1. Data Exploration and Preprocessing

```
# Step 1: Install necessary libraries (only if required)
!pip install scikit-learn pandas matplotlib seaborn
# Step 2: Import libraries
import pandas as pd
import numpy as np
from sklearn.model_selection import train_test_split
from sklearn.preprocessing import StandardScaler
from sklearn.impute import SimpleImputer
import matplotlib.pyplot as plt
import seaborn as sns
# Step 3: Load the dataset (assuming it's a CSV file)
df = pd.read_csv('/content/Breast Cancer Diagnosis Dataset with Tumor Characteristics.csv')
# Step 4: Exploratory Data Analysis (EDA)
print("First five rows of the dataset:")
print(df.head())
# Check for missing values
print("Checking for missing values:")
print(df.isnull().sum())
# Step 5: Convert categorical target (diagnosis) to numeric (Malignant = 1, Benign = 0)
df['diagnosis'] = df['diagnosis'].map({'M': 1, 'B': 0})
# Step 6: Define features (X) and target (y)
X = df.drop('diagnosis', axis=1) # Features
y = df['diagnosis'] # Target
# Step 7: Split data into training and testing sets (80% train, 20% test)
X_train, X_test, y_train, y_test = train_test_split(X, y, test_size=0.2, random_state=42)
# Step 8: Handle missing values with SimpleImputer (impute using mean)
imputer = SimpleImputer(strategy='mean')
# Apply imputation to training and testing sets
X_train = imputer.fit_transform(X_train)
X_test = imputer.transform(X_test)
# Step 9: Normalize features using StandardScaler
scaler = StandardScaler()
X_train = scaler.fit_transform(X_train)
X_test = scaler.transform(X_test)
print("Data preprocessing complete.")
```

4	16.6/	152.20	15/5.0	0.13/4	
	compactness_worst	concavity_worst	concave points_worst	symmetry_worst	\
0	0.6656	0.7119	0.2654	0.4601	
1	0.1866	0.2416	0.1860	0.2750	
2	0.4245	0.4504	0.2430	0.3613	
3	0.8663	0.6869	0.2575	0.6638	
4	0.2050	0.4000	0.1625	0.2364	
	fractal_dimension_w	vorst Unnamed: 32			
0	0.1	.1890 NaN			
1	0.0	8902 NaN			
2	0.0	98758 NaN			
3	0.1	.7300 NaN			
4	0.0	7678 NaN			

[5 rows x 33 columns]

2. Model Development

```
# Step 10: Import required libraries for model development
from sklearn.neighbors import KNeighborsClassifier
from sklearn.linear_model import LogisticRegression

# Step 11: Develop K-Nearest Neighbors (KNN) model
knn = KNeighborsClassifier(n_neighbors=3)
knn.fit(X_train, y_train)

# Step 12: Develop Logistic Regression model for comparison
log_reg = LogisticRegression()
log_reg.fit(X_train, y_train)

print("Model development complete.")

Nodel development complete."
```

3. Model Evaluation

```
# Step 13: Import evaluation metrics
from sklearn.metrics import accuracy_score, classification_report, confusion_matrix
# Step 14: Evaluate KNN model
y_pred_knn = knn.predict(X_test)
print("KNN Model Performance:")
print("Accuracy:", accuracy_score(y_test, y_pred_knn))
print("Classification Report:\n", classification_report(y_test, y_pred_knn))
# Step 15: Confusion matrix for KNN
conf_matrix_knn = confusion_matrix(y_test, y_pred_knn)
sns.heatmap(conf_matrix_knn, annot=True, fmt='d', cmap='Blues')
plt.title('Confusion Matrix for KNN')
plt.xlabel('Predicted')
plt.ylabel('Actual')
plt.show()
# Step 16: Evaluate Logistic Regression model
y_pred_log_reg = log_reg.predict(X_test)
print("Logistic Regression Model Performance:")
print("Accuracy:", accuracy_score(y_test, y_pred_log_reg))
print("Classification Report:\n", classification_report(y_test, y_pred_log_reg))
# Step 17: Confusion matrix for Logistic Regression
conf_matrix_log_reg = confusion_matrix(y_test, y_pred_log_reg)
```

```
sns.heatmap(conf_matrix_log_reg, annot=True, fmt='d', cmap='Blues')
plt.title('Confusion Matrix for Logistic Regression')
plt.xlabel('Predicted')
plt.ylabel('Actual')
plt.show()

print("Model evaluation complete.")
```



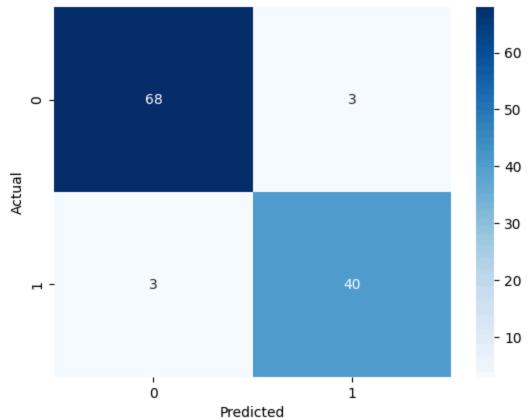
KNN Model Performance:

