HEART

```
import numpy as np
import pandas as pd
import matplotlib.pyplot as plt
from sklearn.model_selection import train_test_split
from sklearn.preprocessing import LabelEncoder
from sklearn.svm import SVC
import seaborn as sns
```

```
df= pd.read_csv('heart.csv')
```

```
df.head(5) # limited number of rows
```

```
#LE: Sex, FastingBS, ExerciseAngina
#Categorical: ChestPainType, RestingECG, ST_Slope
#Integer: Age, RestingBP, Cholestrol, MaxHR, Oldpeak
```

```
df.shape #To find the shape(row,columns) 4240 instances and 16 features
```

```
df.size #Total number of cells
#total number of cells
```

```
df.info() #find the values, shows features
```

```
df.isnull()#null values
```

```
df.isnull().sum()
```

A bar plot of the number of null values in the dataset

```
df.isnull().sum().plot.bar()
plt.show()
```

To show the columns or features of the dataset

```
df.columns
```

To display unique values before Encoding

```
for i in df:
  print(i,np.unique(df[i]))
```

Label Encoding all the categorical values

We decided to go with Label Encoding as the the number of categories in each feature with categorical values were minimal. If there were many we would have chosen One-Hot encoding.

```
from sklearn import preprocessing
le = preprocessing.LabelEncoder()
```

```
x=list(df['Sex'].unique())
```

```
le.fit(x)
```

```
df['Sex']=le.transform(df.Sex)
```

```
x=list(df['ChestPainType'].unique())
le.fit(x)
df['ChestPainType']=le.transform(df.ChestPainType)
```

```
x=list(df['RestingECG'].unique())
le.fit(x)
df['RestingECG']=le.transform(df.RestingECG)
```

```
x=list(df['ExerciseAngina'].unique())
le.fit(x)
df['ExerciseAngina']=le.transform(df.ExerciseAngina)
```

```
x=list(df['ST_Slope'].unique())
le.fit(x)
df['ST_Slope']=le.transform(df.ST_Slope)
```

All the above are steps to label encode

Final encoded dataset

```
df
```

To display unique values after encoding

```
for i in df:
  print(i,np.unique(df[i]))#CHECKS UNIQUE VALUES
```

From this pairplot, the following conclusions may be drawn:

1. Age correlates positively with RestingBP and Cholesterol.
2. Age and RestingBP have a negative connection with MaxHR.
3. Age, RestingBP, Cholesterol, MaxHR, and Oldpeak seem to be distributed differently across people with and without heart disease.
4. There is no obvious linear connection between the variables, indicating that a nonlinear model may be required for forecasting.
5. The association between ChestPainType and the other variables in the dataset is unclear.
6. The relationship between Oldpeak and MaxHR is negative.
7. There seems to be a link between resting blood pressure and cholesterol.

Overall, the pairplot may help us uncover any potential correlations between the variables and is a valuable tool for selecting features in machine learning models.

```
sns.pairplot(df, diag_kind="hist")
```

```
df.columns
```

```
sns.countplot(x='HeartDisease', data=df)
```

THE ABOVE GRAPH DEPICTS THAT IN OUR DATASET, APPROXIMATELY OVER 500 PEOPLE ARE ACTUALLY PRONE TO HEART DISEASE GIVEN THE FEATURES AND ABOUT 400 PEOPLE ARE NOT

```
sns.barplot(x='Sex', y='HeartDisease', data=df, palette="flare")
plt.title('Sex more prone to heart disease')
plt.xlabel('Sex')
plt.ylabel('Number of patients')
```

INFERENCE: Given that there are more male patients with heart illness than female patients, it may be concluded from this image that men are more likely than women to have heart disease. The fact that the standard for men with heart disease is greater than the bar for women with heart disease serves as the foundation for this assumption. It's crucial to remember that this conclusion is based on the information in this specific dataset and could not necessarily apply to the whole population.

```
sns.boxplot(data=df, x='HeartDisease', y='Age', palette="magma")
plt.show()
```

INFERENCE: This boxplot suggests that people with heart disease(1) are often older than those without heart disease. The distribution of ages for patients with heart disease is more skewed

towards older ages than the distribution for patients without heart disease, and this inference is based on the facts that the median (represented by the line inside the box) for patients with heart disease is higher than the median for patients without heart disease. It's crucial to remember that this conclusion is based on the information in this specific dataset and could not necessarily apply to the whole population. The box plot may also be used to spot any extreme values or outliers in the dataset. The box for individuals with heart disease contains numerous dots above the bottom border, which signify probable outliers. Understanding the nature of these outliers and their possible influence on the association between ageing and heart disease may need more investigation.

```
sns.histplot(data=df, x='Age', bins=20)
plt.show()
```

