# Heart Failure Prediction (Predykcja niewydolności serca)

This project was done for SKN Data Science by Zofia Seweryńska.

Project was done using the following dataset from Kaggle:

#### **Dataset:**

#### Kaggle Heart Failure Prediction Dataset

It consists 11 clinical features for predicting heart disease events:

Age: wiek pacjenta [lata]

Sex: płeć pacjenta [M: mężczyzna, F: kobieta]

ChestPainType: rodzaj bólu w klatce piersiowej [TA: typowa dławica piersiowa, ATA: atypowa

dławica piersiowa, NAP: ból nie-dławicowy, ASY: bezobjawowy]

RestingBP: ciśnienie tętnicze spoczynkowe [mm Hg]

Cholesterol: stężenie cholesterolu w surowicy [mg/dl]

FastingBS: poziom glukozy na czczo [1: jeśli > 120 mg/dl, 0: w przeciwnym razie]

RestingECG: wynik spoczynkowego EKG [Normal: prawidłowy, ST: nieprawidłowości odcinka

ST-T (inwersja załamka T i/lub uniesienie lub obniżenie ST > 0,05 mV), LVH: przerost lewej

komory wg kryteriów Estesa]

MaxHR: maksymalne osiągnięte tętno [wartość liczbowa między 60 a 202]

ExerciseAngina: dławica wysiłkowa [Y: tak, N: nie]

Oldpeak: obniżenie odcinka ST (ang. oldpeak) [wartość liczbowa w mm] ST\_Slope: nachylenie

odcinka ST podczas wysiłku [Up: wznoszące, Flat: płaskie, Down: opadające]

HeartDisease: klasa wyjściowa [1: choroba serca, 0: brak choroby]

# 1. Pre-processing of the Data Set

Here data set will be analyzed and important features will be described.

## 1.1 Importing Libraries

```
import os
import zipfile
import seaborn as sns
import matplotlib.pyplot as plt
import pandas as pd
import numpy as np
import math
from sklearn.preprocessing import StandardScaler
import statistics
from sklearn.model_selection import train_test_split
from sklearn.linear_model import LogisticRegression
```

```
from sklearn.metrics import classification_report, confusion_matrix
from sklearn.ensemble import RandomForestClassifier
from sklearn.model_selection import GridSearchCV
from sklearn.svm import SVC
```

## 1.2 Kaggle Data Set Download

```
In [3]: # os.environ['KAGGLE_CONFIG_DIR'] = r'C:\Users\zosia\.kaggle'
    # !kaggle datasets download -d fedesoriano/heart-failure-prediction -p heart_failure
    # with zipfile.ZipFile("heart_failure_data/heart-failure-prediction.zip", 'r') as z
    # zip_ref.extractall("heart_failure_data")
```

## 1.3 Data Extraction

```
In [3]: #extracting data
        df = pd.read_csv("heart_failure_data/heart.csv")
        df_original = df.copy()
        #Handling missing values
        print("Data quality check:")
        print(f"Cholesterol = 0 (missing): {(df['Cholesterol'] == 0).sum()} patients")
        print(f"RestingBP = 0 (missing): {(df['RestingBP'] == 0).sum()} patients")
        # Replace Os with NaN
        df['Cholesterol'] = df['Cholesterol'].replace(0, np.nan)
        df['RestingBP'] = df['RestingBP'].replace(0, np.nan)
        # Nan with median
        df = df.fillna({'Cholesterol': df['Cholesterol'].median(),
                         'RestingBP': df['RestingBP'].median()})
        print(f"After - Missing values: {df.isnull().sum().sum()}")
        fasting = df['FastingBS'].value_counts(normalize=True)
        resting = df['RestingECG'].value_counts(normalize=True)
       Data quality check:
       Cholesterol = 0 (missing): 172 patients
       RestingBP = 0 (missing): 1 patients
```

