Machine Learning

Topic: Heart Disease Risk Detection

Introduction

A heart attack is a medical emergency that usually occurs when a blood clot blocks blood flow to the heart. Without blood, tissue loses oxygen and dies. According to the CDC, In the United States, someone has a heart attack every 40 seconds. Every year, about 805,000 people in the United States have a heart attack. Of these, 605,000 are a first heart attack 200,000 happen to people who have already had a heart attack. About 1 in 5 heart attacks is silent—the damage is done, but the person is not aware of it. Using the following dataset, we will take an exploratory look at the factors that lead to heart attacks and try to predict which are the biggest culprits are.

Data Source :

> **Kaggle Dataset**

Required Libraries ...

In [1]:
```
import pandas as pd
import numpy as np
import matplotlib.pyplot as plt
%matplotlib inline
import seaborn as sns
import plotly as py
import plotly.graph_objects as go
import plotly.express as px
import statsmodels.api as sm
from sklearn import preprocessing
from sklearn.metrics import confusion_matrix
from sklearn.metrics import accuracy_score
from sklearn.model_selection import train_test_split
from sklearn.model_selection import GridSearchCV
from sklearn.linear_model import LogisticRegression
from sklearn.svm import SVC
from sklearn.tree import DecisionTreeClassifier
from sklearn.neighbors import KNeighborsClassifier
```

Dataset

In [2]:
```
df = pd.read_csv("C:\\Users\\ferna\\OneDrive\\Desktop\\projects\\Machine Learning\\HeartAttackClassData.csv")
```

Variable Description

Age: Age of patient

Sex: Sex of patient

Cp: Type of chest pain:

Value (0): typical angina

Value (1): atypical angina

Value (2): non-anginal pain

Value (3): asymptomatic

trtbps: resting blood pressure (in mm Hg)

chol: cholestorol levels measured in mg/dl

fbs: (fasting blood sugar > 120 mg/dl (Diabetic))

Value (0): false

Value (1): true

restecg: resting electrocardiographic results

Value (0): normal

Value (1): heart showing some abnormalities

Value (2): Left Ventricular Hypertrophy (a term for a heart's left pumping chamber that has thickened and may not be pumping efficiently).

thalachh: Maximum heart rate achieved

exng: exercise induced angina

Value (0): no

Value (1): yes

oldpeak: ST depression induced by exercise relative to rest. (ST depression is a type of abnormality. the ST segment is the flat, isoelectric part of the ECG and it represents the interval between ventricular depolarization and repolarization)

slp: the slope of the peak exercise ST segment

Value (0): upsloping

Value (1): flat

Value (2): downslope

caa: The number of major vessels

thall: thalassemia (an inherited blood disorder that causes your body to have less hemoglobin than normal)   Value (0): silent carrier; One gene is missing or damaged, this means you don't have signs of the disease, but you can pass the damaged gene on to your child

Value (1): carrier; Two genes are missing. You may have mild anemia.

Value (2): Hemoglobin H disease; Three genes are missing, you may have moderate to severe anemia. Blood transfusions are often needed.   You have a greater risk of having a child with alpha thalassemia major.

Value (3): Alpha thalassemia major; All 4 genes are missing. This causes severe anemia. In most cases, a baby with this condition will die before   birth.

output: diagnosis of heart disease

Value (0): lower risk of heart disease

Value (1): higher risk of heart disease

In [3]:
```
df.head()
```

Out[3]:

	age	sex	cp	trtbps	chol	fbs	restecg	thalachh	exng	oldpeak	slp	caa	thall	output
0	63	1	3	145	233	1	0	150	0	2.3	0	0	1	1
1	37	1	2	130	250	0	1	187	0	3.5	0	0	2	1
2	41	0	1	130	204	0	0	172	0	1.4	2	0	2	1
3	56	1	1	120	236	0	1	178	0	0.8	2	0	2	1
4	57	0	0	120	354	0	1	163	1	0.6	2	0	2	1

Analysis

In [4]:
```
print('The shape of the dataset is:',df.shape)
```

```
The shape of the dataset is: (303, 14)
```

In [5]:
```
df.isnull().sum()
```

```
Out[5]: age         0
        sex         0
        cp          0
        trtbps      0
        chol        0
        fbs         0
        restecg     0
        thalachh    0
        exng        0
        oldpeak     0
        slp         0
        caa         0
        thall       0
        output      0
        dtype: int64
```

Luckily, we do not have any missing values.

```
In [6]: df.describe().transpose()
```

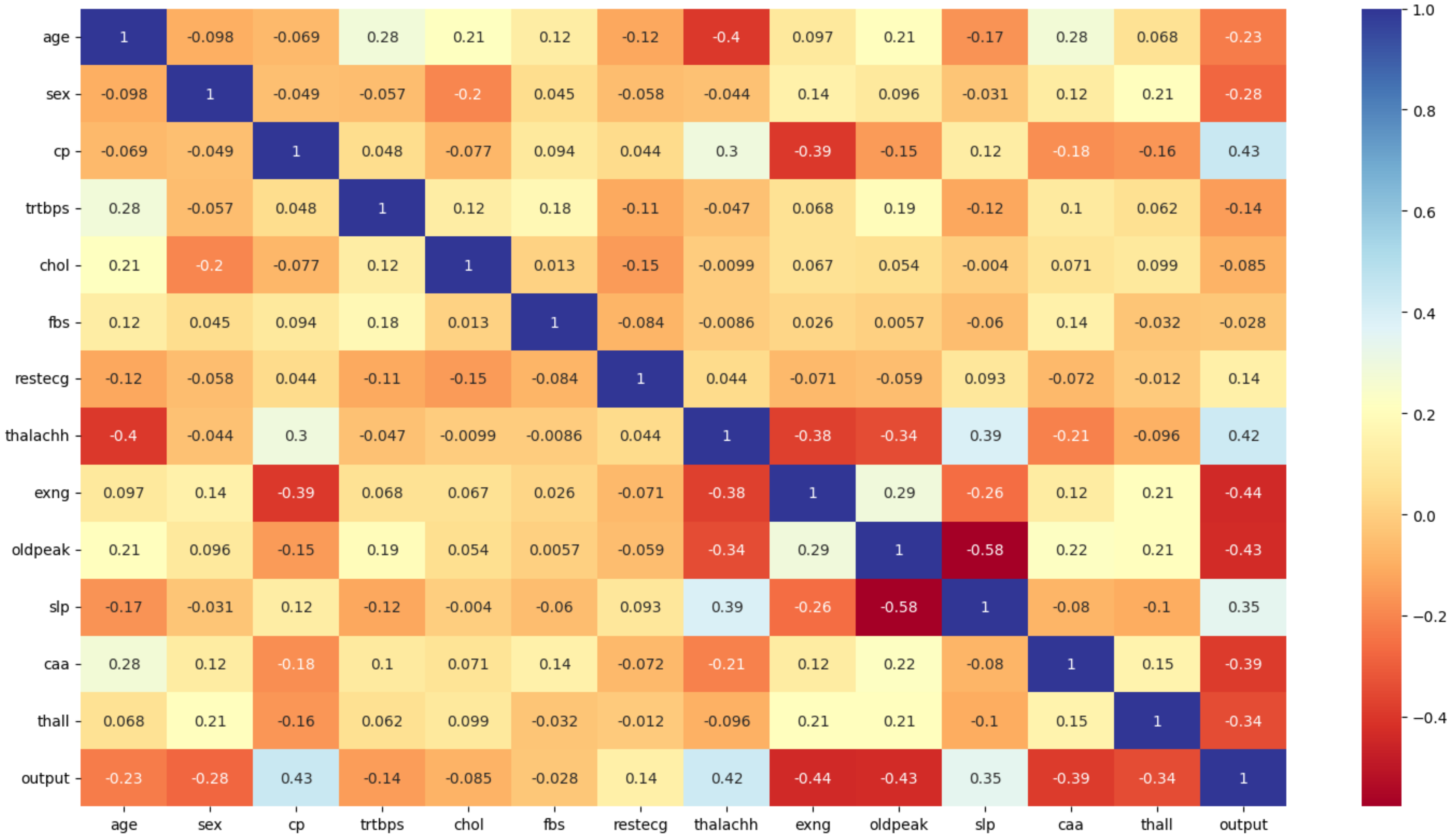
Out[6]:

	count	mean	std	min	25%	50%	75%	max
age	303.0	54.366337	9.082101	29.0	47.5	55.0	61.0	77.0
sex	303.0	0.683168	0.466011	0.0	0.0	1.0	1.0	1.0
cp	303.0	0.966997	1.032052	0.0	0.0	1.0	2.0	3.0
trtbps	303.0	131.623762	17.538143	94.0	120.0	130.0	140.0	200.0
chol	303.0	246.264026	51.830751	126.0	211.0	240.0	274.5	564.0
fbs	303.0	0.148515	0.356198	0.0	0.0	0.0	0.0	1.0
restecg	303.0	0.528053	0.525860	0.0	0.0	1.0	1.0	2.0
thalachh	303.0	149.646865	22.905161	71.0	133.5	153.0	166.0	202.0
exng	303.0	0.326733	0.469794	0.0	0.0	0.0	1.0	1.0
oldpeak	303.0	1.039604	1.161075	0.0	0.0	0.8	1.6	6.2
slp	303.0	1.399340	0.616226	0.0	1.0	1.0	2.0	2.0
caa	303.0	0.729373	1.022606	0.0	0.0	0.0	1.0	4.0
thall	303.0	2.313531	0.612277	0.0	2.0	2.0	3.0	3.0
output	303.0	0.544554	0.498835	0.0	0.0	1.0	1.0	1.0

The mean age of the observations is 54 with the average participant having Hemoglobin H disease as shown in the 'thall' column men also appear to make up the majority of the observations and a little more than half of the participants are at risk of heart disease.

In [7]:

```
plt.figure(figsize = (15, 8))
sns.heatmap(df.corr(),cmap='RdYlBu', annot=True)
plt.tight_layout()
```



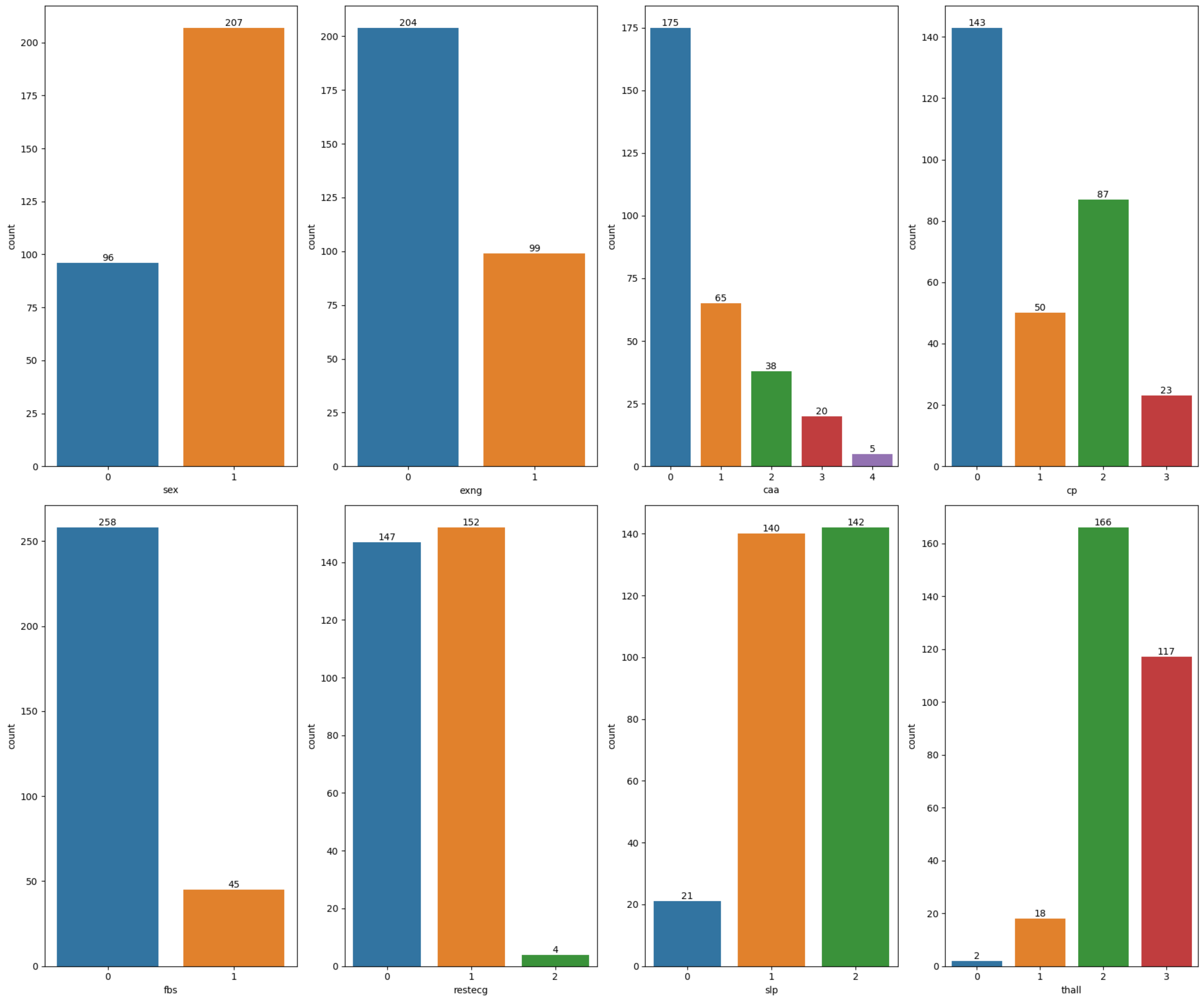
Not many of the variables have a direct correlation with the output columns. The three highest correlated variables are chest pain(cp), maximum heart rate achieved (thalachh), and the slope of the ST depression (slp).

