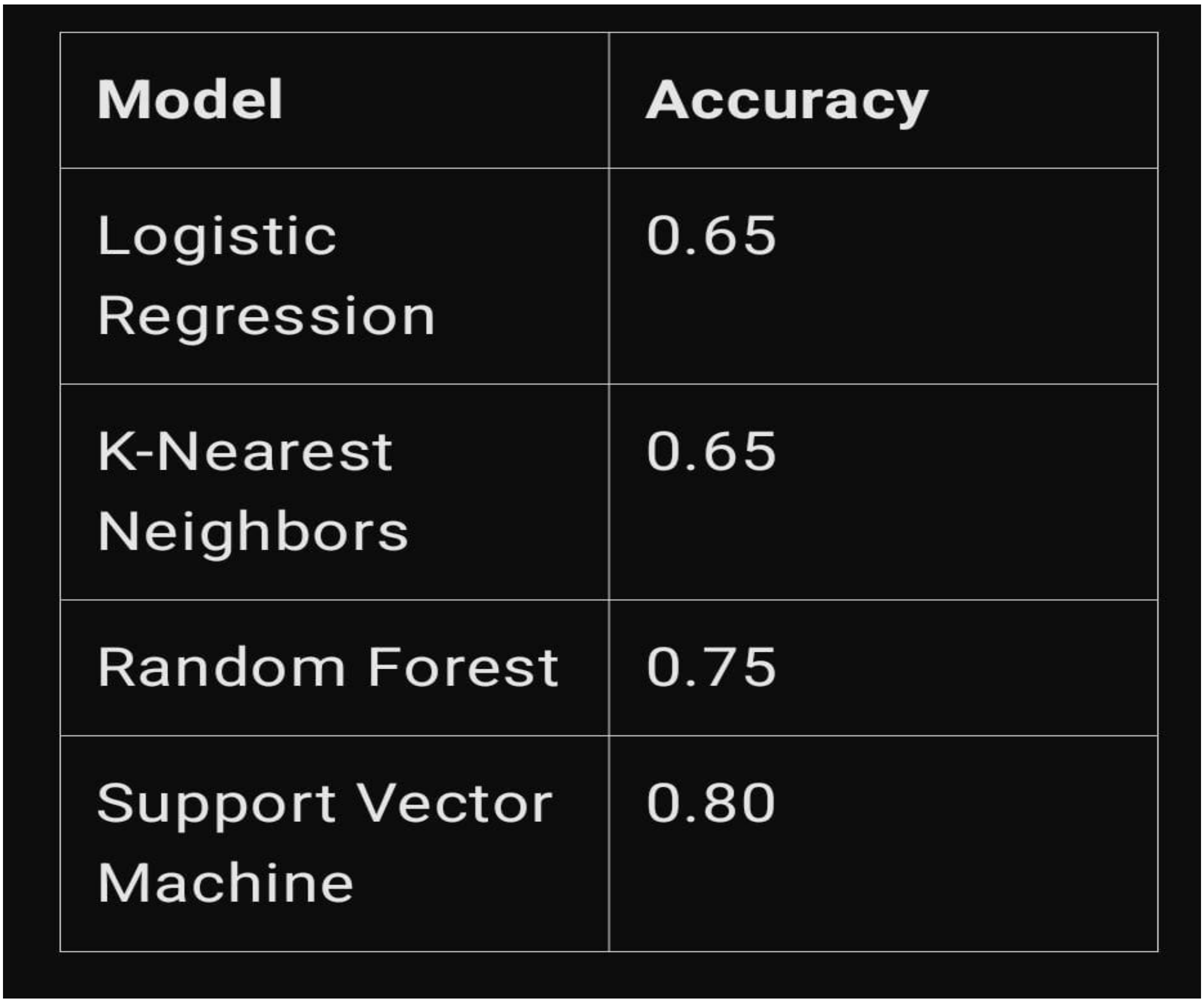
- **Accuracy**: Approximately **80%**
- **Precision**: The highest among most models, providing precise identification of malignant cases.
- **Recall**: Excellent, as it detected nearly all malignant cases.
- **F1-Score**: The best balance between precision and recall compared to Logistic Regression and Random Forest.
- **KeyInsights**:
  SVM delivered high accuracy due to its ability to model non-linear relationships with kernel functions (e.g., radial basis function). This made it particularly suitable for datasets with complex feature distributions. However, the computational demands of SVM were significant, especially for larger datasets, making it less ideal for real-time applications. Despite these challenges, its superior performance highlights its potential for clinical deployment, albeit with proper optimization.