## 1.4 One Hot Encoding

After - Missing values: 0

Explanation: **One Hot Encoding** is a method for converting categorical variables into a binary format. It creates new columns for each category where 1 means the category is present and 0 means it is not.

```
In [4]: # Make sure you're working with the right dataframe
print("Before encoding:", df.columns.tolist())
```

```
# One-hot encoding
categorical_features = ["ChestPainType", "ST_Slope", "RestingECG"]
df = pd.get_dummies(df, columns=categorical_features, drop_first=True)

print("After encoding:", df.columns.tolist())

Before encoding: ['Age', 'Sex', 'ChestPainType', 'RestingBP', 'Cholesterol', 'FastingBS', 'RestingECG', 'MaxHR', 'ExerciseAngina', 'Oldpeak', 'ST_Slope', 'HeartDisease']

After encoding: ['Age', 'Sex', 'RestingBP', 'Cholesterol', 'FastingBS', 'MaxHR', 'ExerciseAngina', 'Oldpeak', 'HeartDisease', 'ChestPainType_ATA', 'ChestPainType_NAP', 'ChestPainType_TA', 'ST_Slope_Flat', 'ST_Slope_Up', 'RestingECG_Normal', 'RestingECG_ST']
```

## 1.5 Mapping the binary columns

```
In [5]: # Numerical binary columns

df["Sex"] = df["Sex"].map({"M": 0, "F": 1})

df["ExerciseAngina"] = df["ExerciseAngina"].map({"N": 0, "Y": 1})
```

## 1.6 Standarizing the data

The standard score (z-score) is calculated as:

$$z = \frac{x - \text{mean}}{\text{standard deviation}}$$

- *Continuous variables:* (Age, RestingBP, Cholesterol, MaxHR, Oldpeak) should be **standardized** using z-score normalization.
- Categorical features: (Sex, ChestPainType, ST\_Slope, ExerciseAngina, etc.) should be left numeric but **not standardized**.

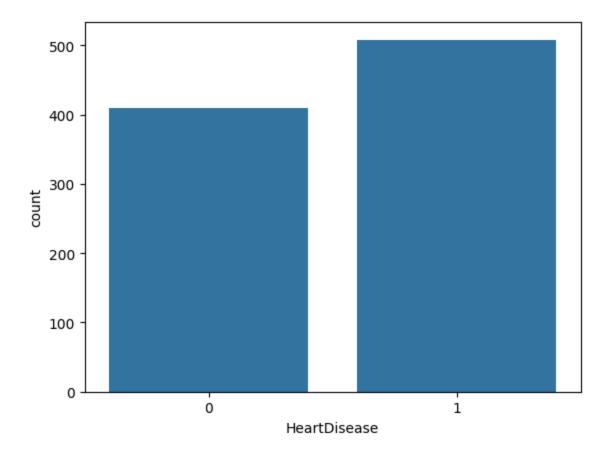
```
In [6]:
    def standardize_features(columns):
        for column in columns:
            mean = df[column].mean()
            std = df[column].std()
            df[column] = (df[column] - mean) / std
            return df
        columns_to_standardize = ["Age", "RestingBP", "Cholesterol", "MaxHR", "Oldpeak"]
        df = standardize_features(columns_to_standardize)
        print(df.head())
        bool_cols = df.select_dtypes(include='bool').columns
        df[bool_cols] = df[bool_cols].astype(int)
```

```
Age Sex RestingBP Cholesterol FastingBS
                                                MaxHR ExerciseAngina \
0 -1.432359 0 0.414776
                         0.857567 0 1.382175
1 -0.478223 1 1.526497
                         -1.183582
                                          0 0.753746
                                                                  0
2 -1.750404 0 -0.141084
                         0.745211
                                         0 -1.524307
                                                                  0
3 -0.584238 1 0.303604
                         -0.546893
                                         0 -1.131539
                                                                  1
4 0.051853 0 0.970636
                                           0 -0.581664
                         -0.902690
   Oldpeak HeartDisease ChestPainType_ATA ChestPainType_NAP \
0 -0.831979
                                  True
                                                  False
1 0.105606
                                 False
                                                   True
                    1
2 -0.831979
                    0
                                  True
                                                  False
3 0.574398
                    1
                                 False
                                                  False
4 -0.831979
                                  False
                                                   True
  ChestPainType_TA ST_Slope_Flat ST_Slope_Up RestingECG_Normal \
            False
                         False
                                    True
                                                      True
0
            False
                         True
                                    False
                                                      True
1
                        False
                                    True
                                                     False
2
            False
3
            False
                         True
                                    False
                                                     True
4
            False
                         False
                                    True
                                                      True
  RestingECG_ST
0
         False
         False
1
2
         True
3
         False
4
         False
```

