DSC680 Project3: Beast Cancer Survival Prediction

Assignment 10.1

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In [1]:
```
# pip install xgboost imbalanced-learn scikit-optimize sweetviz
```

In [2]:
```
# Import the necessary libraries
import pandas as pd
import numpy as np
import seaborn as sns
import matplotlib.pyplot as plt
from sklearn.preprocessing import LabelEncoder, OrdinalEncoder
from sklearn.linear_model import LogisticRegression
from sklearn.svm import SVC
from sklearn.model_selection import GridSearchCV
from sklearn.ensemble import RandomForestClassifier
from sklearn.tree import DecisionTreeClassifier
from sklearn.model_selection import train_test_split
from sklearn.metrics import roc_curve, roc_auc_score, confusion_matrix, accuracy_sc
import sweetviz as sv
from sklearn.model_selection import train_test_split
from xgboost import XGBClassifier
from sklearn.metrics import classification_report, confusion_matrix, accuracy_score
from sklearn.preprocessing import LabelEncoder
from sklearn.feature_selection import mutual_info_classif
from scipy import stats as ss
from scipy.stats import chi2_contingency
from sklearn.preprocessing import OneHotEncoder
from imblearn.over_sampling import SMOTE

# Ignore warnings
import warnings
warnings.filterwarnings('ignore')

%matplotlib inline
```

In [3]:
```
# Load the Breast Cancer dataset into the data frame
breast_cancer_df = pd.read_csv('BRCA.csv')
breast_cancer_df
```

Out[3]:

	Patient_ID	Age	Gender	Protein1	Protein2	Protein3	Protein4	Tumour_Stage	Histology
0	TCGA-D8-A1XD	36.0	FEMALE	0.080353	0.42638	0.54715	0.273680	III	Infiltrating Ductal Carcinoma
1	TCGA-EW-A1OX	43.0	FEMALE	-0.420320	0.57807	0.61447	-0.031505	II	Mucinous Carcinoma
2	TCGA-A8-A079	69.0	FEMALE	0.213980	1.31140	-0.32747	-0.234260	III	Infiltrating Ductal Carcinoma
3	TCGA-D8-A1XR	56.0	FEMALE	0.345090	-0.21147	-0.19304	0.124270	II	Infiltrating Ductal Carcinoma
4	TCGA-BH-A0BF	56.0	FEMALE	0.221550	1.90680	0.52045	-0.311990	II	Infiltrating Ductal Carcinoma
...	...	...	...	...	...	...	...	...	...
336	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
337	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
338	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
339	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
340	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN

341 rows × 16 columns

In [4]:
```
# Display the information to understand the dataset
breast_cancer_df.info()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 341 entries, 0 to 340
Data columns (total 16 columns):
 #   Column              Non-Null Count  Dtype  
---  ------              --------------  -----  
 0   Patient_ID          334 non-null    object 
 1   Age                 334 non-null    float64
 2   Gender              334 non-null    object 
 3   Protein1            334 non-null    float64
 4   Protein2            334 non-null    float64
 5   Protein3            334 non-null    float64
 6   Protein4            334 non-null    float64
 7   Tumour_Stage        334 non-null    object 
 8   Histology           334 non-null    object 
 9   ER status           334 non-null    object 
 10  PR status           334 non-null    object 
 11  HER2 status         334 non-null    object 
 12  Surgery_type        334 non-null    object 
 13  Date_of_Surgery     334 non-null    object 
 14  Date_of_Last_Visit  317 non-null    object 
 15  Patient_Status      321 non-null    object 
dtypes: float64(5), object(11)
memory usage: 42.8+ KB
```

In [5]:
```
# Check for any missing values
breast_cancer_df.isna().sum()
```

Out[5]:
```
Patient_ID             7
Age                    7
Gender                 7
Protein1               7
Protein2               7
Protein3               7
Protein4               7
Tumour_Stage           7
Histology              7
ER status              7
PR status              7
HER2 status            7
Surgery_type           7
Date_of_Surgery        7
Date_of_Last_Visit    24
Patient_Status        20
dtype: int64
```

In [6]:
```
# Drop the missing values
# breast_cancer_df.dropna(how='all', inplace=True)
# breast_cancer_df.dropna(subset='Patient_Status', inplace = True)

# Filter rows with at least one NaN value
breast_cancer_df = breast_cancer_df.dropna()
breast_cancer_df.info()
```

```
<class 'pandas.core.frame.DataFrame'>
Index: 317 entries, 0 to 333
Data columns (total 16 columns):
 #   Column              Non-Null Count  Dtype  
---  ------              --------------  -----  
 0   Patient_ID          317 non-null    object 
 1   Age                 317 non-null    float64
 2   Gender              317 non-null    object 
 3   Protein1            317 non-null    float64
 4   Protein2            317 non-null    float64
 5   Protein3            317 non-null    float64
 6   Protein4            317 non-null    float64
 7   Tumour_Stage        317 non-null    object 
 8   Histology           317 non-null    object 
 9   ER status           317 non-null    object 
 10  PR status           317 non-null    object 
 11  HER2 status         317 non-null    object 
 12  Surgery_type        317 non-null    object 
 13  Date_of_Surgery     317 non-null    object 
 14  Date_of_Last_Visit  317 non-null    object 
 15  Patient_Status      317 non-null    object 
dtypes: float64(5), object(11)
memory usage: 42.1+ KB
```

In [7]:
```
breast_cancer_df
```

Out[7]:

	Patient_ID	Age	Gender	Protein1	Protein2	Protein3	Protein4	Tumour_Stage	Histology
0	TCGA-D8-A1XD	36.0	FEMALE	0.080353	0.42638	0.54715	0.273680	III	Infiltrating Ductal Carcinoma
1	TCGA-EW-A1OX	43.0	FEMALE	-0.420320	0.57807	0.61447	-0.031505	II	Mucinous Carcinoma
2	TCGA-A8-A079	69.0	FEMALE	0.213980	1.31140	-0.32747	-0.234260	III	Infiltrating Ductal Carcinoma
3	TCGA-D8-A1XR	56.0	FEMALE	0.345090	-0.21147	-0.19304	0.124270	II	Infiltrating Ductal Carcinoma
4	TCGA-BH-A0BF	56.0	FEMALE	0.221550	1.90680	0.52045	-0.311990	II	Infiltrating Ductal Carcinoma
...	...	...	...	...	...	...	...	...	...
329	TCGA-AN-A04A	36.0	FEMALE	0.231800	0.61804	-0.55779	-0.517350	III	Infiltrating Ductal Carcinoma
330	TCGA-A8-A085	44.0	MALE	0.732720	1.11170	-0.26952	-0.354920	II	Infiltrating Lobular Carcinoma
331	TCGA-A1-A0SG	61.0	FEMALE	-0.719470	2.54850	-0.15024	0.339680	II	Infiltrating Ductal Carcinoma
332	TCGA-A2-A0EU	79.0	FEMALE	0.479400	2.05590	-0.53136	-0.188480	I	Infiltrating Ductal Carcinoma
333	TCGA-B6-A40B	76.0	FEMALE	-0.244270	0.92556	-0.41823	-0.067848	I	Infiltrating Ductal Carcinoma

317 rows × 16 columns

In [8]:
```python
# Check if there are duplicate rows in the data set
breast_cancer_df.duplicated().sum()
```

Out[8]:
```
0
```

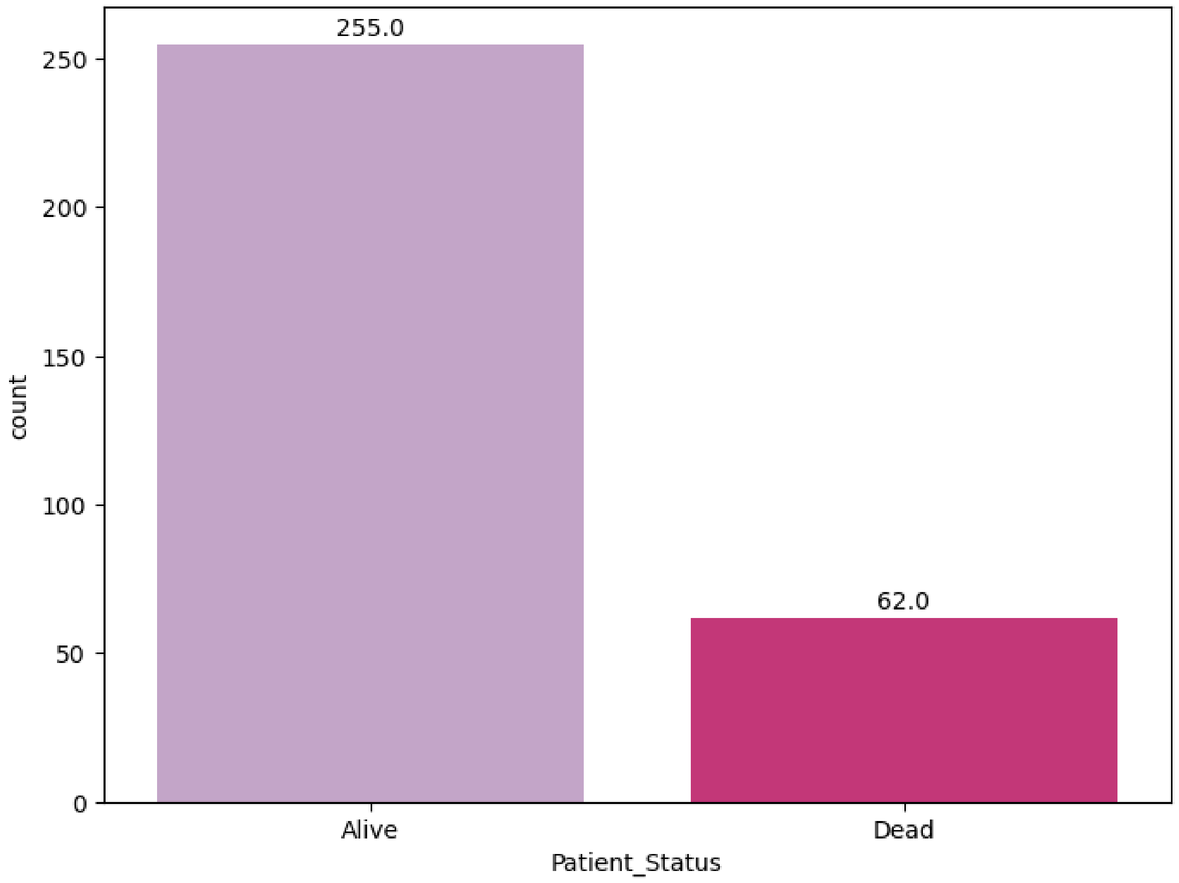
Exploratory Data Analysis

In [9]:
```python
breast_cancer_df.describe()
```

Out[9]:

	Age	Protein1	Protein2	Protein3	Protein4
count	317.000000	317.000000	317.000000	317.000000	317.000000
mean	58.725552	-0.027232	0.949557	-0.095104	0.006713
std	12.827374	0.543858	0.906153	0.589027	0.625965
min	29.000000	-2.144600	-0.978730	-1.627400	-2.025500
25%	49.000000	-0.350600	0.368840	-0.531360	-0.382240
50%	58.000000	0.005649	0.997130	-0.193040	0.038522
75%	67.000000	0.336260	1.612000	0.251210	0.436250
max	90.000000	1.593600	3.402200	2.193400	1.629900

In [10]:
```
# Target distribution

# Set the figure size and create a count plot
plt.figure(figsize=(8, 6))
ax = sns.countplot(x=breast_cancer_df['Patient_Status'], palette='PuRd')

# Add labels to each bar in the plot
for p in ax.patches:
    ax.text(p.get_x()+p.get_width()/2, p.get_height()+3, f'{p.get_height()}', ha="c

plt.show()
```