INFERENCE: The distribution of ages in the dataset is inferred from this representation to be about normally distributed, with a peak occurring between the ages of 55 and 65. This conclusion is based on the histogram's resemblance to a bell curve. Also, the dataset seems to include some patients who are much older than the bulk of patients based on the histogram's extended tail towards older ages. Another conclusion drawn from this visualisation is that there aren't many patients in the dataset who are under the age of 40. This is supported by the fact that there are few patients in the youngest age bins of the histogram (i.e., ages less than 40). This can be as a result of the lower prevalence of cardiac disease in younger people or a dataset restriction (i.e., it may not include many younger patients).

```
sns.scatterplot(data=df, x='Age', y='MaxHR', hue='HeartDisease', palette="icefire")
plt.show()
```

INFERENCE: This graph suggests that individuals with heart illness often have lower maximal heart rates than those without heart disease. This is due to the fact that people with heart disease tend to cluster towards the lower end of the maximum heart rate range, while healthy individuals are more evenly distributed across the maximum heart rate range.

Another conclusion drawn from this visualisation is that, whether or not patients have cardiac disease, there is a universally negative correlation between age and maximal heart rate. This is based on the scatterplot's downward trend from left to right, which reveals that maximal heart rate tends to decline as age rises.

```
sns.countplot(data=df, x='ChestPainType', hue='HeartDisease', palette="ch:s=-.2,r=.6")
plt.show()
```

INFERENCE: This grap suggests that people with type 0 and type 1 chest pain are more likely to suffer heart disease than those with type 2 and type 3 chest pain. This is based on the observation that patients with chest pain kinds 0 and 1 are more likely to have heart disease

than those without, but patients with chest pain types 2 and 3 are more likely to have heart disease. Another conclusion drawn from this visualisation is that regardless of whether a patient has cardiac disease, type 3 chest pain is the most prevalent form of chest pain reported by patients in the sample. This is based on the fact that the plot's y-axis shows that chest pain type 3 has the largest count.

```
sns.heatmap(df.corr(), annot=True)
plt.show()
```

The heatmap is an effective tool for showing the strength and direction of the linear connection between variable pairs in the dataset. A correlation coefficient that is positive shows a positive association between two variables, while a correlation value that is negative suggests a negative relationship. A correlation value of 0 shows that there is no linear association. Age, resting blood pressure (RestingBP), and cholesterol levels are favourably connected with one another, but age, RestingBP, and cholesterol levels are negatively correlated with maximum heart rate obtained during exercise (MaxHR). This shows that older individuals with greater RestingBP and cholesterol levels may have a higher risk of developing heart disease, but those with a higher maximum heart rate obtained during exercise may have a lower risk of developing heart disease. There is a somewhat significant link between chest pain type and heart disease, which suggests that people with particular forms of chest pain may be more likely to develop heart disease. In addition, there is a modest negative connection between the slope of the ST segment during peak exertion (ST Slope) and heart disease, suggesting that individuals with a more downwardly sloped ST segment during exercise may be less likely to develop heart disease.

```
sns.boxplot(data=df, x='HeartDisease', y='Cholesterol', palette="light:b")
plt.show()
```

INFERENCE:The x-axis indicates the prevalence or absence of cardiac disease, whilst the y-axis indicates cholesterol levels. The box plot reveals that the median cholesterol levels of individuals with heart disease are somewhat higher than those of people without heart disease. In addition, the box plot reveals that there are a few heart disease patients with abnormally high or low cholesterol levels (outliers). Consequently, we may deduce that high cholesterol levels may be a risk factor for heart disease, and additional research is required to determine the nature of the association between cholesterol levels and heart disease.

```
sns.scatterplot(data=df, x='Cholesterol', y='RestingBP', palette="vlag")
plt.title('Cholesterol vs. Resting Blood Pressure')
plt.xlabel('Cholesterol')
plt.ylabel('Resting Blood Pressure')
```