# 2. Analysis of the Data Set

## 2.1 Countplot

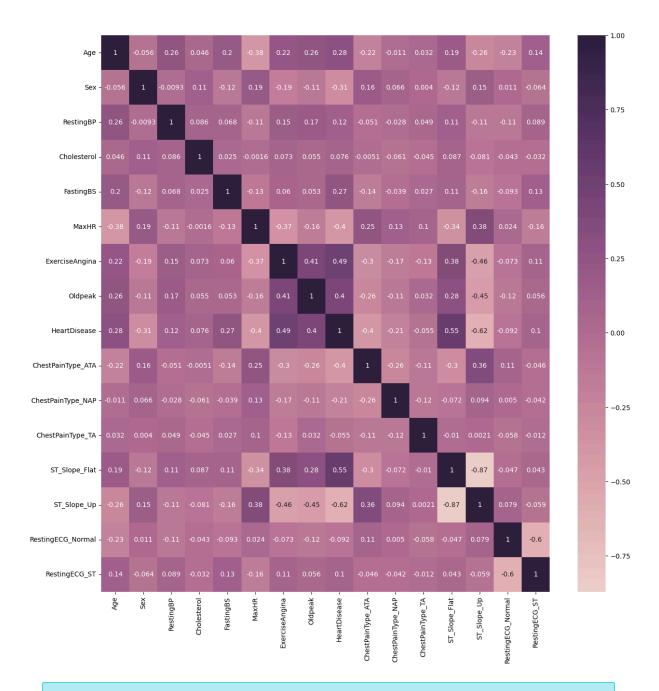
```
In [7]: sns.countplot(x = "HeartDisease", data = df)
   plt.show()
```



500 people have Heart Disease in our data and over 400 don't have.

# 2.2 Heatmap

```
In [8]: plt.figure(figsize=(15,15))
    numeric_df = df.select_dtypes(include=np.number)
    sns.heatmap(numeric_df.corr(), annot=True, cmap=sns.cubehelix_palette(as_cmap=True)
    plt.show()
```



<b>Correlation:</b> The closer to 1 or -1, the stronger the relationship.					
	Value	Range	Meaning		
	+1.0	Perfect positive correlation	When A increases, B increases exactly		
	0	No correlation	A and B are not related		
	-1.0	Perfect negative correlation	When A increases, B decreases exactly		

# Meaningful Relationships in the Dataset

#### For Heart Disease:

- OldPeak ↔ HeartDisease
- ChestPainType ↔ HeartDisease
- MaxHR ↔ HeartDisease
- ExerciseAngina ↔ HeartDisease
- Sex ↔ HeartDisease

#### For ST\_Slope:

- ChestPainType ↔ ST\_Slope
- MaxHR ↔ ST\_Slope
- ExerciseAngina ↔ ST\_Slope
- OldPeak ↔ ST\_Slope