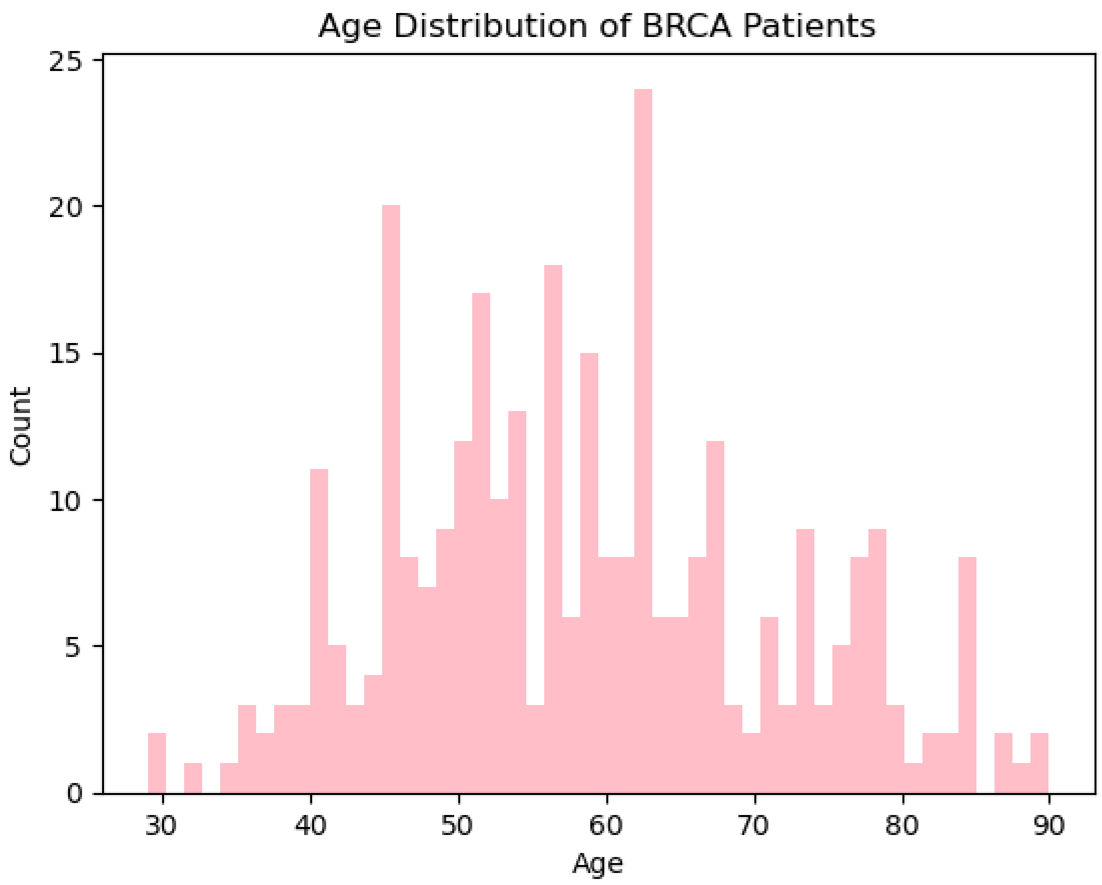
In [11]:
```
breast_cancer_df['Gender'].value_counts()
```

Out[11]:
```
Gender
FEMALE    313
MALE        4
Name: count, dtype: int64
```

Gender is not a useful feature in this case as there are only a few male patients

In [12]:
```
breast_cancer_df['Age'].hist(bins = 50, grid = False, color='pink')
plt.xlabel(xlabel = "Age")
plt.ylabel(ylabel = "Count")
plt.title("Age Distribution of BRCA Patients")
```

Out[12]:
```
Text(0.5, 1.0, 'Age Distribution of BRCA Patients')
```



`Age` is normally distributed, with slight right skewness and most of population is around 45-65 years old.

In [13]:
```
# Separate categorical and numerical columns
categorical_columns = breast_cancer_df.select_dtypes(include=['object']).columns
numerical_columns = breast_cancer_df.select_dtypes(include=['float64', 'int64']).co
```

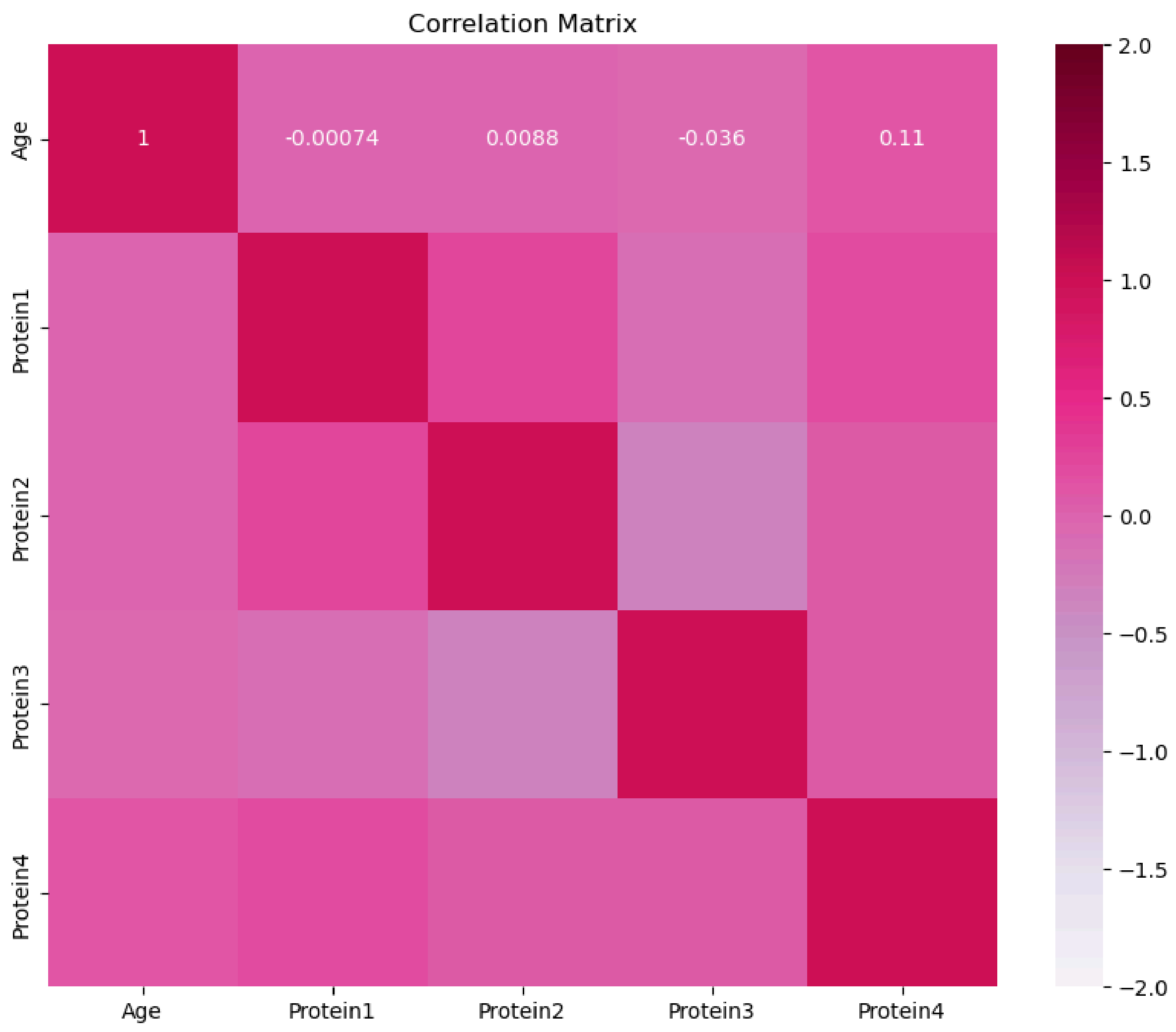
In [14]:
```
# Calculate the Inter Quartile Range for each numerical column
Q1 = breast_cancer_df[numerical_columns].quantile(0.25)
Q3 = breast_cancer_df[numerical_columns].quantile(0.75)
```

```
IQR = Q3 - Q1

# Identify outliers for each numerical column
outliers = {}
for column in numerical_columns:
    lower_bound = Q1[column] - 1.5 * IQR[column]
    upper_bound = Q3[column] + 1.5 * IQR[column]
    outliers[column] = breast_cancer_df[(breast_cancer_df[column] < lower_bound) |

# Count the number of outliers for each numerical column
outlier_counts = {col: len(outliers[col]) for col in numerical_columns}

# Display the number of outliers for each numerical column
outlier_counts
```

Out[14]:
```
{'Age': 0, 'Protein1': 7, 'Protein2': 0, 'Protein3': 5, 'Protein4': 4}
```

In [15]:
```
# Remove observations with outliers from the dataframe
for col in numerical_columns:
    breast_cancer_df = breast_cancer_df[(breast_cancer_df[col] >= Q1[col] - 1.5 * I
```

In [16]:
```
# Evaluate the Spearman correlation between numerical columns
correlation_matrix = breast_cancer_df[numerical_columns].corr(method='spearman')
# Plot the correlation matrix as a heatmap
plt.figure(figsize=(10, 8))
sns.heatmap(correlation_matrix, annot=True, vmin = -2, vmax = 2, cmap='PuRd')
plt.title('Correlation Matrix')
plt.show()
```



```
In [17]: # Separate the features and the target variable
         X = breast_cancer_df[numerical_columns]
         y = breast_cancer_df['Patient_Status']
         # Encode the target variable
         label_encoder = LabelEncoder()
         y = label_encoder.fit_transform(y)
```

```
In [18]: # Drop the Age column from the dataframe
         breast_cancer_df = breast_cancer_df.drop('Age', axis=1)
```

```
In [19]: breast_cancer_df
```

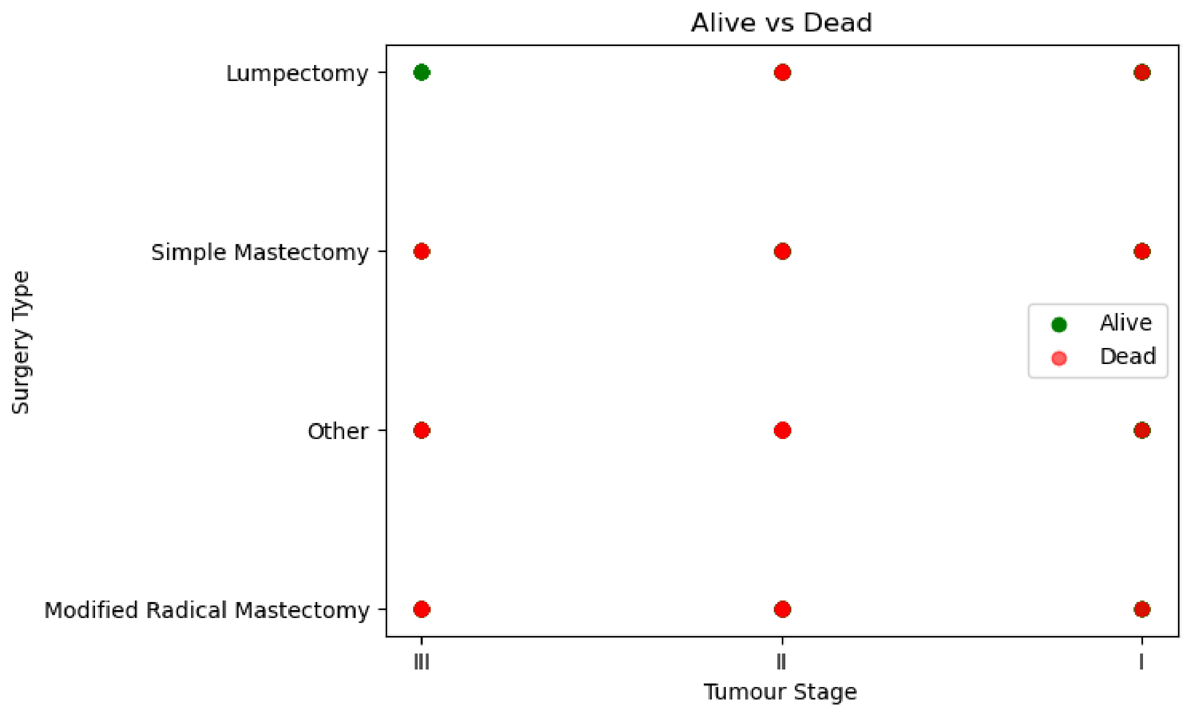
Out[19]:

	Patient_ID	Gender	Protein1	Protein2	Protein3	Protein4	Tumour_Stage	Histology	stat
0	TCGA-D8-A1XD	FEMALE	0.080353	0.42638	0.54715	0.273680	III	Infiltrating Ductal Carcinoma	Posit
1	TCGA-EW-A1OX	FEMALE	-0.420320	0.57807	0.61447	-0.031505	II	Mucinous Carcinoma	Posit
2	TCGA-A8-A079	FEMALE	0.213980	1.31140	-0.32747	-0.234260	III	Infiltrating Ductal Carcinoma	Posit
3	TCGA-D8-A1XR	FEMALE	0.345090	-0.21147	-0.19304	0.124270	II	Infiltrating Ductal Carcinoma	Posit
4	TCGA-BH-A0BF	FEMALE	0.221550	1.90680	0.52045	-0.311990	II	Infiltrating Ductal Carcinoma	Posit
...	...	...	...	...	...	...	...	...	
329	TCGA-AN-A04A	FEMALE	0.231800	0.61804	-0.55779	-0.517350	III	Infiltrating Ductal Carcinoma	Posit
330	TCGA-A8-A085	MALE	0.732720	1.11170	-0.26952	-0.354920	II	Infiltrating Lobular Carcinoma	Posit
331	TCGA-A1-A0SG	FEMALE	-0.719470	2.54850	-0.15024	0.339680	II	Infiltrating Ductal Carcinoma	Posit
332	TCGA-A2-A0EU	FEMALE	0.479400	2.05590	-0.53136	-0.188480	I	Infiltrating Ductal Carcinoma	Posit
333	TCGA-B6-A40B	FEMALE	-0.244270	0.92556	-0.41823	-0.067848	I	Infiltrating Ductal Carcinoma	Posit

301 rows × 15 columns

In [20]:

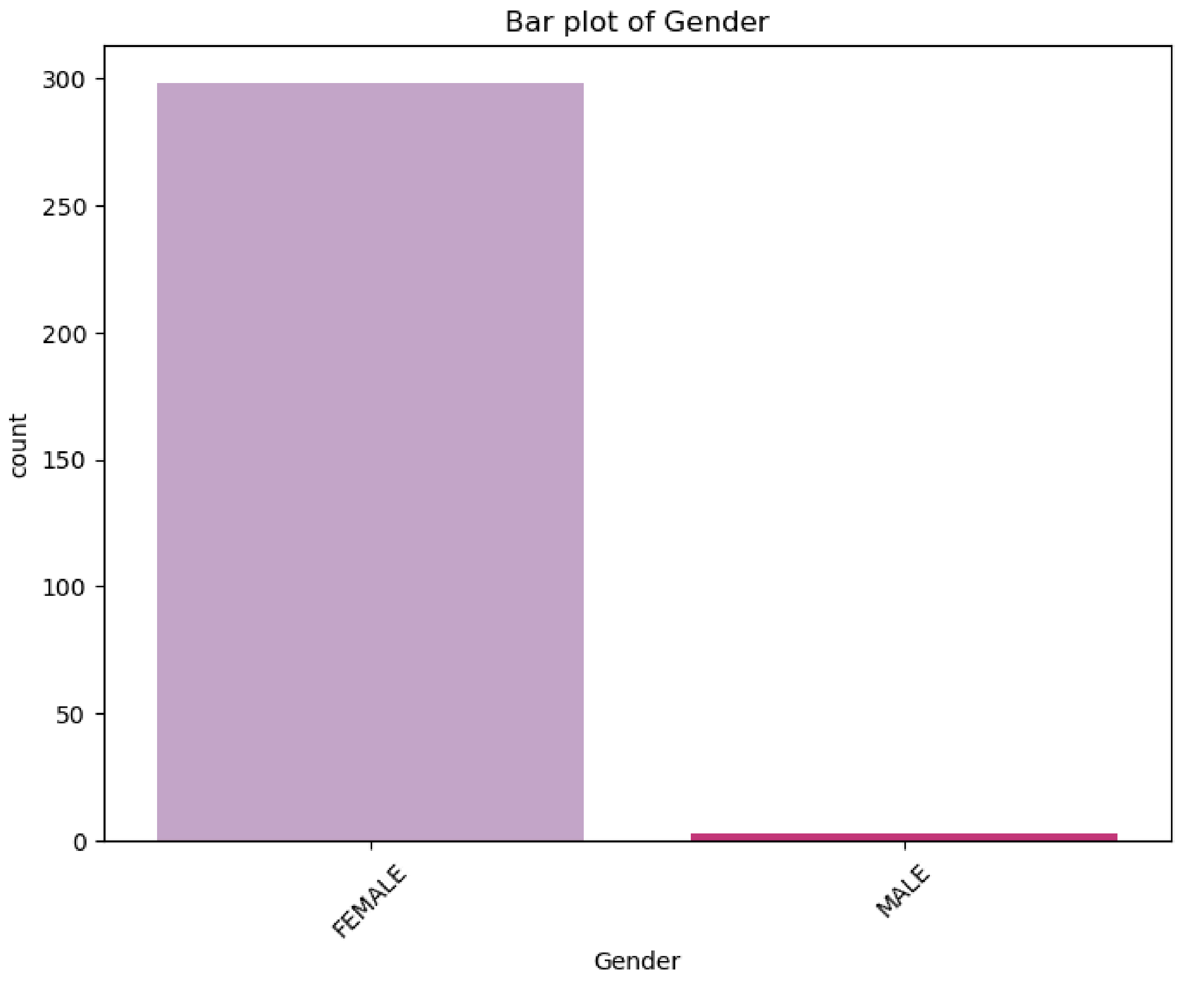
```python
# Plot Scatter plot on Tumor Stage vs Surgery Type
A = breast_cancer_df[breast_cancer_df.Patient_Status == "Alive"]
D = breast_cancer_df[breast_cancer_df.Patient_Status == "Dead"]

#T= breast_cancer_df[breast_cancer_df.Tumour_Stage =="III"]

plt.title("Alive vs Dead")
plt.xlabel("Tumour Stage")
plt.ylabel("Surgery Type")
plt.scatter(A.Tumour_Stage, A.Surgery_type, color = "Green", label = "Alive", alpha
plt.scatter(D.Tumour_Stage, D.Surgery_type, color = "Red", label = "Dead", alpha =
plt.legend()
plt.show()
```

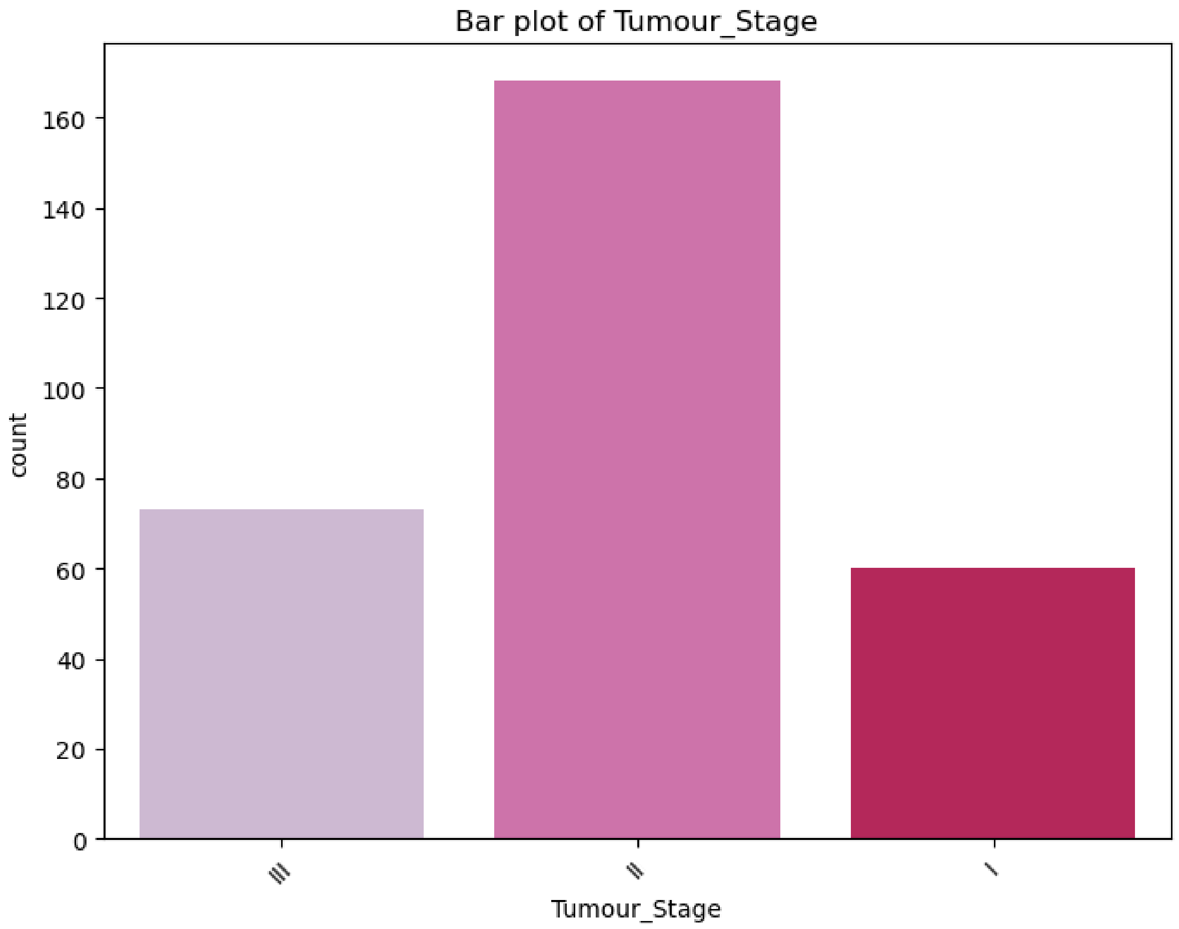


From the above graph, we can see that for Tumor Stage 3, Lumpectomy can be performed to help the patient.