In [8]:
```
categorical = ['sex','exng','caa','cp','fbs','restecg','slp','thall']
continuous = ["age","trtbps","chol","thalachh","oldpeak"]
target = ["output"]
print("The categorial variables are : ", categorical)
print("The continuous variables are : ", continuous)
print("The target variable is :  ", target)
```

```
The categorial variables are :  ['sex', 'exng', 'caa', 'cp', 'fbs', 'restecg', 'slp', 'thall']
The continuous variables are :  ['age', 'trtbps', 'chol', 'thalachh', 'oldpeak']
The target variable is :   ['output']
```

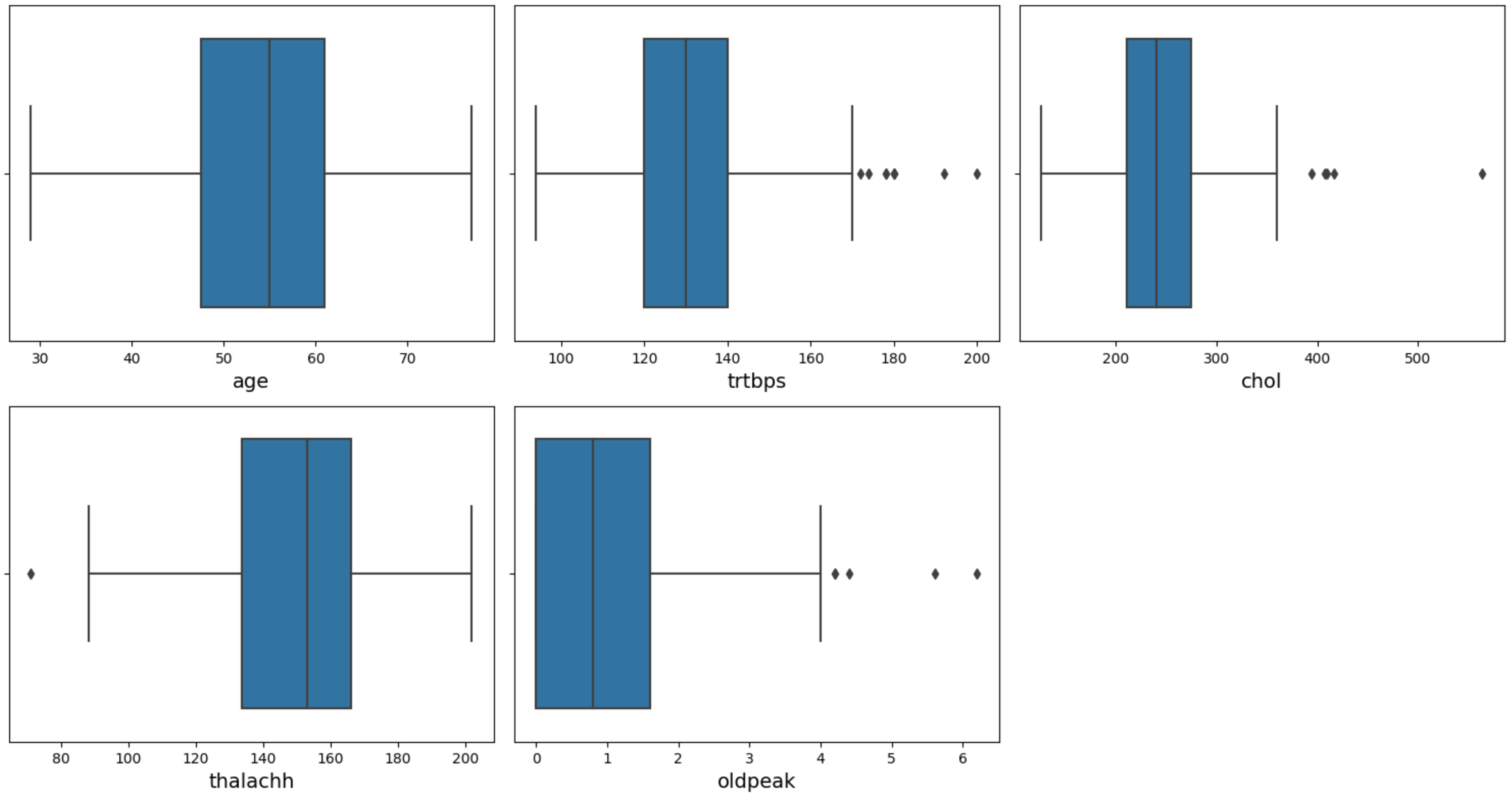
In [9]:

```
fig = plt.figure(figsize=(18,15))
grid = fig.add_gridspec(2,4)

ax0 = fig.add_subplot(grid[0,0])
sns.countplot(data=df, x=categorical[0], ax=ax0)
ax0.bar_label(ax0.containers[0])

ax1 = fig.add_subplot(grid[0,1])
sns.countplot(data=df, x=categorical[1], ax=ax1)
ax1.bar_label(ax1.containers[0])

ax2 = fig.add_subplot(grid[0,2])
sns.countplot(data=df, x=categorical[2], ax=ax2)
ax2.bar_label(ax2.containers[0])

ax3 = fig.add_subplot(grid[0,3])
sns.countplot(data=df, x=categorical[3], ax=ax3)
ax3.bar_label(ax3.containers[0])

ax4 = fig.add_subplot(grid[1,0])
sns.countplot(data=df, x=categorical[4], ax=ax4)
ax4.bar_label(ax4.containers[0])

ax5 = fig.add_subplot(grid[1,1])
sns.countplot(data=df, x=categorical[5], ax=ax5)
ax5.bar_label(ax5.containers[0])

ax6 = fig.add_subplot(grid[1,2])
sns.countplot(data=df, x=categorical[6], ax=ax6)
ax6.bar_label(ax6.containers[0])

ax7 = fig.add_subplot(grid[1,3])
sns.countplot(data=df, x=categorical[7], ax=ax7)
ax7.bar_label(ax7.containers[0])

plt.tight_layout()
```


count
sex
96
207
0
1
exng
204
99
caa
175
65
38
20
5
cp
143
50
87
23
fbs
258
45
restecg
147
152
4
slp
21
140
142
thall
2
18
166
117