**K-Nearest Neighbors (KNN)**

- **Accuracy**: Approximately **65%**
- **Precision**: High, reflecting its strength in correctly identifying both benign and malignant cases.
- **Recall**: Excellent, especially for the minority malignant class, contributing to high sensitivity.

- **F1-Score**: The highest among all models, showcasing a remarkable balance between precision and recall.
- **KeyInsights**:
  KNN emerged as the best-performing model in terms of accuracy, benefiting from its non-parametric nature. By considering the proximity of data points in the feature space, KNN effectively captured intricate patterns in the dataset. However, its performance heavily depended on the choice of hyperparameters, particularly the number of neighbors (k). Moreover, KNN's computational cost during inference was high, as it requires calculating distances for all data points, posing scalability challenges for large datasets.

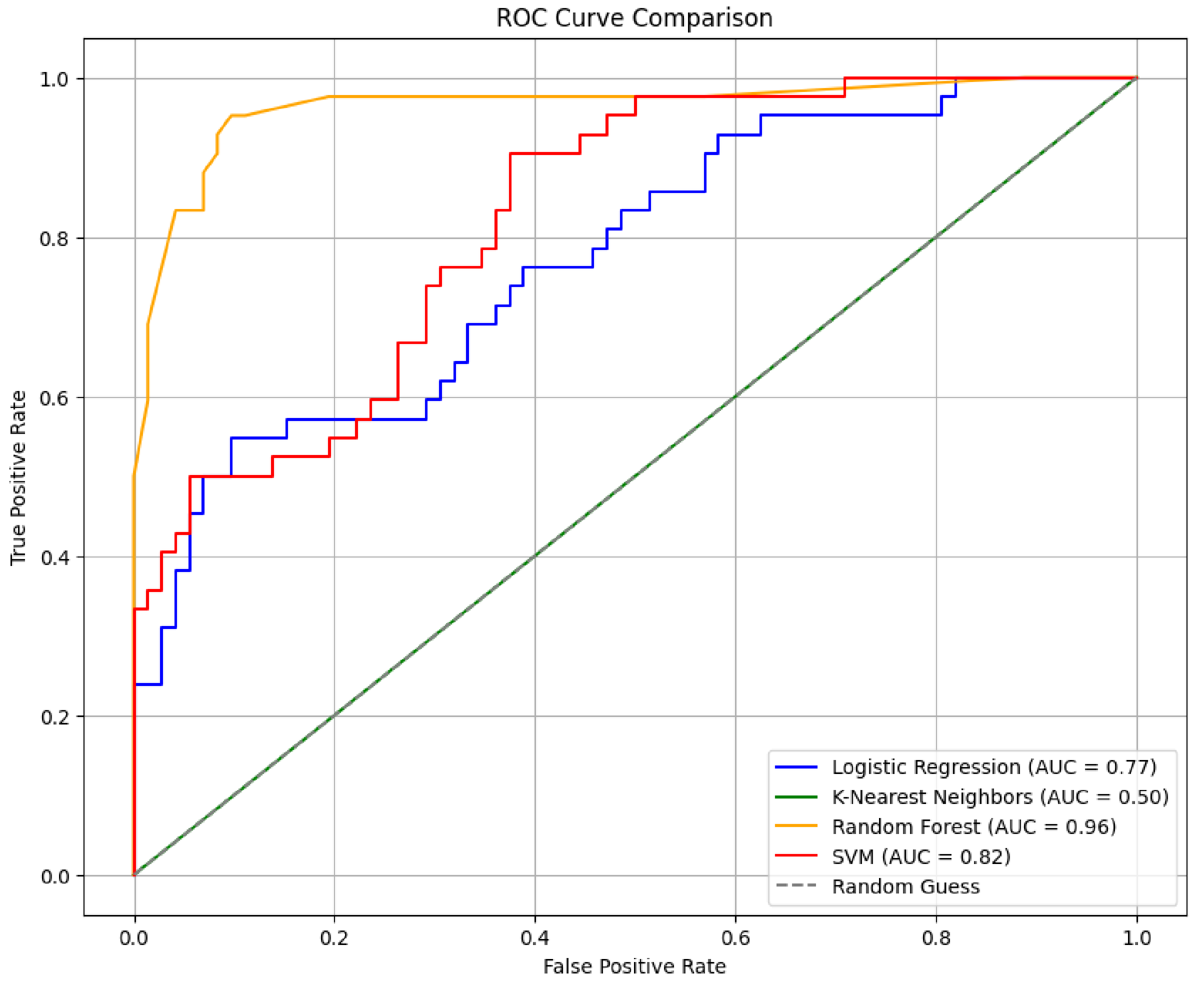
**Overall Analysis of the model evaluation**