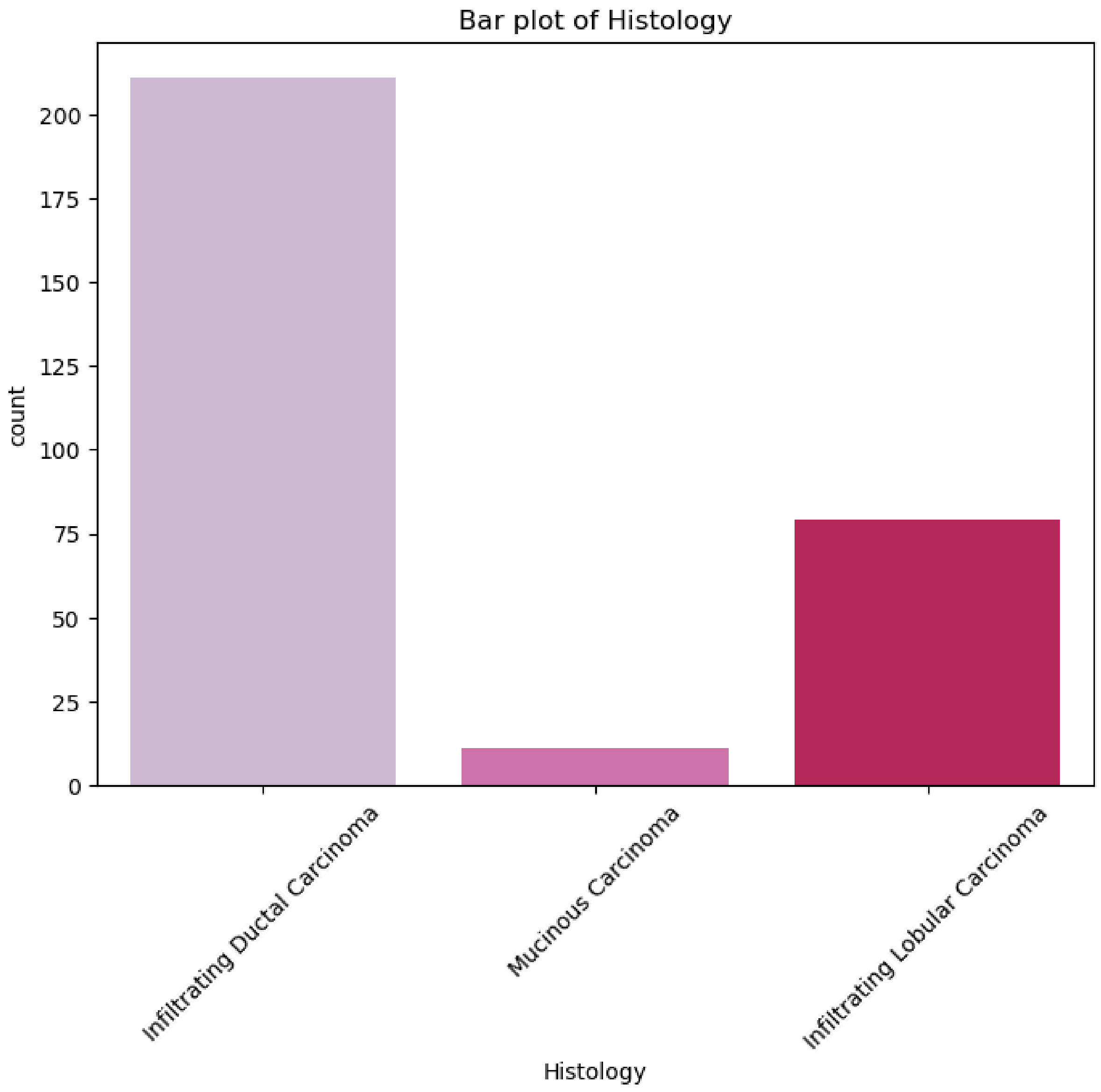
In [21]:
```
# Apply kernel PCA to the numerical columns to create new features to add to the da
from sklearn.decomposition import KernelPCA
numerical_columns_pca = breast_cancer_df.select_dtypes(include=['float64', 'int64']
kpca = KernelPCA(n_components=2, kernel='rbf', random_state=42)
kpca_features = kpca.fit_transform(breast_cancer_df[numerical_columns_pca])
breast_cancer_df['KPCA1'] = kpca_features[:, 0]
breast_cancer_df['KPCA2'] = kpca_features[:, 1]
```

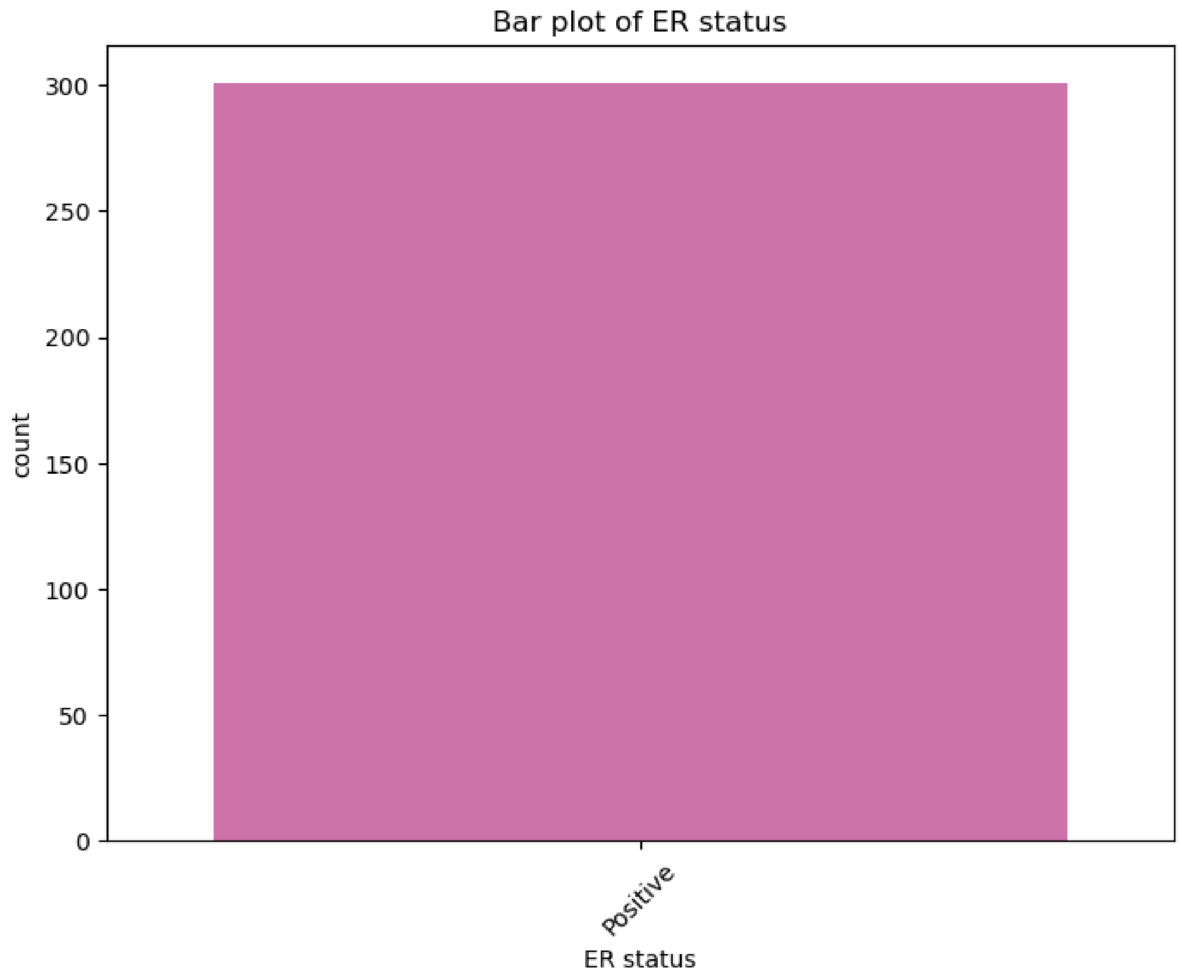
In [22]:
```
# Bar plot of the categorical columns to evaluate the distribution
for col in categorical_columns:
    if(col != 'Date_of_Surgery' and col != 'Date_of_Last_Visit' and col != 'Patient
        plt.figure(figsize=(8, 6))
        sns.countplot(data=breast_cancer_df, x=col, palette='PuRd')
        plt.title(f'Bar plot of {col}')
        plt.xticks(rotation=45)
        plt.show()
```