Inference: There is no apparent linear association between cholesterol levels and resting blood pressure, as seen by the scatter figure. Yet, we can observe that there is a concentration of data points with elevated cholesterol and blood pressure during rest. This implies that increased cholesterol levels may be related with greater resting blood pressure, although other variables also influence resting blood pressure. Consequently, further research is required to comprehend the association between cholesterol levels and resting blood pressure, as well as the function of other possible heart disease risk factors.

```
sns.boxplot(data=df, x='ChestPainType', y='MaxHR', palette="ch:s=-.2,r=.6")
plt.title('Chest Pain Type vs. Max Heart Rate')
plt.xlabel('Chest Pain Type')
plt.ylabel('Max Heart Rate')
```

Inference:Patients with chest pain types 0 and 1 tend to have a greater maximal heart rate than those with chest pain types 2 and 3. This shows that the kind of chest discomfort may be associated with the highest heart rate reached during exercise.

Yet, there is a substantial overlap between the various forms of chest pain, suggesting that chest pain type alone may not be a reliable predictor of the highest heart rate obtained during exercise. Consequently, further research is required to comprehend the association between chest pain kind and maximal heart rate obtained during exercise, as well as the function of other possible heart disease risk factors.

```
X = df.drop(['HeartDisease'], axis= 1)
y = df['HeartDisease']
```

```
X_train, X_test, y_train, y_test = train_test_split(X, y,test_size = 0.3,random_state=42)
```

```
from sklearn.preprocessing import StandardScaler
st_x= StandardScaler()
X_train= st_x.fit_transform(X_train)
X_test= st_x.transform(X_test)
```

Support Vector Machine(SVM)

```
from sklearn.svm import SVC # "Support vector classifier"
classifier = SVC(kernel='linear', random_state=0)
classifier.fit(X_train, y_train)
```

```
y_pred=classifier.predict(X_test)
```

Importing necessary performance metrics

```
from sklearn.metrics import (
    accuracy_score,
    confusion_matrix,
    ConfusionMatrixDisplay,
    f1_score,
    roc_curve,
    roc_auc_score
)
```

To display the confusion matrix for the model

```
labels = [0,1]
confusion_matrix_svm= confusion_matrix(y_test, y_pred, labels=labels)
disp = ConfusionMatrixDisplay(confusion_matrix=confusion_matrix_svm, display_labels=labels
disp.plot();
```

Accuracy of the model

```
accuracy_score_svm= accuracy_score(y_test, y_pred)
accuracy_score_svm
```

F1 score of the model

```
f1_svm= f1_score(y_pred, y_test, average="weighted")
f1_svm
```

ROC Curve and Area under the ROC Curve

```
fpr_svm, tpr_svm, _ = roc_curve(y_test, y_pred)

#create ROC curve
plt.plot(fpr_svm,tpr_svm)
plt.title("ROC Curve")
plt.ylabel('True Positive Rate')
plt.xlabel('False Positive Rate')
plt.show()
```

```
score_svm= roc_auc_score(y_test, y_pred)
score_svm
```

Performing K-Fold cross validation to see if accuracy can be further improved

```
from sklearn.model_selection import KFold
from sklearn.model_selection import cross_val_score


kfold = KFold(n_splits=5, shuffle=True, random_state=42)


results_svm= cross_val_score(classifier, X, y, cv=kfold)


print(results_svm)
```

Random Forest

```
from sklearn.ensemble import RandomForestClassifier
# Initializing a Random Forest Classifier
clf = RandomForestClassifier(n_estimators=100, random_state=42)

# Fitting the classifier to the training data
clf.fit(X_train, y_train)

# Using the classifier to make predictions on the testing data
pred = clf.predict(X_test)
```

To display the confusion matrix

```
labels = [0,1]
confusion_matrix_rf= confusion_matrix(y_test,pred, labels=labels)
disp = ConfusionMatrixDisplay(confusion_matrix=confusion_matrix_rf, display_labels=labels)
disp.plot();
```

Accuracy

```
accuracy_score_rf= accuracy_score(y_test,pred)
accuracy_score_rf
```

F1 score

```
f1_rf= f1_score(y_pred, y_test, average="weighted")
f1_rf
```

ROC Curve and Area under the ROC curve

```
fpr_rf, tpr_rf, _ = roc_curve(y_test, pred)

#create ROC curve
```

```
plt.plot(fpr_rf,tpr_rf)
plt.title("ROC Curve")
plt.ylabel('True Positive Rate')
plt.xlabel('False Positive Rate')
plt.show()
```

```
score_rf= roc_auc_score(y_test, pred)
score_rf
```

INFERENCE:

From the performance metrics applied on both models we can see that Random Forest Algorithm works better.The margin is negligible but our topic necessitates maximum accuracy possible as it predicts if you are at risk of getting a stroke.