Above we can see the total value counts for each categorical variable. Men make up the overwhelming majority of the observations, more than doubling the amount of women. Most participants do not have exercise induced angina specifically (exng) but a majority do have typical anginal pain (1). Most particpants are not diabetic (fbs) but most do seem to contain Hemoglobin H disease (thall) which is represented by the value (2).

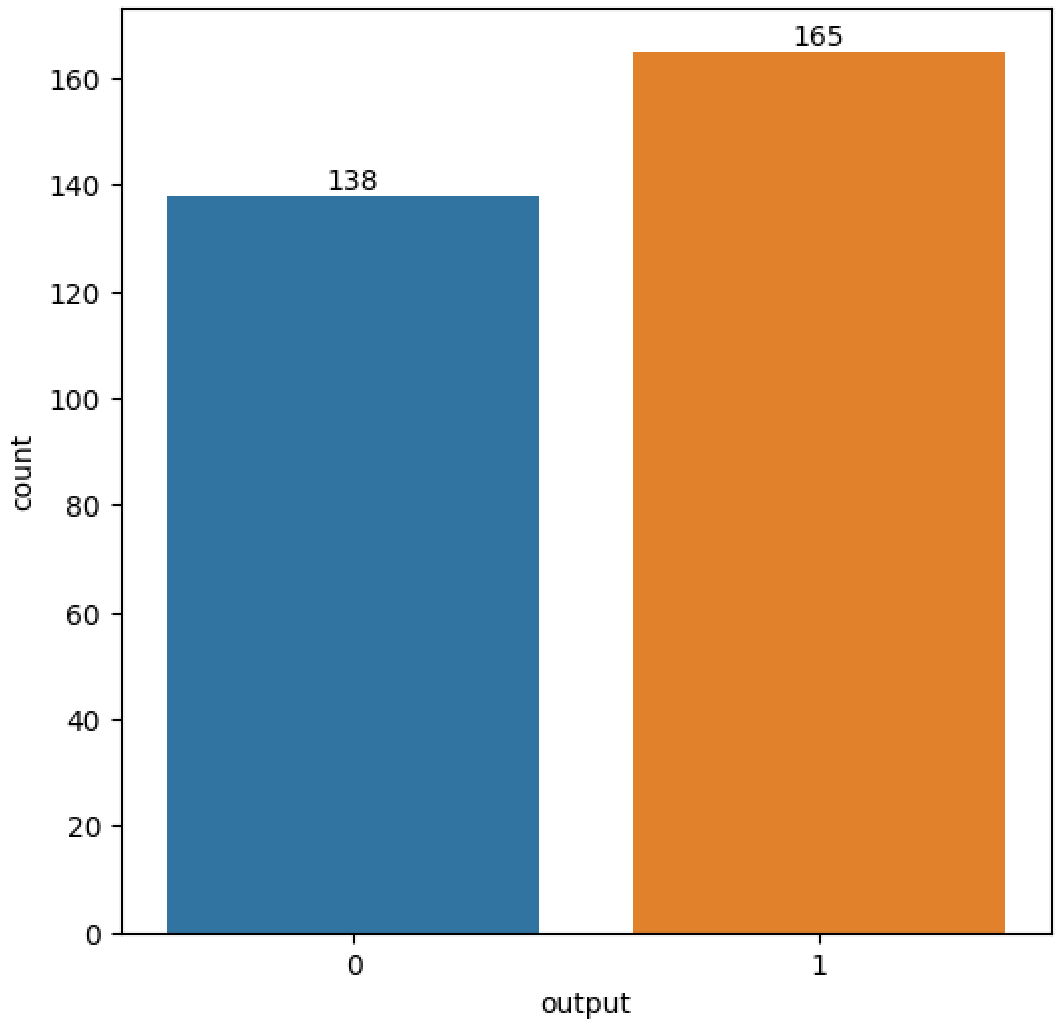
In [10]:
```
fig = plt.figure(figsize=(15,8))
grid = fig.add_gridspec(2,3)

ax0 = fig.add_subplot(grid[0,0])
sns.boxplot(data=df, x=continuous[0], ax=ax0)
ax0.set_xlabel('age', fontsize=14)

ax1 = fig.add_subplot(grid[0,1])
sns.boxplot(data=df, x=continuous[1], ax=ax1)
ax1.set_xlabel('trtbps', fontsize=14)

ax2 = fig.add_subplot(grid[0,2])
sns.boxplot(data=df, x=continuous[2], ax=ax2)
ax2.set_xlabel('chol', fontsize=14)

ax3 = fig.add_subplot(grid[1,0])
sns.boxplot(data=df, x=continuous[3], ax=ax3)
ax3.set_xlabel('thalachh', fontsize=14)

ax4 = fig.add_subplot(grid[1,1])
sns.boxplot(data=df, x=continuous[4], ax=ax4)
ax4.set_xlabel('oldpeak', fontsize=14)

plt.tight_layout()
```



These boxplots show us the distribution of the continuous variables. There are outliers for resting blood pressure(trtbps), cholesterol, and oldpeak. There is also one lower outlier for max heart rate (thalachh).

In [11]:
```
fig = plt.figure(figsize=(6,6))
out = sns.countplot(x='output', data=df)
out.bar_label(out.containers[0])
```

Out[11]:
```
[Text(0, 0, '138'), Text(0, 0, '165')]
```



165 of the participants are at risk of heart disease.

Split and Scale

Before continuing we will build a function to plot a confusion matrix for each model built ...