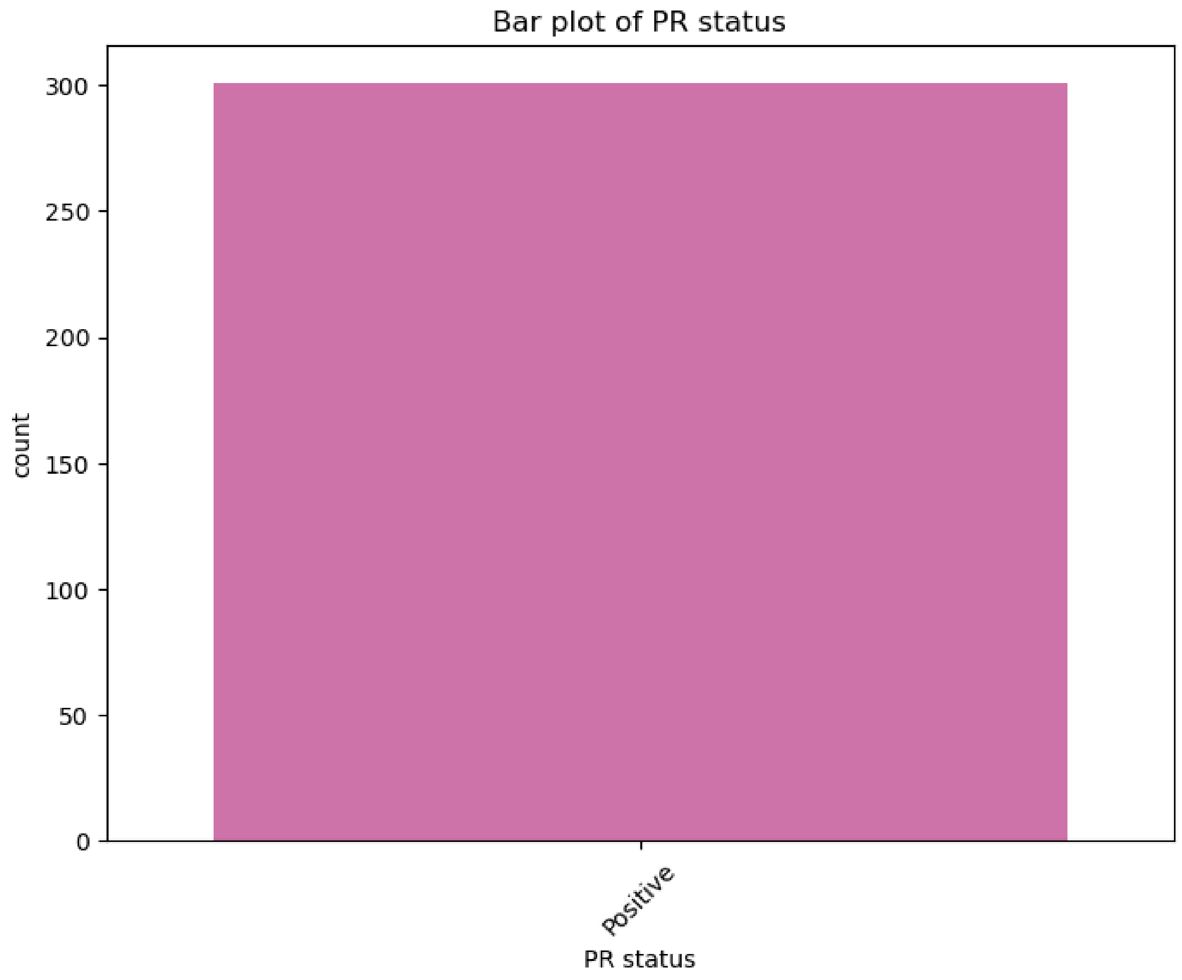

Bar plot of Gender
count
300
250
200
150
100
50
0
FEMALE
MALE
Gender

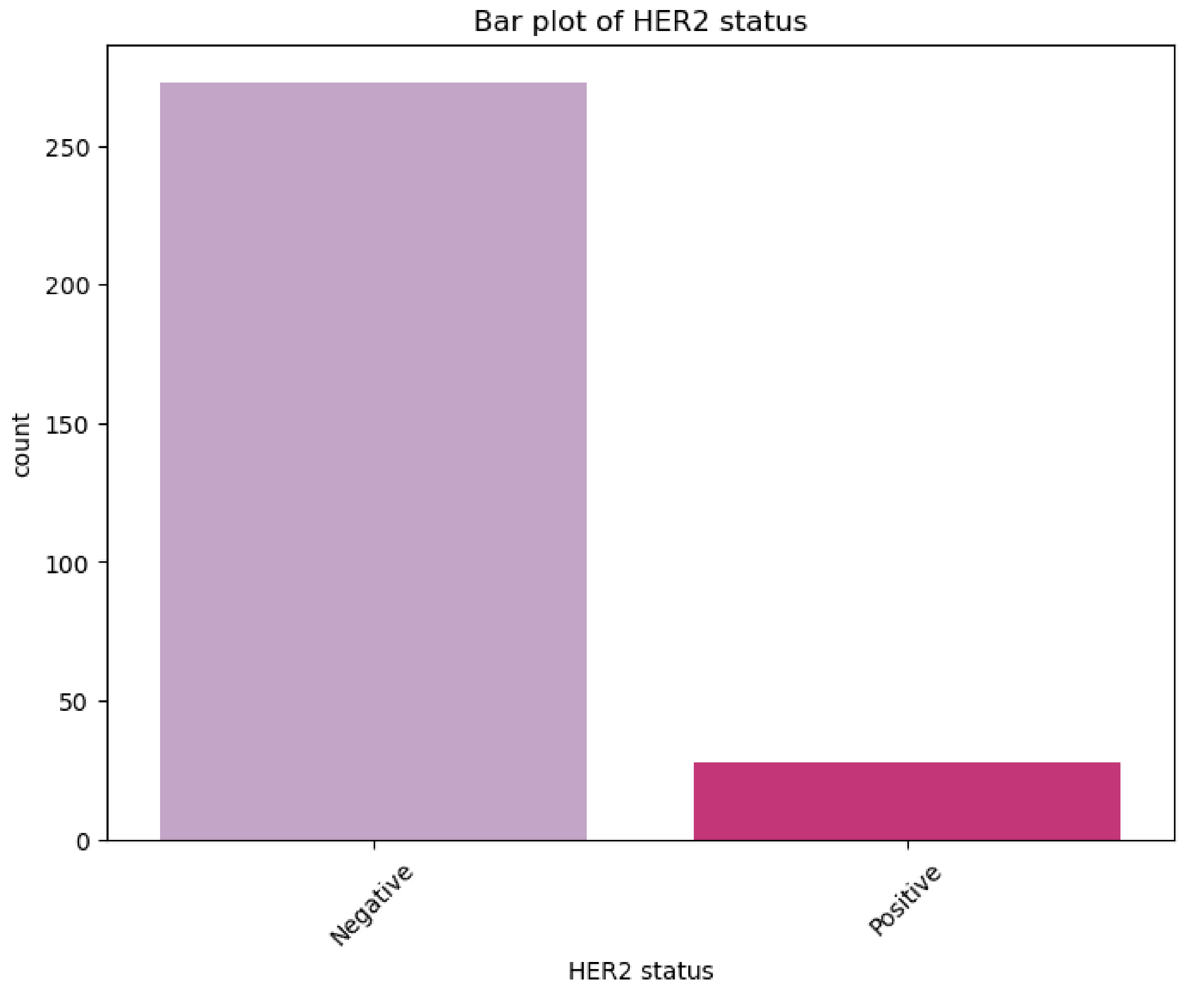


Bar plot of Tumour_Stage
count
0
20
40
60
80
100
120
140
160
III
II
I
Tumour_Stage

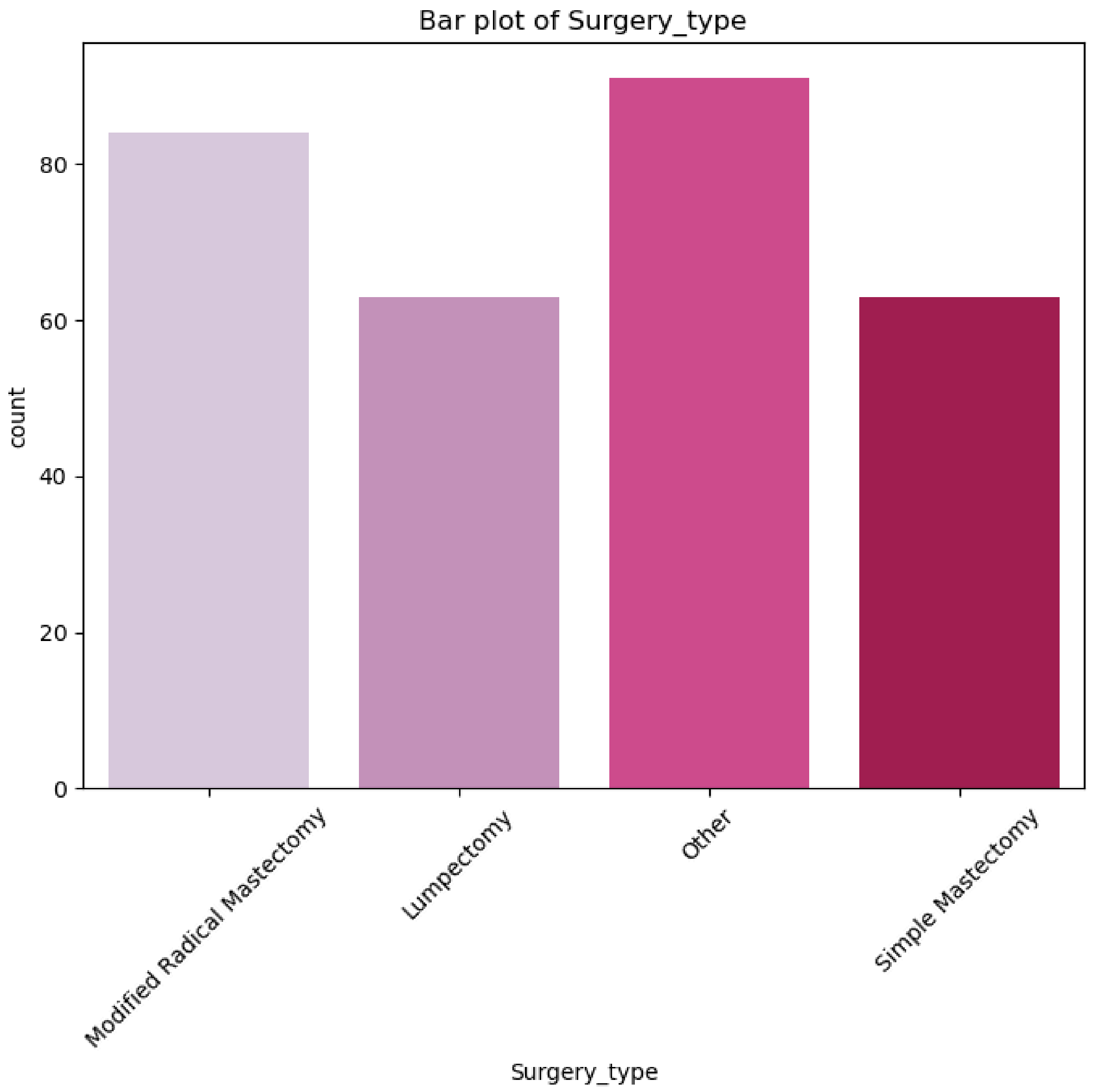

Bar plot of Histology
count
200
175
150
125
100
75
50
25
0
Infiltrating Ductal Carcinoma
Mucinous Carcinoma
Infiltrating Lobular Carcinoma
Histology


Bar plot of ER status
count
300
250
200
150
100
50
0
Positive
ER status


Bar plot of PR status
count
300
250
200
150
100
50
0
Positive
PR status



Bar plot of HER2 status
count
250
200
150
100
50
0
Negative
Positive
HER2 status



In [23]:
```
# Drop the columns because they have one or almost unique value
breast_cancer_df=breast_cancer_df.drop(columns=['ER status','PR status','Gender'])

# Extract again the categorical columns
categorical_columns = breast_cancer_df.select_dtypes(include=['object']).columns
```

In [24]:
```
# Calculate the contingency table between columns

categorical_columns = ['Tumour_Stage', 'Histology', 'HER2 status', 'Surgery_type']
for col in categorical_columns:
    contingency_table = pd.crosstab(breast_cancer_df[col], breast_cancer_df['Patien
    print(f'Contingency Table for {col}:')
    print(contingency_table)
    print('\n')
```

```
Contingency Table for Tumour_Stage:
Patient_Status  Alive  Dead
Tumour_Stage
I                  51     9
II                135    33
III                56    17


Contingency Table for Histology:
Patient_Status                  Alive  Dead
Histology
Infiltrating Ductal Carcinoma     169    42
Infiltrating Lobular Carcinoma     65    14
Mucinous Carcinoma                  8     3


Contingency Table for HER2 status:
Patient_Status  Alive  Dead
HER2 status
Negative          218    55
Positive           24     4


Contingency Table for Surgery_type:
Patient_Status               Alive  Dead
Surgery_type
Lumpectomy                      55     8
Modified Radical Mastectomy     68    16
Other                           68    23
Simple Mastectomy               51    12
```

In [25]:
```
# Encode the categorical columns with one hot encoding except for Date_of_Surgery,
# Select the categorical columns to encode
categorical_columns_encode = ['Tumour_Stage', 'Histology', 'HER2 status', 'Surgery_

# Create a OneHotEncoder object
encoder = OneHotEncoder(handle_unknown='ignore', sparse_output=False, dtype=int)

# Apply encoding to the specified columns
encoded_features = encoder.fit_transform(breast_cancer_df[categorical_columns_encod

# Create a DataFrame with the encoded features
encoded_df = pd.DataFrame(encoded_features, columns=encoder.get_feature_names_out(c

# Remove the original columns and add the encoded ones
df_encoded = breast_cancer_df.drop(columns=categorical_columns_encode).reset_index(
df_encoded = pd.concat([df_encoded, encoded_df], axis=1)



# Encode the target variable Patient_Status with LabelEncoder
df_encoded['Patient_Status'] = label_encoder.fit_transform(df_encoded['Patient_Stat

df = df_encoded
```

In [26]:
```
#Introduce the variable Difference_Days and divide the date of surgery and date of

# Change the data type of the 'Date_of_Surgery' and 'Date_of_Last_Visit' columns to
df['Date_of_Surgery'] = pd.to_datetime(df['Date_of_Surgery'])
df['Date_of_Last_Visit'] = pd.to_datetime(df['Date_of_Last_Visit'])

# Calculate the difference in days between the date of last visit and the date of s
df['Difference_Days'] = (df['Date_of_Last_Visit'] - df['Date_of_Surgery']).dt.days

# Extract the day, month, and year from the 'Date_of_Surgery' and 'Date_of_Last_Vis
df["Month_of_Surgery"] = df["Date_of_Surgery"].apply(lambda x : x.month)
df["Day_of_Surgery"] = df["Date_of_Surgery"].apply(lambda x : x.day)
df["Year_of_Surgery"] = df["Date_of_Surgery"].apply(lambda x : x.year)
df["Month_of_Last_visit"] = df["Date_of_Last_Visit"].apply(lambda x : x.month)
df["Day_of_Last_visit"] = df["Date_of_Last_Visit"].apply(lambda x : x.day)
df["Year_of_Last_visit"] = df["Date_of_Last_Visit"].apply(lambda x : x.year)

# Drop the 'Date_of_Surgery' and 'Date_of_Last_Visit' columns and change the displa
df = df.drop(['Date_of_Surgery', 'Date_of_Last_Visit'], axis=1)
df['Patient_Status'] = df.pop('Patient_Status')
```

Model Development

In [27]:
```
df = df.drop('Patient_ID', axis=1)
X = df.drop(columns=['Patient_Status'])
y = df['Patient_Status']

# Split dataset into training and test set after feature generation
X_train, X_test, y_train, y_test = train_test_split(X, y, test_size=0.3, random_sta
# Check dimensions of the sets
print(f'Training set size: {X_train.shape[0]}')
print(f'Test set size: {X_test.shape[0]}')
```

```
Training set size: 210
Test set size: 91
```