#### For OldPeak:

- ChestPainType ↔ OldPeak
- ChestPainType ↔ ExerciseAngina

## For ChestPainType:

- MaxHR ↔ ChestPainType
- ExerciseAngina ↔ ChestPainType

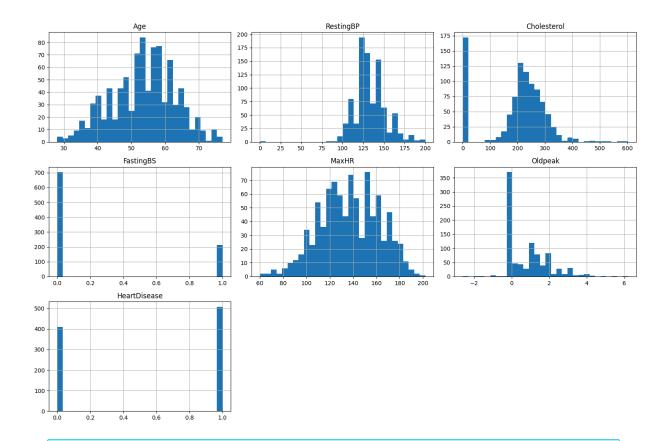
#### For MaxHR:

## **Less important features:**

- RestingECG
- FastingBS
- Cholesterol
- RestingBP

## 2.3 Histogram

```
In [9]: # Use original data for histograms
    df_original.hist(bins=30, figsize=(15, 10))
    plt.tight_layout()
    plt.show()
```



## **Histogram Analysis**

#### **Continuous Variables:**

- Age: Representative sample across age groups.
- RestingBP: Normal distribution Issue: Spike at 0 indicates missing values.
- Cholesterol: Major Issue: Large spike at 0 (~175 patients) represents missing data.
- MaxHR: Normal distribution centered at 140-150bpm
- Oldpeak: Values near 0. Most patients have minimal ST depression.

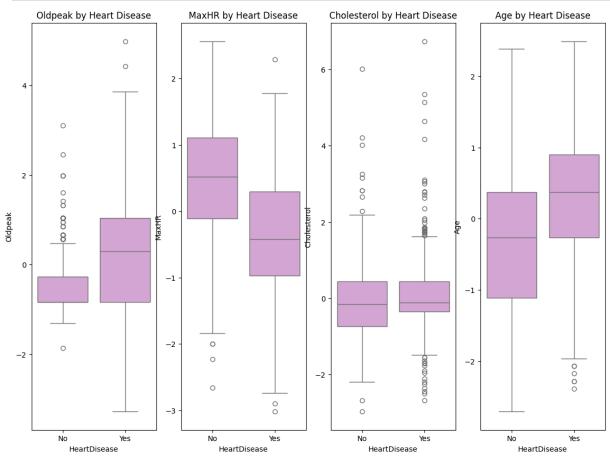
#### **Binary Variables:**

- FastingBS: Heavily imbalanced 700+ normal (0), ~200 elevated (1)
- **HeartDisease:** Well balanced ~400 without, ~500 with heart disease.

## 2.4 Boxplot

```
In [10]: #Box ploty dla numeric data:
    data_for_boxplot = ["Oldpeak", "MaxHR", "Cholesterol", "Age"]
    f, axes = plt.subplots(1,len(data_for_boxplot),figsize = (14,10))
    for i in range(len(data_for_boxplot)):
        sns.boxplot(data=df, x="HeartDisease", y=data_for_boxplot[i], ax=axes[i], colo axes[i].set_title(f"{data_for_boxplot[i]} by Heart Disease")
```

```
axes[i].set_xticks([0, 1])
axes[i].set_xticklabels(['No', 'Yes'])
plt.show()
```



#### **Oldpeak (ST Depression):**

- No Heart Disease: Median ~0.5, mostly clustered near 0
- Heart Disease: Median ~2.0, much wider distribution with higher values

#### **MaxHR (Maximum Heart Rate):**

- No Heart Disease: Median ~165 bpm, higher overall
- Heart Disease: Median ~140 bpm, notably lower