Accuracy: 0.9473684210526315

Classification Report:

	precision	recall	f1-score	support
0	0.96	0.96	0.96	71
1	0.93	0.93	0.93	43
accuracy			0.95	114
macro avg	0.94	0.94	0.94	114
weighted avg	0.95	0.95	0.95	114





Logistic Regression Model Performance:

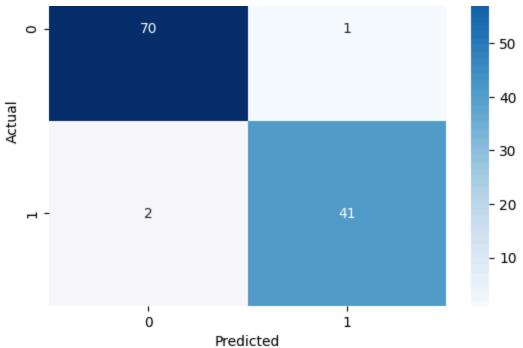
Accuracy: 0.9736842105263158

Classification Report:

	precision	recall	f1-score	support
0 1	0.97 0.98	0.99 0.95	0.98 0.96	71 43
accuracy macro avg weighted avg	0.97 0.97	0.97 0.97	0.97 0.97 0.97	114 114 114







Model evaluation complete.

Logistic Regression is better than KNN for this task. It has an accuracy of 97.4%, while KNN is at 94.7%.

Logistic Regression is also more accurate in predicting malignant tumors, with 98% precision compared to KNN's 93%. Overall, Logistic Regression is the better choice.

4. Report and Visualizations

```
# Step 18: Compare models and report findings
print("Comparison of KNN and Logistic Regression Models:")

# KNN Results
knn_accuracy = accuracy_score(y_test, y_pred_knn)
print(f"KNN Accuracy: {knn_accuracy}")
print("KNN Classification Report:\n", classification_report(y_test, y_pred_knn))

# Logistic Regression Results
log_reg_accuracy = accuracy_score(y_test, y_pred_log_reg)
print(f"Logistic Regression Accuracy: {log_reg_accuracy}")
print("Logistic Regression Classification Report:\n", classification_report(y_test, y_pred_l

# Step 19: Optional Visualizations (decision boundaries if applicable, or data distribution)
# Example: Distribution of diagnosis values in the dataset
sns.countplot(x='diagnosis', data=df)
plt.title('Distribution of Diagnosis in the Dataset')
plt.show()
```

print("Report and visualizations complete.")

Comparison of KNN and Logistic Regression Models: KNN Accuracy: 0.9473684210526315

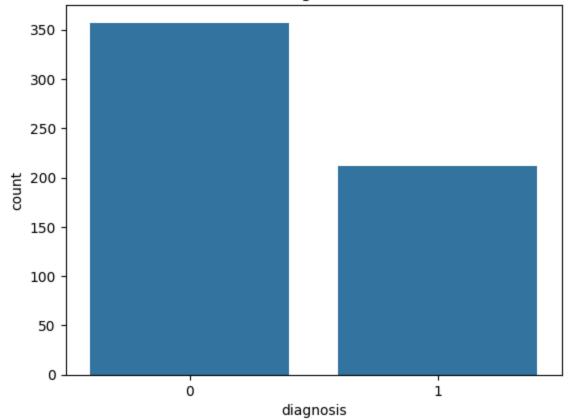
KNN Classification Report:

	precision	recall	f1-score	support
0	0.96	0.96	0.96	71
1	0.93	0.93	0.93	43
accuracy			0.95	114
macro avg	0.94	0.94	0.94	114
weighted avg	0.95	0.95	0.95	114

Logistic Regression Accuracy: 0.9736842105263158 Logistic Regression Classification Report:

	precision	recall	f1-score	support
0	0.97	0.99	0.98	71
1	0.98	0.95	0.96	43
accuracy			0.97	114
macna ava	0 07	9 07	0 07	111
weighted avg	0.97	0.97	0.97	114

Distribution of Diagnosis in the Dataset



Report and visualizations complete.

1. Data Preprocessing

- Loaded Dataset: Analyzed the data structure and checked for missing values.
- Handled Missing Values: Used mean imputation to replace missing values.
- Converted Target: Changed diagnosis labels ('M' for malignant and 'B' for benign) to 1 and 0.
- Split Data: Divided the dataset into training (80%) and testing (20%) sets.
- Normalized Features: Scaled the features for better model performance.

2. Model Development

• KNN: Used K-Nearest Neighbors with 3 neighbors.