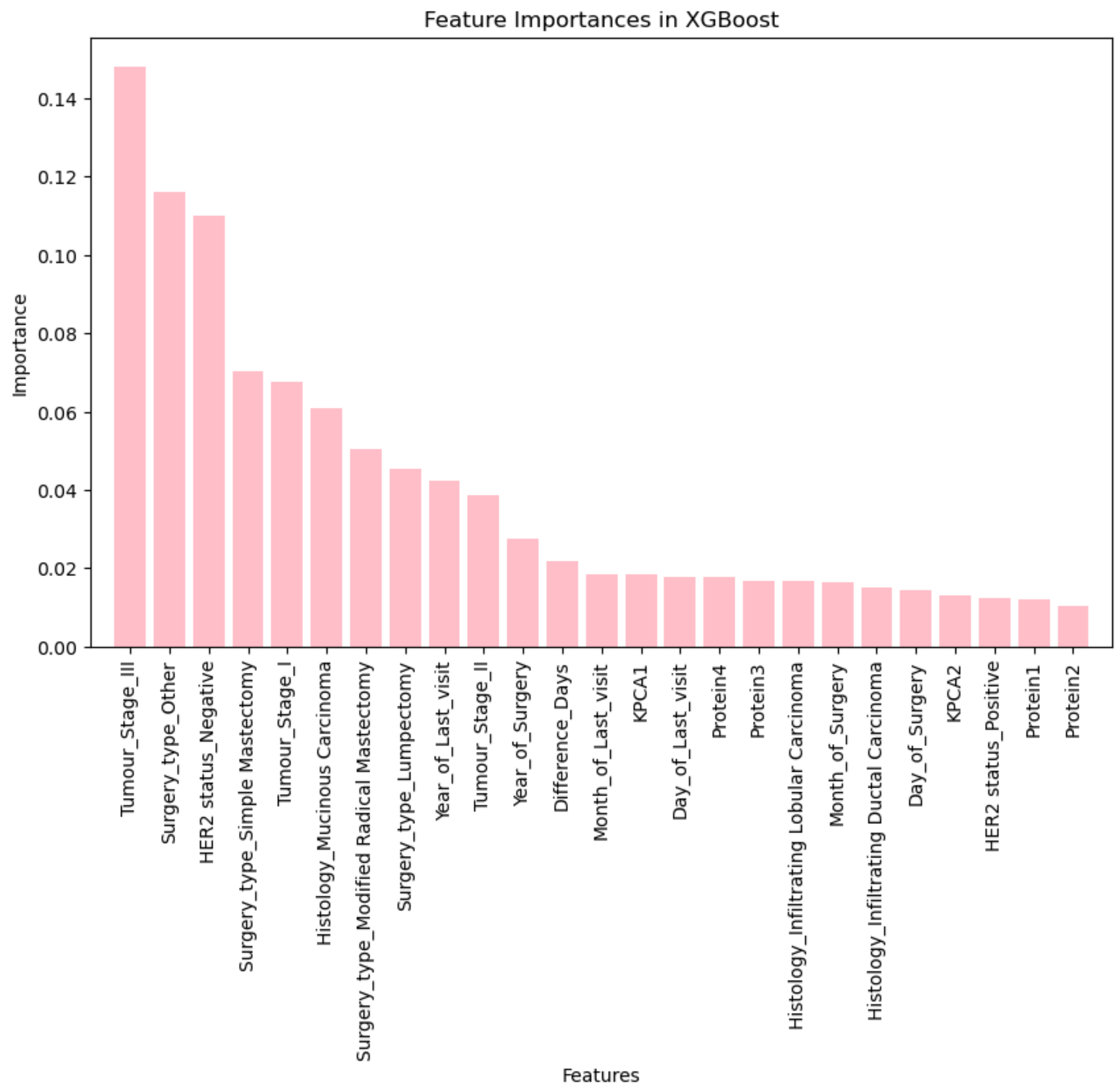
In [28]:
```
# Use SMOTE to balance the training set
# Create a SMOTE object
smote = SMOTE(random_state=42)

# Apply SMOTE to the training set
X_train_balanced, y_train_balanced = smote.fit_resample(X_train, y_train)

# Check the dimensions of the balanced training set
print(f'Balanced training set size: {X_train_balanced.shape[0]}')

X_train = X_train_balanced
y_train = y_train_balanced
```

```
Balanced training set size: 338
```

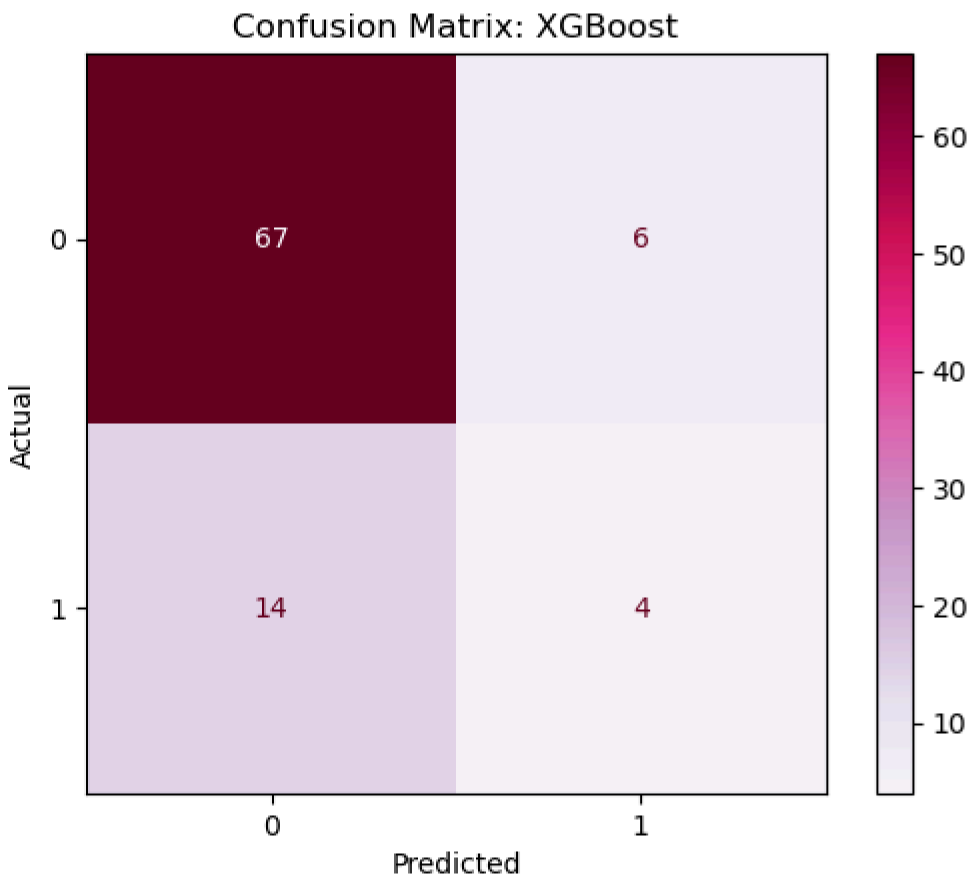
In [29]:
```
# Function to plot a confusion matrix
def plot_confusion_matrix(y_true, y_pred, title):
    """
    Plots a confusion matrix using seaborn's heatmap visualization.

    Parameters:
    - y_true: array-like of true labels.
    - y_pred: array-like of predicted labels.
    - title: str, title of the plot.

    This function calculates the confusion matrix from true and predicted labels,
    then visualizes it with annotations and a color map of 'Blues'.
    """
    cm = confusion_matrix(y_true, y_pred)  # Calculate confusion matrix
    cmd = ConfusionMatrixDisplay(cm)
    cmd.plot(cmap='PuRd');
    plt.title(title)  # Set the title of the plot
    plt.xlabel('Predicted')  # Set x-axis label
    plt.ylabel('Actual')  # Set y-axis label


# Function to plot features importance
def plot_feature_importance(model, feature_names, title):
    """
    Plots the feature importance for tree-based machine learning models.

    Parameters:
    - model: the trained model object that has the attribute 'feature_importances_'
    - feature_names: list or array of feature names.
    - title: str, title of the plot.

    This function plots the feature importances provided by the model, sorting them
    in descending order and displaying a bar plot.
    """
    importances = model.feature_importances_
    indices = np.argsort(importances)[::-1]

    plt.figure(figsize=(10, 6))
    plt.title(title)
    plt.bar(range(len(importances)), importances[indices], align='center', color='p
    plt.xticks(range(len(importances)), [feature_names[i] for i in indices], rotati
    plt.xlim([-1, len(importances)])
    plt.xlabel('Features')
    plt.ylabel('Importance')
    plt.show()
```

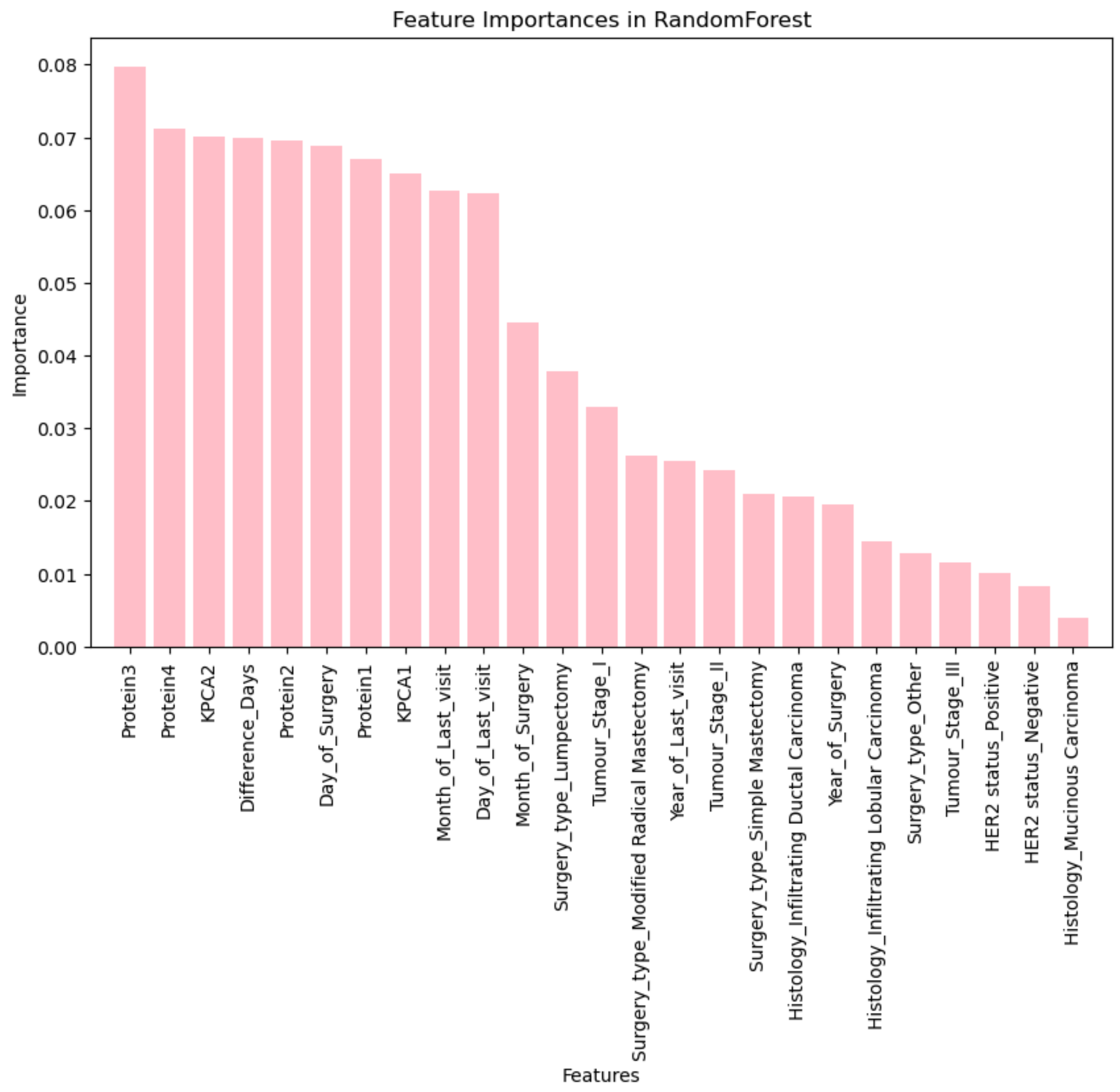
In [30]:
```
# Define the models to train, in this case, we will use XGBoost
models = {
    'XGBoost': XGBClassifier(),
    'RandomForest' : RandomForestClassifier(n_estimators=500),
    'DecisionTree' : DecisionTreeClassifier(criterion='gini',max_depth=15)
}

# Dictionary to store the accuracy for comparison
model_accuracies = {}

# Train and evaluate the models
for name, model in models.items():
    model.fit(X_train, y_train)
    y_pred = model.predict(X_test)
    accuracy = accuracy_score(y_test, y_pred)
    model_accuracies[name] = accuracy  # Store the accuracy of each model

    print(f"Model: {name}")
    print("Accuracy:", accuracy)
    print(classification_report(y_test, y_pred))

    # Optional: Feature importance and confusion matrix
    # Ensure these functions are defined or available in your environment
    plot_feature_importance(model, X.columns, f'Feature Importances in {name}')
    plot_confusion_matrix(y_test, y_pred, f'Confusion Matrix: {name}')

# Find the best model based on accuracy
best_model_name = max(model_accuracies, key=model_accuracies.get)
best_model = models[best_model_name]
```

```
Model: XGBoost
Accuracy: 0.7802197802197802
              precision    recall  f1-score   support

           0       0.83      0.92      0.87        73
           1       0.40      0.22      0.29        18

    accuracy                           0.78        91
   macro avg       0.61      0.57      0.58        91
weighted avg       0.74      0.78      0.75        91
```