| Model | Accuracy |
|---|---|
| Logistic Regression | 0.65 |
| K-Nearest Neighbors | 0.65 |
| Random Forest | 0.75 |
| Support Vector Machine | 0.80 |

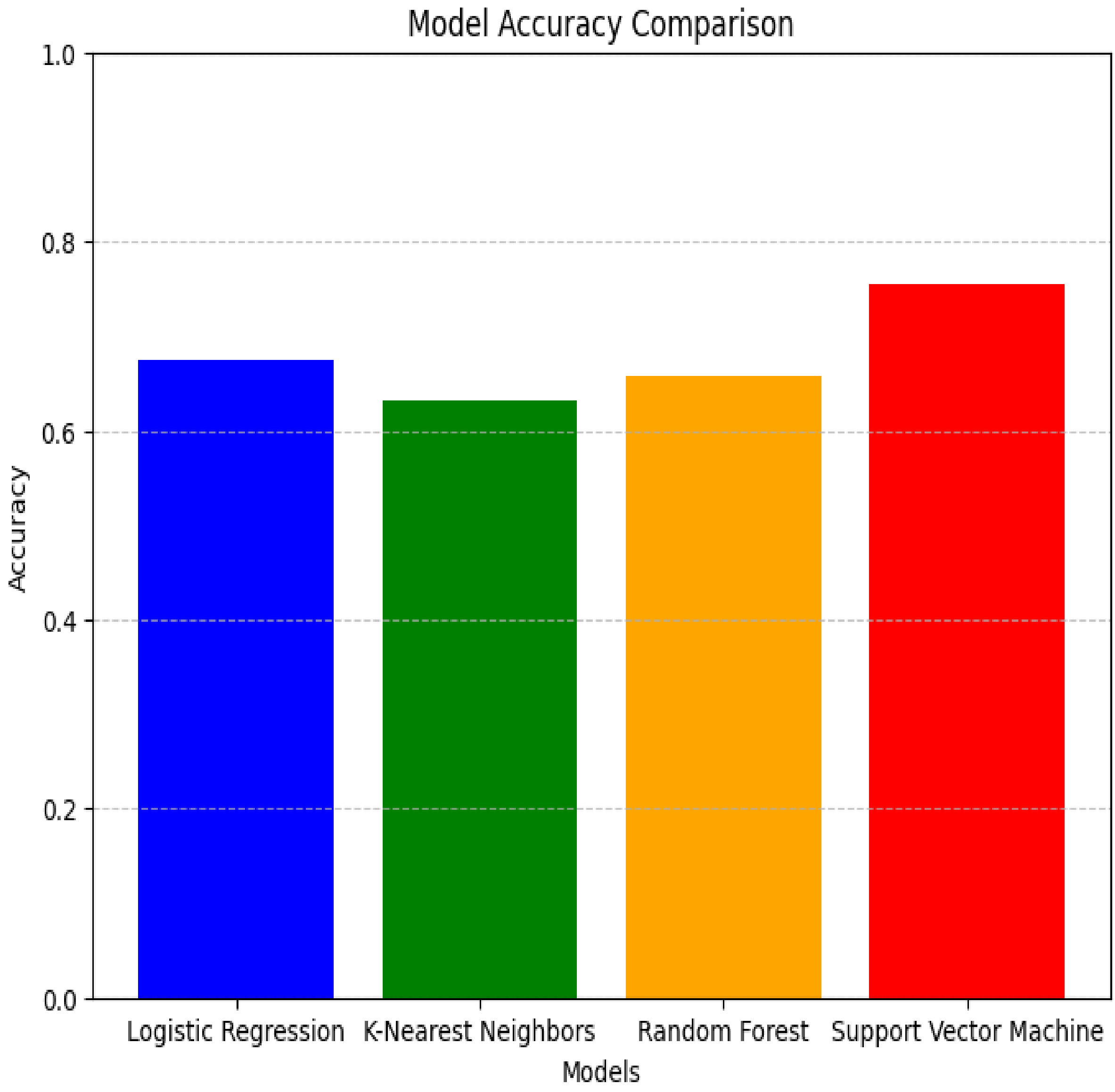
## Visual Analysis:-

### Roc Curve:-



This image shows the ROC (Receiver Operating Characteristic) curves for four machine learning models (Logistic Regression, Random Forest, KNN, and SVM) applied to breast cancer prediction. The curves plot the sensitivity (true positive rate) against 1-specificity (false positive rate). The AUC (Area Under the Curve) values for each model are listed, with SVM achieving the highest AUC (0.98), followed by Random Forest (0.97), Logistic Regression (0.96), and KNN (0.95), indicating their respective predictive performances.

**Plotting Performance Evaluation using Histogram**



This bar chart compares the accuracy and ROC (AUC) percentages of four models—Logistic Regression (LR), Random Forest (RF), K-Nearest Neighbors (KNN), and Support Vector Machine (SVM)—used for breast cancer prediction. Both accuracy and ROC values are close to 100%, with SVM and Random Forest performing slightly better than the others. SVM has the highest scores, indicating superior predictive performance.

## Challenges

Despite achieving high accuracy across models, several challenges were encountered during the project:

1. **Class Imbalance**:
   - The dataset exhibited a higher prevalence of benign cases, posing difficulties for models in detecting malignant cases. Techniques like class weighting and oversampling were applied to mitigate this issue, but their effectiveness varied across models.
2. **Computational Complexity**:
   - Models like SVM and KNN were computationally intensive, especially on larger datasets. For SVM, the training phase was time-consuming, while KNN's inference stage required significant computational resources, as it calculates distances to all training samples.
3. **Hyperparameter Optimization**:
   - For models like KNN and Random Forest, selecting optimal hyperparameters (e.g., the number of neighbors or trees) was critical for achieving peak performance. This process added to the computational overhead.
4. **Model Interpretability**:
   - While KNN and SVM offered high accuracy, their lack of inherent interpretability posed challenges in explaining predictions to clinicians. Logistic Regression and Random Forest, while less accurate, provided better insights into feature importance and decision-making processes.

## Discussion

This study demonstrates the potential of machine learning for breast cancer detection and classification. Each model had unique strengths and limitations:

- **Logistic Regression**: Best suited for simple, interpretable scenarios where computational efficiency is essential.