In [12]:
```
def plot_confusion_matrix(y,y_predict):
    cm = confusion_matrix(y, y_predict)
    ax= plt.subplot()
    sns.heatmap(cm, cmap='Spectral',annot=True, ax = ax);
    ax.set_xlabel('Predicted labels')
    ax.set_ylabel('True labels')
    ax.set_title('Confusion Matrix');
    ax.xaxis.set_ticklabels(['No risk', 'At risk']); ax.yaxis.set_ticklabels(['No risk', 'At risk'])
```

In [13]:
```
X = df.drop(['output'],axis = 1)
Y= df['output']
```

In [14]:
```
X_train, X_test, Y_train, Y_test = train_test_split(X,Y, test_size = 0.2, random_state = 42)
```

Since we do have some outliers among our continous variables we will use the RobustScaler to scale them. This scales features using statistics that are robust to outliers by removing the median and scaling the data according to the interquartile range. The IQR is the range between the 1st quartile (25th percentile) and the 3rd quartile (75th percentile).

In [15]:
```
scaler = preprocessing.RobustScaler()
X_train[continuous] = scaler.fit_transform(X_train[continuous])
X_test[continuous]  = scaler.transform(X_test[continuous])
```

In [16]:
```
print("The shape of X_train is:", X_train.shape)
print("The shape of X_test is:", X_test.shape)
print("The shape of Y_train is:", Y_train.shape)
print("The shape of Y_test is:", Y_test.shape)
```

```
The shape of X_train is: (242, 13)
The shape of X_test is: (61, 13)
The shape of Y_train is: (242,)
The shape of Y_test is: (61,)
```

Building Models

Logistic Regression

In [17]:
```
import warnings
warnings.filterwarnings('ignore')
```

In [18]:
```python
lr = LogisticRegression()
lr_params = {'C':[0.01,0.1,1],
             'penalty':['l1','l2','elasticnet'],
             'solver':['liblinear','lbfgs']}
```

In order to ensure that our models are as accurate as possible, we will tune hyperparameters using the dictionary above named **lr_params** and provide multiple options for each.

Hyperparameters are different parameter values that are used to control the learning process and have a significant effect on the performance of machine learning models. With that being said, hyperparameter optimization is the process of finding the right combination of hyperparameter values to achieve maximum performance on the data in a reasonable amount of time. This process plays a vital role in the prediction accuracy of a machine learning algorithm.

For our Logistic Regression model we will tune the **C**, **penalty**, and **solver** hyperparameters ... - **C** is the inverse of regularization strength, meaning that regularization is increased by making the number smaller and this is usually tuned in powers of 10 as shown. - **penalty** refers to the imposition of a penalty to the logistic model for having too many variables. This results in shrinking the coefficients of the less contributive variables toward zero or even zero. This is also known as regularization. - **solver** refers to the algorithm to be used in the optimization problem.

We will use the GridSearchCV feature which performs an exhaustive search of all possible combinations of the specified parameter values for each estimator, in this case Logistic Regression, in order to build the best model possible.

In [19]:
```python
logreg_cv = GridSearchCV(lr,lr_params,cv=5)
logreg_cv.fit(X_train, Y_train)
```

Out[19]:
```
▸          GridSearchCV
▸ estimator: LogisticRegression
     ▸ LogisticRegression
```

In [20]:
```python
print("Best Parameters :",logreg_cv.best_params_)
print("GridSearch Accuracy :",(logreg_cv.best_score_*100).round(2),'%')
```

```
Best Parameters : {'C': 1, 'penalty': 'l2', 'solver': 'liblinear'}
GridSearch Accuracy : 82.22 %
```

Now that we have run the GridSearch on our training data, we can see that the best parameters for our log regression are 1 for **C**, l2 for **penalty**, and liblinear for **solver**.

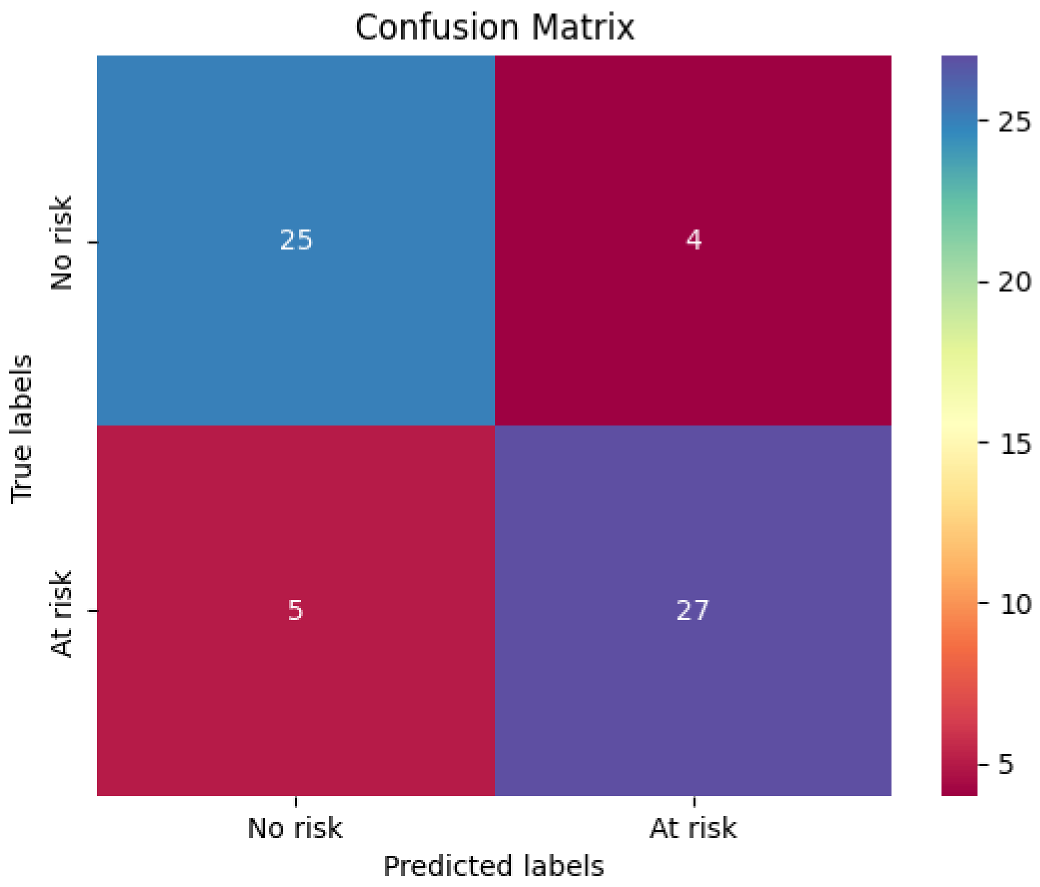
- The 1 for **C** parameter means that the strength of regularization is on the weaker side since this was the highest option given, perhaps because we already scaled our features prior.
- l2 for **penalty** parameter means a ridge regression algorithm was used to regularize the data. This combats the overfitting by forcing weights to be small, but not making them exactly zero.
- liblinear for **solver** refers, as stated, to the optimization algorithm. Liblinear is more efficient with smaller datasets and mostly useful for one-vs-rest problems, both of which apply to our dataset.