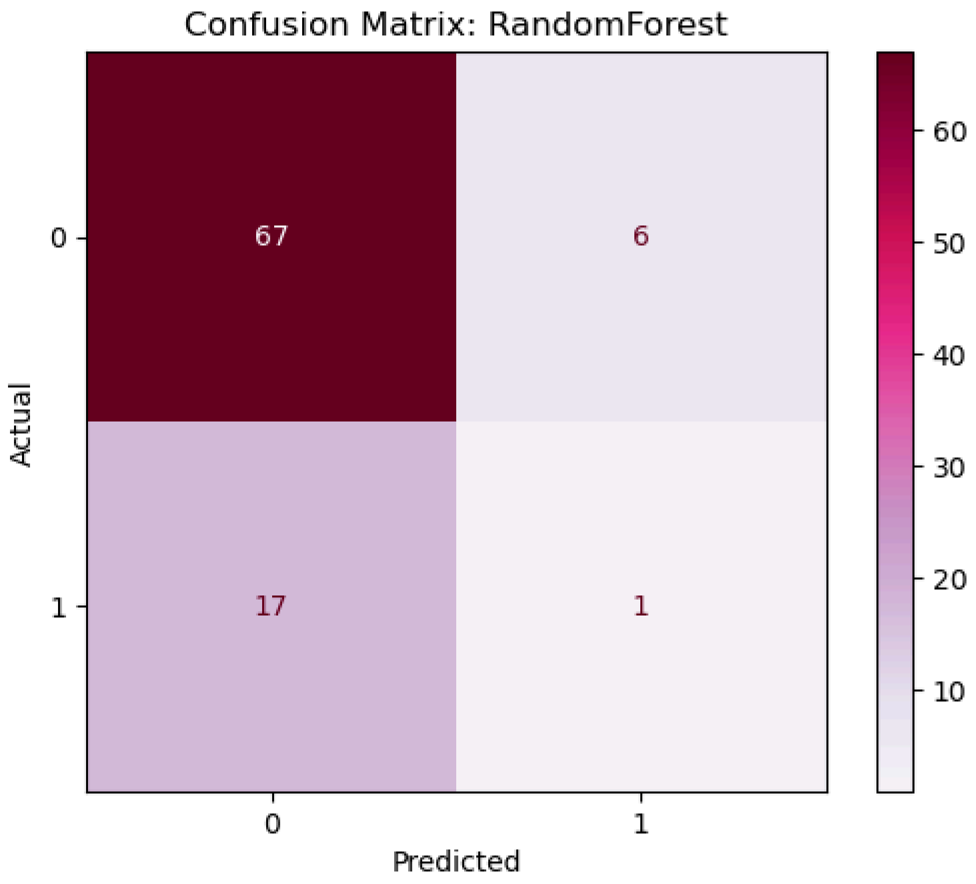


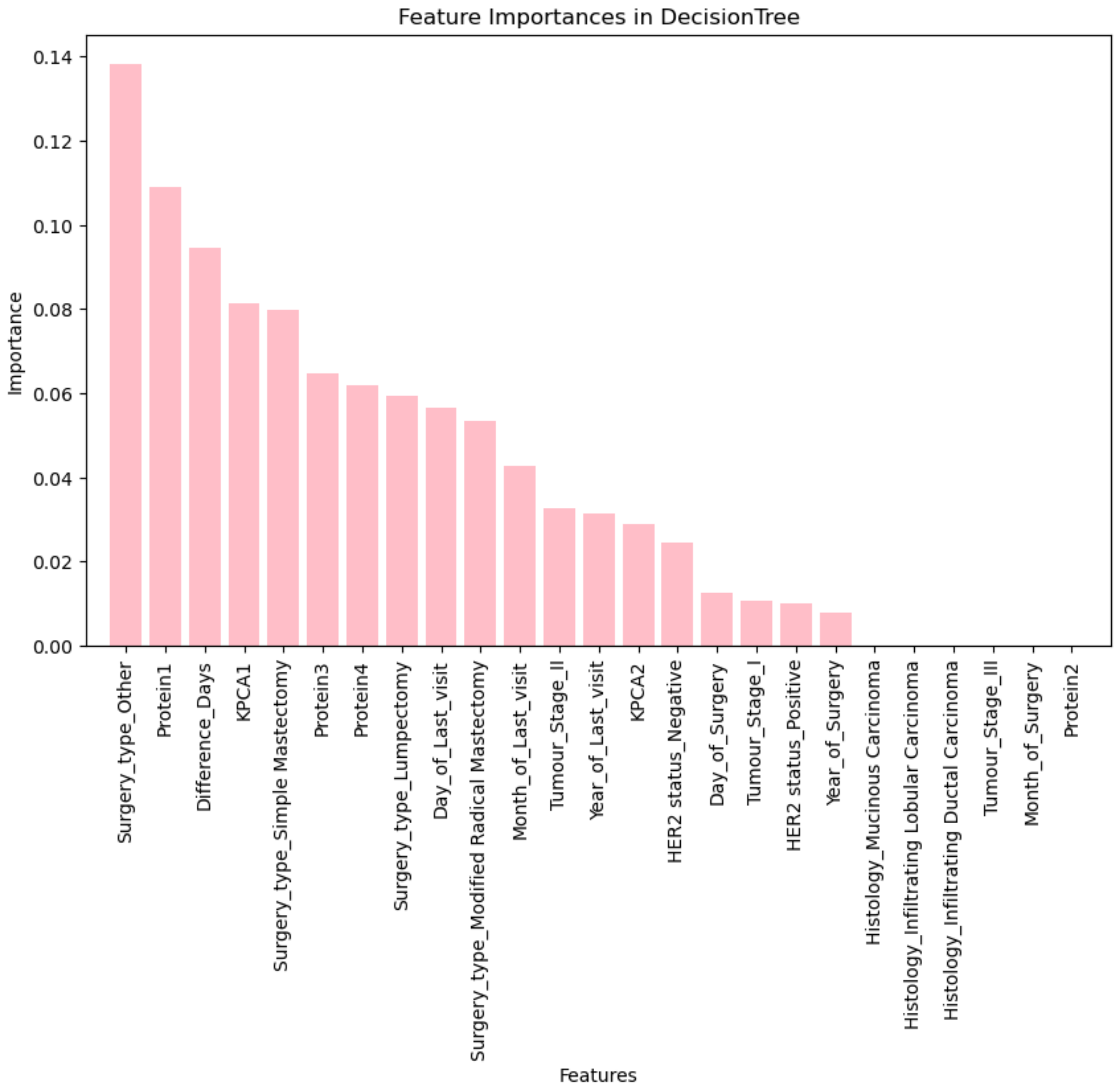
```
Model: RandomForest
Accuracy: 0.7472527472527473
              precision    recall  f1-score   support

           0       0.80      0.92      0.85        73
           1       0.14      0.06      0.08        18

    accuracy                           0.75        91
   macro avg       0.47      0.49      0.47        91
weighted avg       0.67      0.75      0.70        91
```

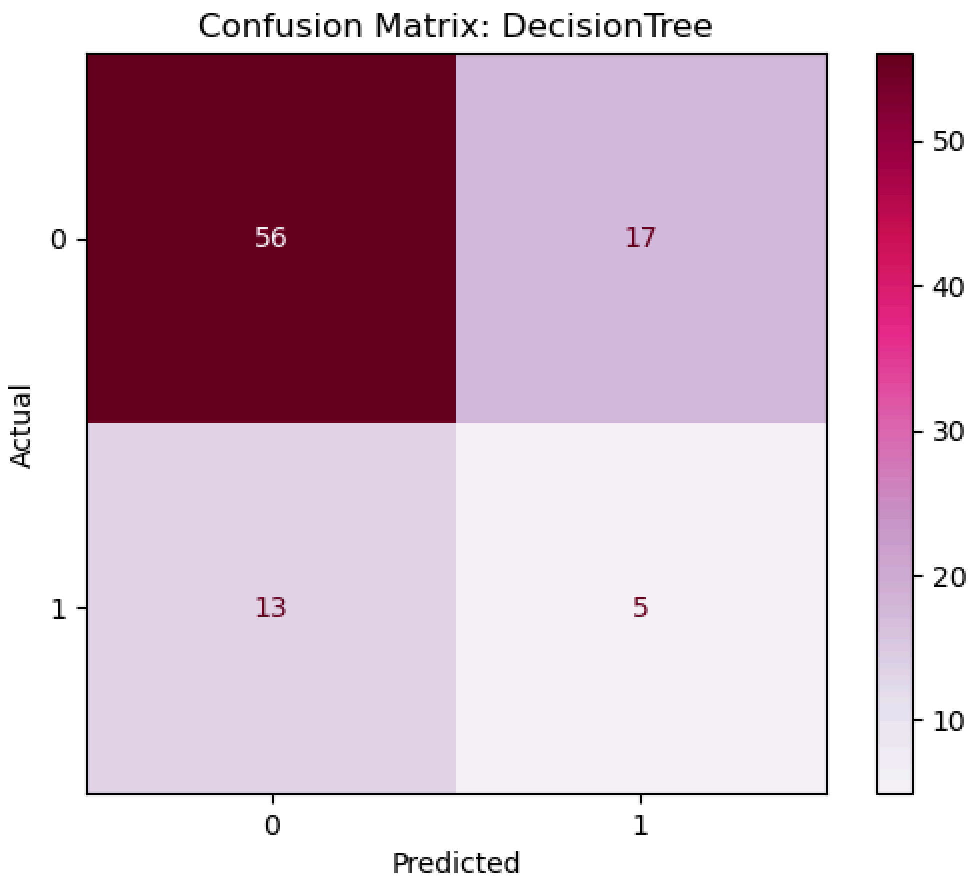

Confusion Matrix: XGBoost
Actual
Predicted
0
1
0
1
67
6
14
4
60
50
40
30
20
10



```
Model: DecisionTree
Accuracy: 0.6703296703296703
              precision    recall  f1-score   support

           0       0.81      0.77      0.79        73
           1       0.23      0.28      0.25        18

    accuracy                           0.67        91
   macro avg       0.52      0.52      0.52        91
weighted avg       0.70      0.67      0.68        91
```


Confusion Matrix: RandomForest
Actual
Predicted
0
1
0
1
67
6
17
1
60
50
40
30
20
10