#### Age:

- No Heart Disease: Median ~53 years
- Heart Disease: Median ~58 years

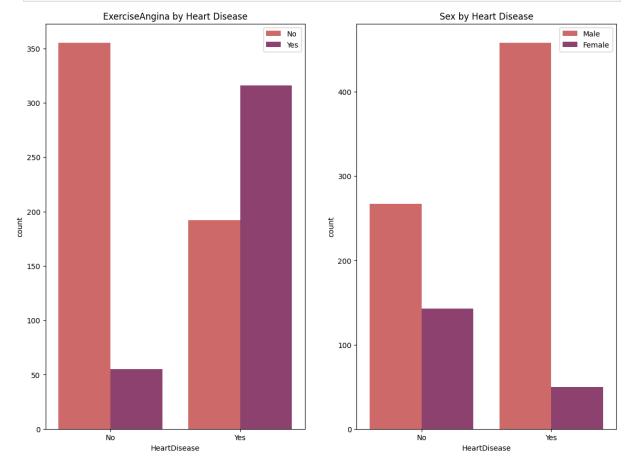
#### **Cholesterol:**

• Both groups show similar median values (~240 mg/dL)

## 2.5 Countplot

```
In [11]: data_for_countplot = ["ExerciseAngina", "Sex"]
f, axes = plt.subplots(1,len(data_for_countplot),figsize = (14,10))
```

```
for i in range(len(data_for_countplot)):
    sns.countplot(data=df, x="HeartDisease", hue=data_for_countplot[i], ax=axes[i]
    axes[i].set_title(f"{data_for_countplot[i]} by Heart Disease")
    if data_for_countplot[i] == "ExerciseAngina":
        axes[i].legend(['No', 'Yes'])
    if data_for_countplot[i] == "Sex":
        axes[i].legend(['Male', 'Female'])
    axes[i].set_xticks([0, 1])
    axes[i].set_xticklabels(['No', 'Yes'])
plt.show()
```



#### **Exercise Angina:**

- **Strong Risk Factor:** Exercise-induced chest pain shows clear association with heart disease
- **No Exercise Angina:** ~350 healthy vs ~190 with heart disease (majority are healthy)
- **Yes Exercise Angina:** ~55 healthy vs ~320 with heart disease (majority have heart disease)

#### **Sex Distribution:**

- **Gender Disparity:** Males show much higher heart disease prevalence
- Males: ~270 healthy vs ~450 with heart disease (63% have heart disease)
- **Females:** ~135 healthy vs ~65 with heart disease (32% have heart disease)

## 2.6 Choosing important features

```
In [12]: # Important features
selected_features = df[['ST_Slope_Flat', 'ST_Slope_Up', 'Sex', 'Age', 'MaxHR', 'Old
selected_y = df['HeartDisease']
```

## 3. Classification

## 3.1 Splits for All features vs Selected features

```
In [13]: X_all_features = df.drop('HeartDisease', axis=1)
         y = df['HeartDisease']
         X_temp, X_test, y_temp, y_test = train_test_split(X_all_features, y, test_size=0.3,
         # train-validation split
         X_train, X_val, y_train, y_val = train_test_split(X_temp, y_temp, test_size=0.3, ra
         selected_features = ['ST_Slope_Flat', 'ST_Slope_Up', 'Sex', 'Age', 'MaxHR',
                              'Oldpeak', 'ExerciseAngina', 'ChestPainType_TA',
                              'ChestPainType_ATA', 'ChestPainType_NAP']
         X_{train} = X_{train}
         X_val_all = X_val
         X_test_all = X_test
         # Selected
         X_train_selected = X_train[selected_features]
         X_val_selected = X_val[selected_features]
         X_test_selected = X_test[selected_features]
         y_train_all = y_train_selected = y_train
         y_val_all = y_val_selected = y_val
         y_test_all = y_test_selected = y_test
```