This combination of parameters produced an acccuracy of 82.22% based off of our training data.

In [21]:
```
y_predict=logreg_cv.predict(X_test)

print("Logistic Regression model accuracy:",
     ( accuracy_score(Y_test, y_predict)*100).round(2),'%')
```

```
Logistic Regression model accuracy: 85.25 %
```

In [22]:
```
plot_confusion_matrix(Y_test,y_predict)
```



When using our new optimized Log Regression to make predictions on our test data, meaning data that the algorithm has yet to see, we find that it predicts risk of heart attack at a rate of 85.25%, making 52 correct predictions out of 61 as shown in the confusion matrix above.

Support Vector Machine

In [23]:
```
svm = SVC()
svm_params = {'C':[0.01,0.1,1],
              'kernel':['linear', 'rbf','poly','sigmoid'],
              'degree':[2,3,4,5],
              'gamma':[0.01,0.1,1.0]}
```

For our Support Vector Classifier we created the **svm_params** dictionary to tune the hyperparameters. The parameters for Support Vector Machines are a little different than that of the Log Regression but, likewise, work to optimize our algorithm and give us the most accurate model possible.

For our Support Vector Classifier we will tune the **C**, **kernel**,**degree**,and **gamma** hyperparameters ... - **C** is the inverse of the regularization strength, same as in the Log Regression model above. - **kernel** refers to the type of hyperplane used to seperate the data. - **degree** refers to the degree of the 'poly' (polynomial) kernel and is ignored by all other kernels. - **gamma** defines how far the influence of a single training example reaches, with low values meaning 'far' from the hyperplane and high values meaning 'close'.

In [24]:
```python
svm_cv = GridSearchCV(svm,svm_params,cv=5)
svm_cv.fit(X_train, Y_train)
```

Out[24]:
```
▸ GridSearchCV
▸ estimator: SVC
    ▸ SVC
```

In [25]:
```python
print('Best Parameters :',svm_cv.best_params_)
print("GridSearch Accuracy :",(svm_cv.best_score_*100).round(2),'%')
```

```
Best Parameters : {'C': 0.01, 'degree': 2, 'gamma': 1.0, 'kernel': 'poly'}
GridSearch Accuracy : 82.64 %
```

Now that we have run the GridSearch on our training data, we can see that the best parameters for our Support Vector Machine are 0.01 for **C**, poly for **kernel**, 2 for **degree**, and 1.0 for **gamma**.

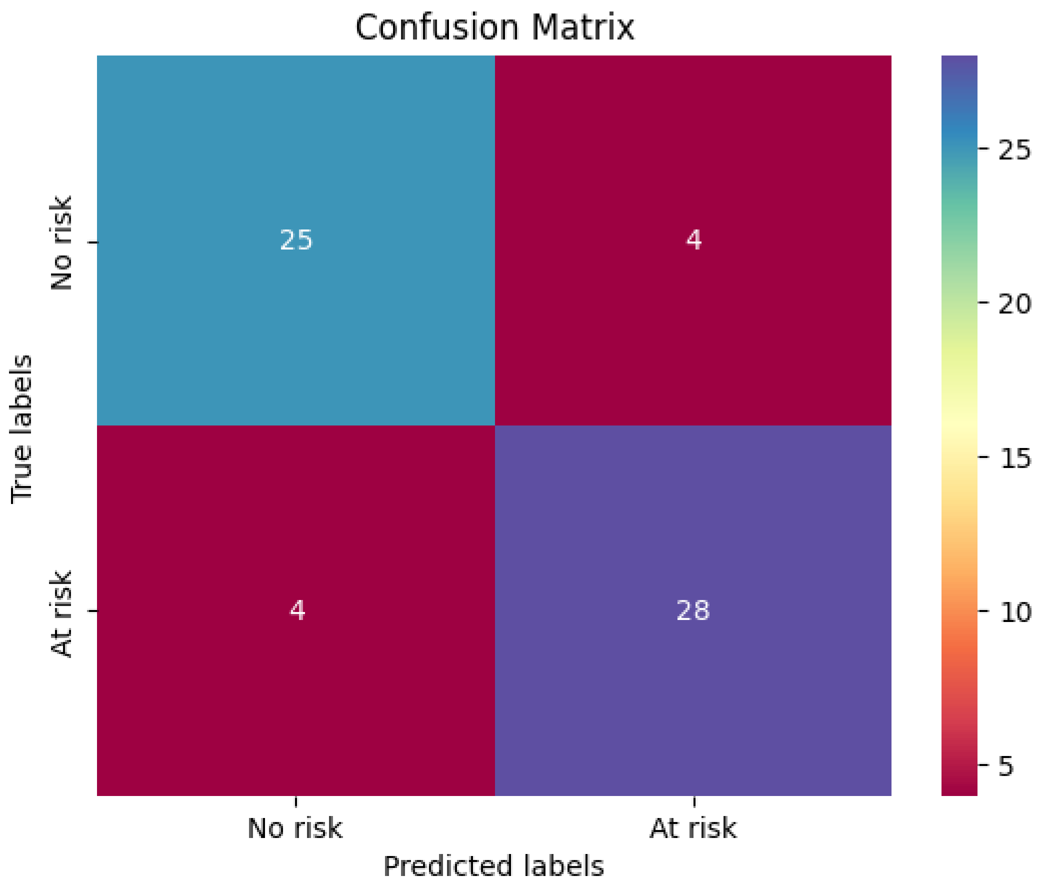
- The 0.01 for **C** parameter means that the strength of regularization is on the stronger end since this was the lowest option given.
- poly for the **kernel** parameter means the model distinguishes curved or nonlinear input space.
- 2 for **degree** refers, as stated, to the degree of the polynomial kernel since that was selected as the best kernel.
- 1 for **gamma** means that the algorithm will consider points closer to the decision boundary(hyperplane) as this was the highest option. This parameter only works with non-linear kernels.

This combination of parameters produced an acccuracy of 82.64% based off of our training data.