Feature Importances in DecisionTree
Importance
0.14
0.12
0.10
0.08
0.06
0.04
0.02
0.00
Surgery_type_Other
Protein1
Difference_Days
KPCA1
Surgery_type_Simple Mastectomy
Protein3
Protein4
Surgery_type_Lumpectomy
Day_of_Last_visit
Surgery_type_Modified Radical Mastectomy
Month_of_Last_visit
Tumour_Stage_II
Year_of_Last_visit
KPCA2
HER2 status_Negative
Day_of_Surgery
Tumour_Stage_I
HER2 status_Positive
Year_of_Surgery
Histology_Mucinous Carcinoma
Histology_Infiltrating Lobular Carcinoma
Histology_Infiltrating Ductal Carcinoma
Tumour_Stage_III
Month_of_Surgery
Protein2
Features



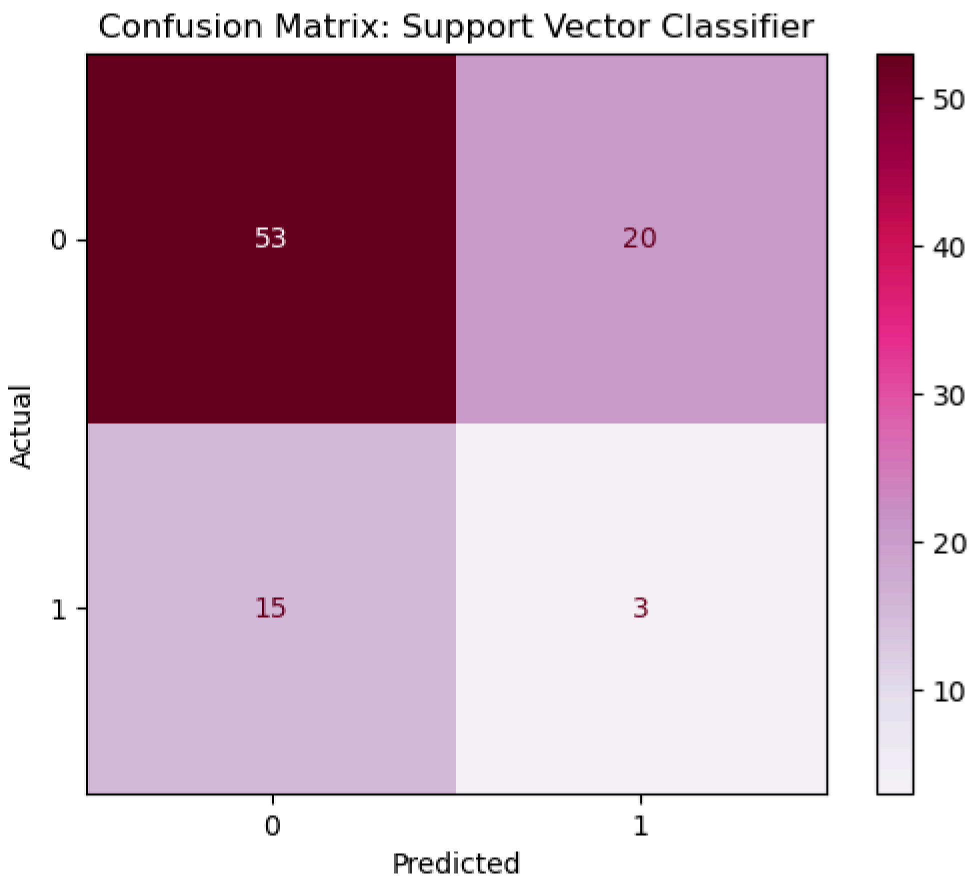
In [31]:
```
svc = SVC(probability=True)
parameters = {'kernel':('linear', 'rbf'), 'C':[1, 10]}
clf = GridSearchCV(svc, parameters, n_jobs=50)
clf.fit(X_train, y_train)
GridSearchCV(estimator=SVC(),
             param_grid={'C': [1, 100], 'kernel': ('linear', 'rbf')})
clf.best_estimator_
```

Out[31]:
```
SVC
SVC(C=1, kernel='linear', probability=True)
```

Support Vector Classifier

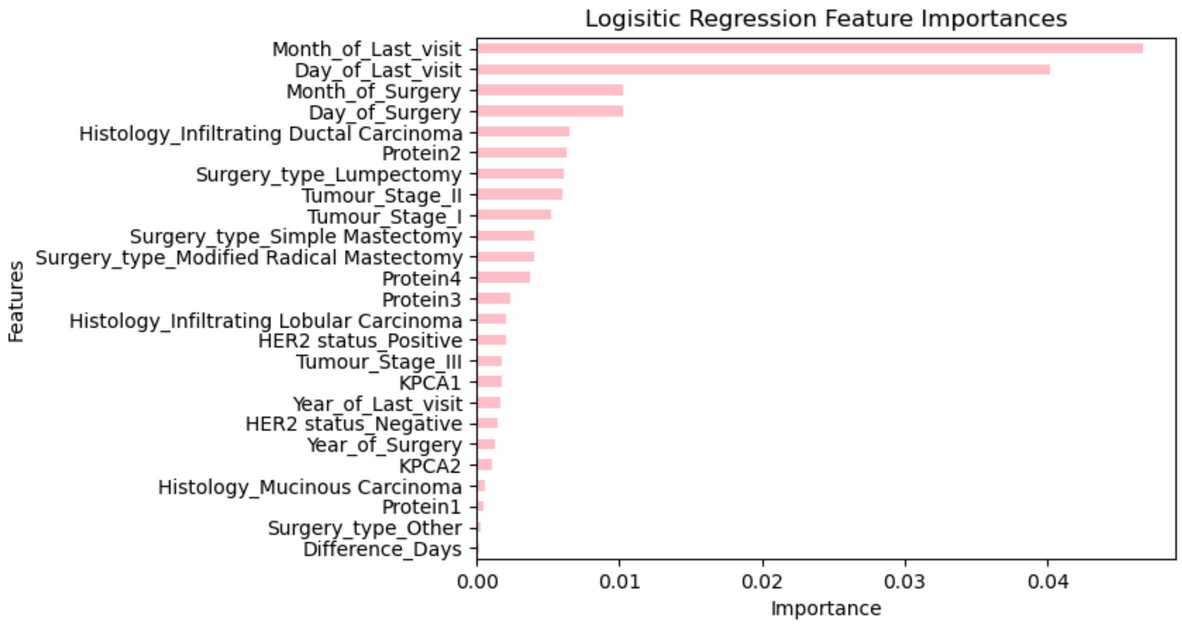
In [32]:
```
svc.fit(X_train, y_train)
y_pred = svc.predict(X_test)
accuracy = accuracy_score(y_test, y_pred)
model_accuracies[name] = accuracy  # Store the accuracy of each model

print(f"Model: Support Vector Classifier")
print("Accuracy:", accuracy)
print(classification_report(y_test, y_pred))

# Ensure these functions are defined or available in your environment
plot_confusion_matrix(y_test, y_pred, f'Confusion Matrix: Support Vector Classifier
best_model_name = max(model_accuracies, key=model_accuracies.get)
best_model = models[best_model_name]
```

```
Model: Support Vector Classifier
Accuracy: 0.6153846153846154
              precision    recall  f1-score   support

           0       0.78      0.73      0.75        73
           1       0.13      0.17      0.15        18

    accuracy                           0.62        91
   macro avg       0.45      0.45      0.45        91
weighted avg       0.65      0.62      0.63        91
```



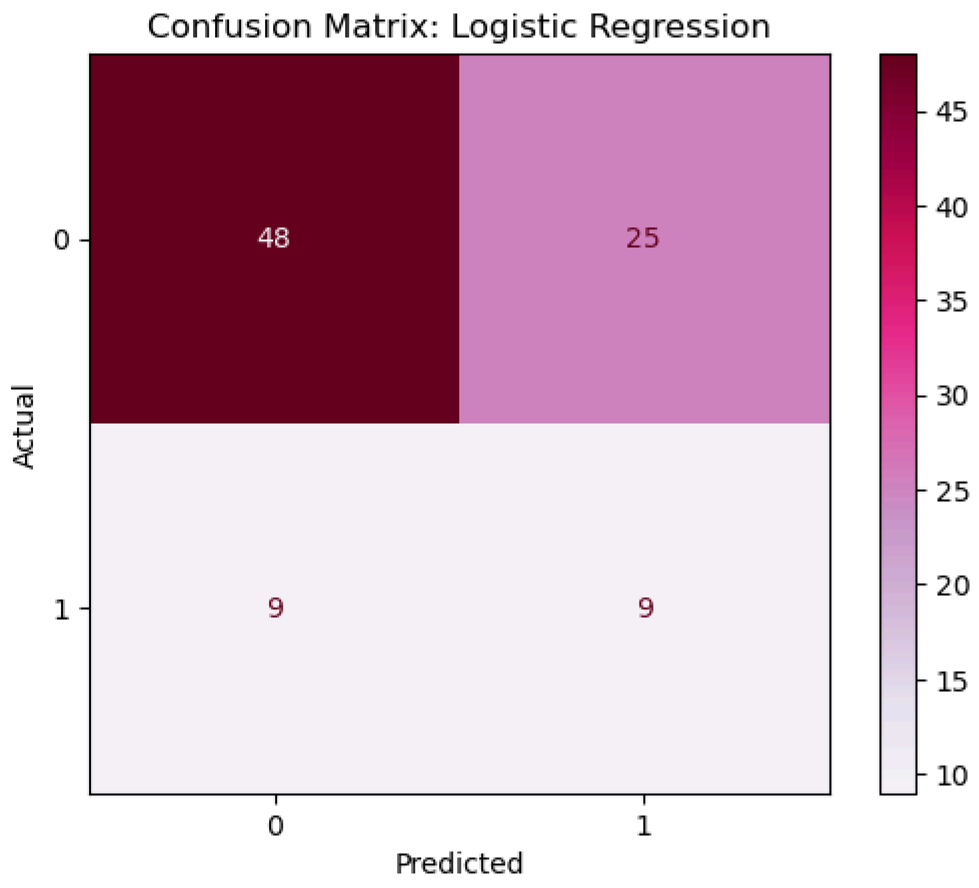
Logistic Regression

In [33]:
```
logit = LogisticRegression(max_iter=3500, penalty='elasticnet', solver = 'saga', l1
logit.fit(X_train, y_train)
logit_importances = logit.coef_[0]
logit_feature_importances = pd.Series(index = X_train.columns, data= np.abs(logit_i
logit_feature_importances = logit_feature_importances.sort_values(ascending=True)
logit_feature_importances.plot(kind='barh', title = 'Logisitic Regression Feature I
plt.show()
```



In [34]:
```
logit.fit(X_train, y_train)
y_pred = logit.predict(X_test)
accuracy = accuracy_score(y_test, y_pred)
model_accuracies[name] = accuracy  # Store the accuracy of each model

print(f"Model: Logistic Regression")
print("Accuracy:", accuracy)
print(classification_report(y_test, y_pred))

# Ensure these functions are defined or available in your environment
plot_confusion_matrix(y_test, y_pred, f'Confusion Matrix: Logistic Regression')

best_model_name = max(model_accuracies, key=model_accuracies.get)
best_model = models[best_model_name]
```

```
Model: Logistic Regression
Accuracy: 0.6263736263736264
              precision    recall  f1-score   support

           0       0.84      0.66      0.74        73
           1       0.26      0.50      0.35        18

    accuracy                           0.63        91
   macro avg       0.55      0.58      0.54        91
weighted avg       0.73      0.63      0.66        91
```



```
In [35]: print("Best Model: ", best_model)
```

```
Best Model:  XGBClassifier(base_score=None, booster=None, callbacks=None,
              colsample_bylevel=None, colsample_bynode=None,
              colsample_bytree=None, device=None, early_stopping_rounds=None,
              enable_categorical=False, eval_metric=None, feature_types=None,
              gamma=None, grow_policy=None, importance_type=None,
              interaction_constraints=None, learning_rate=None, max_bin=None,
              max_cat_threshold=None, max_cat_to_onehot=None,
              max_delta_step=None, max_depth=None, max_leaves=None,
              min_child_weight=None, missing=nan, monotone_constraints=None,
              multi_strategy=None, n_estimators=None, n_jobs=None,
              num_parallel_tree=None, random_state=None, ...)
```