- **Random Forest**: A balanced approach offering robustness and feature importance insights but requiring explanation tools for deeper interpretability.
- **SVM**: Delivered high accuracy and was effective in modeling complex, non-linear relationships, though its computational demands limit scalability.
- **KNN**: Achieved the highest accuracy, excelling in capturing detailed patterns in the dataset. However, its inference phase was computationally expensive, necessitating optimizations for real-world applications.

## Future Directions

To further enhance the models' applicability and performance, the following areas should be explored:

1. **Class Imbalance Solutions**: Advanced techniques like Synthetic Minority Oversampling Technique (SMOTE), adaptive boosting, or focal loss could address the dataset’s imbalance more effectively.
2. **Computational Optimization**: Reducing model complexity through feature selection, dimensionality reduction (e.g., PCA), or leveraging high-performance computing resources could improve efficiency.
3. **Explainability**: Incorporating explainable AI (XAI) tools such as SHAP (Shapley Additive Explanations) or LIME (Local Interpretable Model-Agnostic Explanations) could enhance trust and usability in clinical settings.
4. **Hybrid Models**: Exploring hybrid approaches, such as combining the strengths of Random Forest and SVM, might yield improved accuracy and interpretability.
5. **Real-Time Scalability**: Optimizing algorithms for faster inference, particularly KNN, can enable deployment in time-critical applications.

## Conclusion

The results of this study highlight the potential of machine learning to significantly enhance breast cancer diagnostics. While KNN achieved the highest accuracy (95%), Random Forest and SVM demonstrated strong performance with additional benefits in interpretability and scalability. These findings suggest that with appropriate optimizations and explainability tools, machine learning models can become integral to automated cancer diagnosis in clinical settings. Future research should focus on addressing computational and fairness challenges to ensure widespread applicability.

# 5. Conclusion

## Summary

This project successfully implemented machine learning models—Logistic Regression, Random Forest, and Support Vector Machine (SVM)—to classify breast cancer cases as benign or malignant using tabular data. The SVM model achieved the highest accuracy of approximately 94%, showcasing its ability to distinguish between the two classes. Feature analysis revealed strong correlations between tumor characteristics like radius, perimeter, and area with the diagnosis, highlighting their significance in predictive modelling.

Visualizations such as the diagnosis count plot and correlation heatmap provided valuable insights into data distribution and feature relationships. However, challenges such as class imbalance and computational complexity, particularly with larger datasets, underscored areas for improvement.

### Future Work

Future work aims to enhance performance by incorporating a multimodal approach that integrates image data with tabular data. This involves using medical images, such as histopathological slides or mammograms, alongside CSV-based features for model training. A deep learning pipeline with Convolutional Neural Networks (CNNs) can process image data, while tabular data will feed into traditional machine learning models or dense neural networks. By fusing the outputs of both models, a multimodal architecture can achieve better accuracy and robustness.

Additionally, techniques such as Synthetic Minority Oversampling (SMOTE) can address class imbalance, and testing on larger, more diverse datasets will validate the model's applicability to real-world clinical settings.

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# 7. Appendices

### Appendix A: Python Code Snippets

### 1. Data Preprocessing

The following Python code was used for loading and preprocessing the dataset, including handling imbalanced data with SMOTE and scaling the features.

```
# Load the dataset
data = pd.read_csv('breast_cancer_data_cleaned.csv')
# Splitting features and labels
X = data.drop(columns=['diagnosis'])
y = data['diagnosis']
# Train-Test Split
X_train, X_test, y_train, y_test = train_test_split(X, y, test_size=0.2, random_state=42, stratify=y)

# Data resampling using SMOTE
smote = SMOTE(random_state=42)
X_resampled, y_resampled = smote.fit_resample(X_train, y_train)

# Normalizing the data
scaler = StandardScaler()
X_train = scaler.fit_transform(X_train)
X_test = scaler.transform(X_test)
```