In [26]:
```
y_predict=svm_cv.predict(X_test)

print("Support Vector model accuracy:",
     ( accuracy_score(Y_test, y_predict)*100).round(2),'%')
```

```
Support Vector model accuracy: 86.89 %
```

In [27]:
```
plot_confusion_matrix(Y_test,y_predict)
```



When using our newly optimized Support Vector Machine to make predictions on our test data, we find that it predicts risk of heart attack at an 86.89% rate, making 53 correct predictions out of 61 as shown in the confusion matrix above. One more than our Log Regression Model.

Decision Tree

In [28]:
```
tree = DecisionTreeClassifier()
tree_params = {'criterion':['gini','entropy','log_loss'],
               'splitter': ['best', 'random'],
               'max_depth': ['None',2, 4, 6, 8],
               'min_samples_split': [2, 4, 6, 8, 10],
                 'min_samples_leaf': [1, 2, 3, 4, 5, 6, 7],
                 'max_features': ['auto', 'sqrt','log2']}
```

The parameters dictionary for tuning our Decision Tree model will be named **tree_params** as shown above. As we can see, this model has a few more parameters to tune than the previous two.

- **criterion** is the function that measures the quality of a split. It determines how a decision tree chooses to split data. - **splitter** refers to the strategy used to choose the split at each node. - **max_depth** is the maximum depth of the tree. - **min_samples_split** is the minimum number of samples required to split an internal node. - **min_samples_leaf** is the minimum number of samples required to be at a leaf node. - **max_features** is the maximum number of features to consider when looking for the best split.

In [29]:
```
tree_cv = GridSearchCV(tree,tree_params,cv=5)
tree_cv.fit(X_train, Y_train)
```

Out[29]:
```
▸ GridSearchCV
▸ estimator: DecisionTreeClassifier
    ▸ DecisionTreeClassifier
```

In [30]:
```
print('Best Parameters :',tree_cv.best_params_)
print("GridSearch Accuracy :",(tree_cv.best_score_*100).round(2),'%')
```

```
Best Parameters : {'criterion': 'gini', 'max_depth': 8, 'max_features': 'log2', 'min_samples_leaf': 3, 'min_samples_spl
it': 4, 'splitter': 'best'}
GridSearch Accuracy : 83.06 %
```

According to the GridSearch, we can see that the best parameters for our Decision Tree Model are 'entropy' for **criterion**, 4 for **max_depth**, auto for **max_features**, 5 for **min_samples_leaf**, 6 for **min_samples_split**, and 'best' for **splitter**.

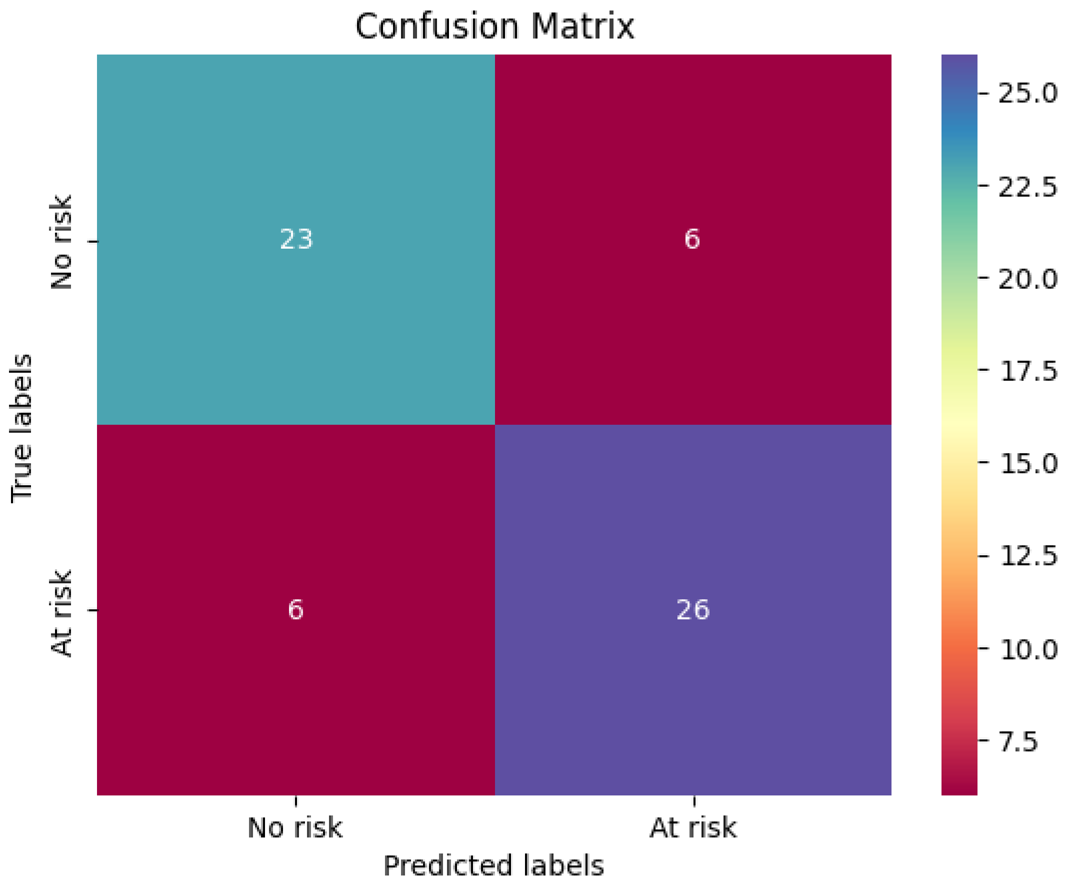
- The 'entropy' option for the **criterion** parameter is the measure of the uncertainty of a random variable. In other words, we can say that entropy is the machine learning metric that measures the unpredictability in the system.
- 'best' for the **splitter** parameter means the model will consider all features and choose the best split.
- 4 for **max_depth** means the tree will be 4 nodes deep.
- 6 for **min_samples_split** means that at least 6 samples are required to split an internal node.
- 5 for **min_samples_leaf** means that a minimum of 5 samples are required to be at a leaf node.
- 'auto' for **max_features** means the algorithm will square root the total number of features and use that number here.

This combination of parameters produced an acccuracy of 81.85% based off of our training data.

```
In [31]: y_predict=tree_cv.predict(X_test)

         print("Decision Tree model accuracy:",
              ( accuracy_score(Y_test, y_predict)*100).round(2),'%')
```

```
Decision Tree model accuracy: 80.33 %
```

```
In [32]: plot_confusion_matrix(Y_test,y_predict)
```



When using our tuned Decision Tree model to make predictions on our test data, we find that it predicts risk of heart attack at 80.03%, mking 49 correct predictions out of 61 as shown in the confusion matrix above. This represents a somewhat steep dropoff from our previous two models, with the biggest issue being false negatives.