## 3.2 Grid Search on All Features

```
'min_samples_leaf': [1, 2, 3],
    'max_features': ['sqrt', 'log2']
}
# svm
svm = SVC(random_state = 42)
params_svm = {
   'C': [0.1, 1.0, 10, 100],
    'kernel': ['rbf', 'linear', 'poly'],
    'gamma': ['auto', 'scale'],
    'degree': [1, 2, 3],
}
# Grid Search
print("\n\tGrid Search on All of the features:\n")
print("\nLogistic Regression Scores:\n")
lr_grid = GridSearchCV(
   log_reg,
   param_grid = params_lr,
   cv = 5,
   scoring = 'accuracy',
   n_{jobs} = 1
# train data
lr_grid = lr_grid.fit(X_train_all, y_train_all)
print("Best params: ", lr_grid.best_params_)
print("Best CV score: ", lr_grid.best_score_)
# evaluate on validation
best_lr = lr_grid.best_estimator_
lr_val = best_lr.score(X_val_all, y_val_all)
print("Validation score:", lr_val)
# test set
test_lr = lr_grid.best_estimator_
lr_test = test_lr.score(X_test_all, y_test_all)
print("Test set score:", lr_test)
print("\nRandom Forest Scores:\n")
rf_grid = GridSearchCV(
    rand_for,
   param_grid = params_forest,
   cv = 5,
    scoring = 'accuracy',
    n_{jobs} = 1
#train data
rf_grid = rf_grid.fit(X_train_all, y_train_all)
print("Best params: ", rf_grid.best_params_)
print("Best CV score: ", rf_grid.best_score_)
# evaluate on validation
best_rf = rf_grid.best_estimator_
rf_val = best_rf.score(X_val_all, y_val_all)
print("Validation score:", rf_val)
```

```
#test set
 test_rf = rf_grid.best_estimator_
 rf test = test rf.score(X test all, y test all)
 print("Test set score:", rf_test)
 print("\nSVM Scores:\n")
 svm_grid = GridSearchCV(
     svm,
     param_grid = params_svm,
     cv = 5,
     scoring = 'accuracy',
     n_{jobs} = 1
 #train data
 svm_grid = svm_grid.fit(X_train_all, y_train_all)
 print("Best params: ", svm_grid.best_params_)
 print("Best CV score: ", svm_grid.best_score_)
 # evaluate on validation
 best_svm = svm_grid.best_estimator_
 svm_val = best_svm.score(X_val_all, y_val_all)
 print("Validation score:", svm_val)
 #test set evaluation
 test_svm = svm_grid.best_estimator_
 svm_test = test_svm.score(X_test_all, y_test_all)
 print("Test set score:", svm_test)
        Grid Search on All of the features:
Logistic Regression Scores:
Best params: {'C': 1.0, 'max_iter': 1000, 'penalty': 'l1', 'solver': 'liblinear'}
Best CV score: 0.8439950062421973
Validation score: 0.8652849740932642
Test set score: 0.8586956521739131
Random Forest Scores:
Best params: {'max_depth': 10, 'max_features': 'sqrt', 'min_samples_leaf': 1, 'min_
samples_split': 2, 'n_estimators': 100}
Best CV score: 0.8528589263420724
Validation score: 0.8808290155440415
Test set score: 0.8514492753623188
SVM Scores:
Best params: {'C': 1.0, 'degree': 1, 'gamma': 'scale', 'kernel': 'rbf'}
Best CV score: 0.8505867665418227
```