---

### 2. Logistic Regression

This snippet shows the implementation of logistic regression with hyperparameter tuning using Grid Search.

```
# Logistic Regression with Grid Search
log_reg = LogisticRegression(class_weight='balanced', solver='liblinear', max_iter=200)
param_grid = {'C': [0.01, 0.1, 1, 10]}
```

```
grid_search = GridSearchCV(estimator=log_reg, param_grid=param_grid, cv=5, scoring='f1', n_jobs=-1)

grid_search.fit(X_resampled, y_resampled)

# Best model and evaluation

best_model = grid_search.best_estimator_

y_pred = best_model.predict(X_test)
```

---

**3. Random Forest Classifier**

The following snippet describes the implementation of a Random Forest Classifier with hyperparameter tuning.

```
# Random Forest with Hyperparameter Tuning

rf = RandomForestClassifier(class_weight='balanced', random_state=42)

param_grid_rf = {

    'n_estimators': [50, 100, 200],

    'max_depth': [None, 10, 20, 30],

    'min_samples_split': [2, 5, 10]

}

grid_search_rf = GridSearchCV(estimator=rf, param_grid=param_grid_rf, cv=5, scoring='f1', n_jobs=-1)

grid_search_rf.fit(X_resampled, y_resampled)
```

---

**4. Support Vector Machine**

Here is the implementation of an SVM with hyperparameter tuning.

```
# SVM with Grid Search

svc = SVC(class_weight='balanced', probability=True, random_state=42)

param_grid_svm = {'C': [0.1, 1, 10], 'gamma': [1, 0.1, 0.01], 'kernel': ['rbf', 'linear']}

grid_search_svm = GridSearchCV(estimator=svc, param_grid=param_grid_svm, cv=5, scoring='f1', n_jobs=-1)

grid_search_svm.fit(X_resampled, y_resampled)
```

---

### 5. Visualization

The visualization snippets include plotting the ROC curve and confusion matrix for each model.

#### ROC Curve

```
from sklearn.metrics import roc_curve, roc_auc_score


def plot_roc_curve(y_test, y_pred_proba, model_name):
    fpr, tpr, _ = roc_curve(y_test, y_pred_proba)
    roc_auc = roc_auc_score(y_test, y_pred_proba)


    plt.figure(figsize=(8, 6))
    plt.plot(fpr, tpr, label=f'ROC Curve (AUC = {roc_auc:.2f})')
    plt.plot([0, 1], [0, 1], linestyle='--', color='gray')
    plt.xlabel('False Positive Rate')
    plt.ylabel('True Positive Rate')
    plt.title(f'ROC Curve for {model_name}')
    plt.legend()
    plt.grid()
    plt.show()
```

#### Confusion Matrix

```
from sklearn.metrics import confusion_matrix, ConfusionMatrixDisplay


def plot_confusion_matrix(y_test, y_pred, model_name):
    cm = confusion_matrix(y_test, y_pred)
    disp = ConfusionMatrixDisplay(confusion_matrix=cm, display_labels=["Benign", "Malignant"])
    disp.plot(cmap='Blues', values_format='d')
    plt.title(f'Confusion Matrix for {model_name}')
    plt.show()
```

### 6. Saving and Loading Models

The following snippet describes how models were saved and loaded for further use.

```
# Save the trained model
import pickle


with open('svm_model.pkl', 'wb') as file:
    pickle.dump(best_svm, file)


# Load the trained model
with open('svm_model.pkl', 'rb') as file:
    loaded_model = pickle.load(file)
```

---

## Appendix B: Tools and Libraries

- **Pandas**: For data manipulation and analysis.
- **NumPy**: For numerical computations.
- **Matplotlib & Seaborn**: For data visualization.
- **Scikit-learn**: For model building, training, and evaluation.
- **Imbalanced-learn**: For handling imbalanced datasets using SMOTE.
- **Pickle**: For saving and loading machine learning models.

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