K-Nearest-Neighbors

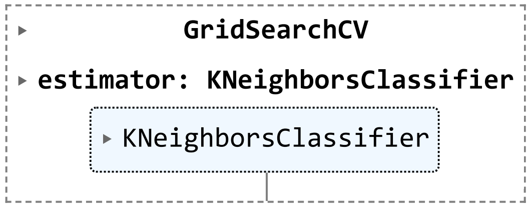
In [33]:
```python
KNN = KNeighborsClassifier()
knn_params = {'n_neighbors': list(range(1,30)),
              'algorithm': ['auto', 'ball_tree', 'kd_tree', 'brute'],
              'p': [1,2]}
```

We will tune our K-Neighbors Classifer model by using the **knn_params** dictionary shown directly above.

- **n_neighbors** refers to number of neighbors to use by default when searching for similarities.
- **algorithm** refers to the algorithm used to compute the nearest neighbors.
- **p** is the power parameter for the Minkowski metric.

In [34]:
```python
knn_cv = GridSearchCV(KNN,knn_params,cv=10)
knn_cv.fit(X_train, Y_train)
```

Out[34]:



In [35]:
```python
print("Best Parameters :",knn_cv.best_params_)
print("GridSearch Accuracy :",knn_cv.best_score_)
```

```
Best Parameters : {'algorithm': 'auto', 'n_neighbors': 7, 'p': 1}
GridSearch Accuracy : 0.8265
```

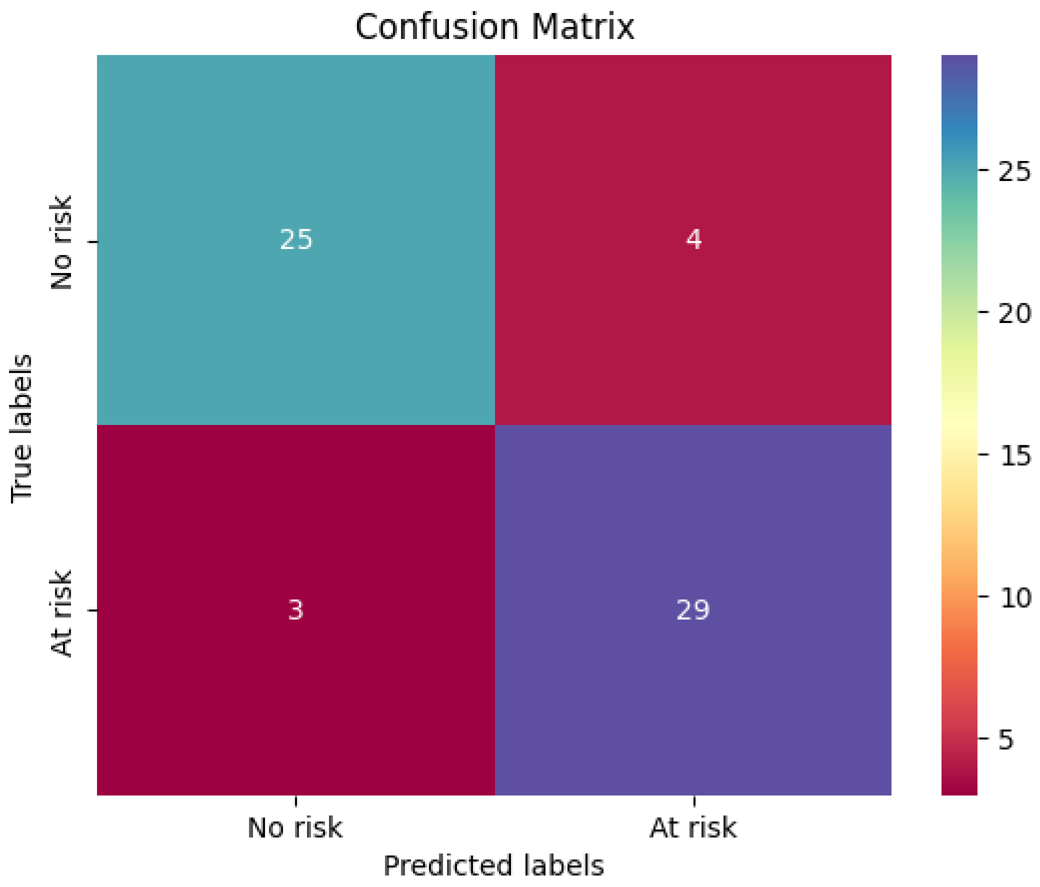
The GridSearch tells us the best parameters are 7 for **n_neighbors**, obtained using the 'auto' option for the **algorithm**, and 1 for the Minkowski metric, denoted in our dictionary as **p**.

- 7 for **n_neighbors** means that the model will look at the 7 closest neighbors for each test observation in order to find similarities and make its prediction.
- 'auto' for the **algorithm** parameter means the model will come up with its own algorithm based on the training data provided.
- 1 for **p** parameter means the Minkowski Distance Metric will be set to 1, or Manhattan Distance. This means the distance between two points is the sum of the absolute differences of their Cartesian coordinates.

In [36]:
```
y_predict=knn_cv.predict(X_test)

print("K-Neighbors model accuracy:",
     ( accuracy_score(Y_test, y_predict)*100).round(2),'%')
```

```
K-Neighbors model accuracy: 88.52 %
```

In [37]:
```
plot_confusion_matrix(Y_test,y_predict)
```



Our optimized K-Nearest-Neighbors model predicts risk of heart attack at a rate of 88.52% when presented with the previously unseen test data, making 54 correct predictions out of 61 as shown in the confusion matrix above.

Comparisons

In [38]:
```
mods = {'LogReg':[logreg_cv.best_score_,logreg_cv.score(X_test, Y_test)],'SVM':[svm_cv.best_score_,svm_cv.score(X_test,
scores = pd.DataFrame.from_dict(mods, orient='index',columns=['Best CV Score','Test Score'])
scores
```

Out[38]:

	Best CV Score	Test Score
LogReg	0.822194	0.852459
SVM	0.826361	0.868852
Tree	0.830612	0.803279
KNN	0.826500	0.885246

The best model for prediction whether or not a patient is at risk of heart failure is the K-Nearest-Neighbors model. This optimized model produced the highest score on the GridSearch using the training set and also had the highest prediction on the unseen test set.