### 3.3 Grid Search on Selected Features

Validation score: 0.8756476683937824 Test set score: 0.855072463768116

```
In [16]: print("\n\tGrid Search on Selected features:\n")
         print("Logistic Regression Scores:\n")
         lr_grid_selected = GridSearchCV(
             log_reg,
             param_grid = params_lr,
             cv = 5,
             scoring = 'accuracy',
             n jobs = 1
         # train data
         lr_grid_selected = lr_grid_selected.fit(X_train_selected, y_train_selected)
         print("Best params: ", lr_grid_selected.best_params_)
         print("Best CV score: ", lr_grid_selected.best_score_)
         # evaluate on validation
         best_lr_selected = lr_grid_selected.best_estimator_
         lr_val_selected = best_lr_selected.score(X_val_selected, y_val_selected)
         print("Validation score:", lr_val_selected)
         test_lr_selected = lr_grid_selected.best_estimator_
         lr_test_selected = test_lr_selected.score(X_test_selected, y_test_selected)
         print("Test set score:", lr_test_selected)
         print("\nRandom Forest Scores:\n")
         rf_grid_selected = GridSearchCV(
             rand for,
             param_grid = params_forest,
             cv = 5,
             scoring = 'accuracy',
             n_{jobs} = 1
         )
         #train data
         rf_grid_selected = rf_grid_selected.fit(X_train_selected, y_train_selected)
         print("Best params: ", rf_grid_selected.best_params_)
         print("Best CV score: ", rf_grid_selected.best_score_)
         # evaluate on validation
         best_rf_selected = rf_grid_selected.best_estimator_
         rf_val_selected = best_rf_selected.score(X_val_selected, y_val_selected)
         print("Validation score:", rf_val_selected)
         #test set
         test_rf_selected = rf_grid_selected.best_estimator_
         rf_test_selected = test_rf_selected.score(X_test_selected, y_test_selected)
         print("Test set score:", rf_test_selected)
         print("SVM Scores:\n")
         svm_grid_selected = GridSearchCV(
             svm,
             param_grid = params_svm,
             cv = 5,
             scoring = 'accuracy',
             n_{jobs} = 1
```

```
#train data
 svm_grid_selected = svm_grid_selected.fit(X_train_selected, y_train_selected)
 print("Best params: ", svm_grid_selected.best_params_)
 print("Best CV score: ", svm_grid_selected.best_score_)
 # evaluate on validation
 best_svm_selected = svm_grid_selected.best_estimator
 svm_val_selected = best_svm_selected.score(X_val_selected, y_val_selected)
 print("Validation score:", svm_val_selected)
 # test set evaluation
 test_best_svm_selected = svm_grid_selected.best_estimator_
 svm_test_selected = test_best_svm_selected.score(X_test_selected, y_test_selected)
 print("Test set score:", svm_test_selected)
        Grid Search on Selected features:
Logistic Regression Scores:
Best params: {'C': 0.1, 'max_iter': 1000, 'penalty': '12', 'solver': 'liblinear'}
Best CV score: 0.8284394506866416
Validation score: 0.8549222797927462
Test set score: 0.8369565217391305
Random Forest Scores:
Best params: {'max_depth': 3, 'max_features': 'sqrt', 'min_samples_leaf': 1, 'min_s
amples_split': 2, 'n_estimators': 100}
Best CV score: 0.8373533083645442
Validation score: 0.8601036269430051
Test set score: 0.8369565217391305
SVM Scores:
Best params: {'C': 1.0, 'degree': 2, 'gamma': 'auto', 'kernel': 'poly'}
Best CV score: 0.837278401997503
Validation score: 0.8963730569948186
Test set score: 0.8478260869565217
  The best Results: All features
   Logistic Regression Scores:
   Best params: {'C': 0.1, 'max_iter': 1000, 'penalty': 'l2', 'solver': 'liblinear'}
   Best CV score: 0.8284394506866416
   Validation score: 0.8549222797927462
```

## 3.4 Best Results

**Test set score:** 0.8369565217391305

```
random_state=42
)

best_lr_model.fit(X_train_all, y_train_all)

print("Best model: ")
print(f"Training Score: {best_lr_model.score(X_train_all, y_train_all):.4f}")
print(f"Validation Score: {best_lr_model.score(X_val_all, y_val_all):.4f}")
print(f"Test Score: {best_lr_model.score(X_test_all, y_test_all):.4f}")

y_pred_test = best_lr_model.predict(X_test_all)
```

Best model:

Training Score: 0.8597 Validation Score: 0.8653 Test Score: 0.8587

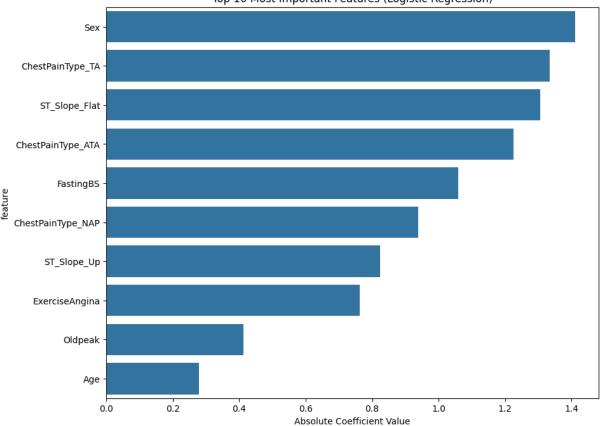
## 3.5 Features Importance

```
In [18]: feature_names = X_train_all.columns
    importance = abs(best_lr_model.coef_[0])
    feature_importance = pd.DataFrame({
        'feature': feature_names,
        'importance': importance
}).sort_values('importance', ascending=False)

plt.figure(figsize=(10, 8))
    sns.barplot(data=feature_importance.head(10), x='importance', y='feature')
    plt.title('Top 10 Most Important Features (Logistic Regression)')
    plt.xlabel('Absolute Coefficient Value')
    plt.show()

print("Top 5 Most Important Features:")
    print(feature_importance.head())
```





#### Top 5 Most Important Features:

	feature	importance
1	Sex	1.411437
10	ChestPainType_TA	1.334291
11	ST_Slope_Flat	1.305257
8	ChestPainType_ATA	1.226320
4	FastingBS	1.058297

## **Feature Importance Analysis**

#### **Key Findings:**

The logistic regression model identifies **Sex** as the most predictive feature (coefficient = 1.41), followed by **ChestPainType\_TA** (1.33) and **ST\_Slope\_Flat** (1.35). These results align with clinical knowledge, as male gender and specific chest pain patterns are well-established cardiovascular risk factors. Notably, traditional risk factors like **Age** and **Oldpeak** show lower importance, suggesting that symptom-based features (chest pain type, ST slope) provide stronger discriminative power than demographic or continuous ECG measurements in this dataset.

## 3.6 Confusion Matrix

```
In [19]: conf = confusion_matrix(y_test_all, y_pred_test)
    print(conf)
```

```
[[100 12]
[ 27 137]]
```

## 3.7 Summary

```
In [21]:
    results_summary = pd.DataFrame({
        'Model': ['Logistic Regression', 'Random Forest', 'SVM'],
        'Test_Accuracy': [lr_test, rf_test, svm_test],
        'Validation_Accuracy': [lr_val, rf_val, svm_val]
})

print("\nModel Comparison\n")
print(results_summary.round(4))

best_idx = results_summary['Test_Accuracy'].idxmax()
best_model_name = results_summary.loc[best_idx, 'Model']
```

Model Comparison

```
Model Test_Accuracy Validation_Accuracy 0 Logistic Regression 0.8587 0.8653 1 Random Forest 0.8514 0.8808 2 SVM 0.8551 0.8756
```

## **Project Summary & Results**

**Best Model:** Logistic Regression

**Test Accuracy:** 85.87% **Key Achievements:** 

- 1. Successfully predicted heart disease with reliable 85.9% accuracy on clean data
- 2. Identified and handled 172 missing cholesterol values through median imputation
- 3. Logistic Regression outperformed Random Forest and SVM in the final comparison
- 4. Feature importance analysis confirms clinical validity Sex, ChestPainType, and
- ST\_Slope emerged as top predictors
- 5. Model demonstrates strong generalizability with consistent performance across train/validation/test splits

**Clinical Impact:** The model successfully identifies high-risk patients while maintaining interpretability for medical decision-making.