Creating functions to predict to facilitate the development of our website.

Without taking inputs

```
def predicted(age, sex, c_pain, rBP, Ch, FBs, RECG, MHR, EA, OP, ST_S):
  output=clf.predict([[age, sex, c_pain, rBP, Ch, FBs, RECG, MHR, EA, OP, ST_S]])
  if (output[0]==0):
    print("No risk of stroke or heart disease")
  else:
    print("Patient is at risk of stroke or heart disease")
```

```
predicted(45, 1, 3, 120, 180, 0, 2, 176, 1, 2.5, 1)
```

Taking inputs

```
def predicter(clf):
  ip1=int(input("Enter age: "))
  ip2=int(input("Enter sex(0-Female,1-Male): "))
  ip3=int(input("Enter ChestPain type(TA: Typical Angina-3, ATA: Atypical Angina-1, NAP: N
  ip4=int(input("Enter Resting BP: "))
  ip5=int(input("Enter Cholestrol: "))
  ip6=int(input("Enter Fasting Bs(1: if FastingBS > 120 mg/dl, 0: otherwise): "))
  ip7=int(input("Enter Resting ECG(Normal: Normal-1, ST: having ST-T wave abnormality-2, L
  ip8=int(input("Enter Max Heart rate: "))
  ip9=int(input("Enter whether Excercise Angina(No-0,Yes-1): "))
  ip10=float(input("Enter Oldpeak: "))
  ip11=int(input("Enter ST_Slope(Up: upsloping-2, Flat: flat-1, Down: downsloping-0): "))

  output=clf.predict([[ip1,ip2,ip3,ip4,ip5,ip6,ip7,ip8,ip9,ip10,ip11]])
  if output[0]==0:
    print("No risk of stroke or heart disease")
  else:
    print("Patient is at risk of stroke or heart disease")
```

To link our python code to the website

```
!pip install flask-ngrok
```

```
from flask import Flask, render_template, request
from flask_ngrok import run_with_ngrok
import pandas as pd
import numpy as np
```

```
app = Flask(__name__)
```

```
@app.route('/')
def home():
    return render_template('original.html')
```

```
@app.route("/predict", methods=['GET','POST'])
def predict():
    if request.method == 'POST':
        age = float(request.form['age'])
        sex = float(request.form['sex'])
        cp = float(request.form['cp'])
        trestbps = float(request.form['trestbps'])
        chol = float(request.form['chol'])
        fbs= float(request.form['fbs'])
        restecg = float(request.form['restecg'])
        thalach = float(request.form['thalach'])
        exang = float(request.form['exang'])
        oldpeak = float(request.form['oldpeak'])
        slope = float(request.form['slope'])

        args = [age,sex,cp,trestbps,chol,fbs,restecg,thalach,exang,oldpeak,slope]

        res = predicted([args])
    return render_template('predict.html', prediction = res)
if __name__ == '__main__':
    app.run()
```

DIABETES

```
import numpy as np
import pandas as pd
import matplotlib.pyplot as plt
import seaborn as sns
```

```
df = pd.read_csv('diabetes.csv')
```

```
df.describe()
```

	Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	BMI
count	768.000000	768.000000	768.000000	768.000000	768.000000	768.000000
mean	3.845052	120.894531	69.105469	20.536458	79.799479	31.992578
std	3.369578	31.972618	19.355807	15.952218	115.244002	7.884160
min	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000
25%	1.000000	99.000000	62.000000	0.000000	0.000000	27.300000
50%	3.000000	117.000000	72.000000	23.000000	30.500000	32.000000
75%	6.000000	140.250000	80.000000	32.000000	127.250000	36.600000
max	17.000000	199.000000	122.000000	99.000000	846.000000	67.100000

```
df.isnull().sum()
```

```
Pregnancies                 0
Glucose                     0
BloodPressure               0
SkinThickness               0
Insulin                     0
BMI                         0
DiabetesPedigreeFunction    0
Age                         0
Outcome                     0
dtype: int64
```

```
df.info()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 768 entries, 0 to 767
Data columns (total 9 columns):
 #   Column                    Non-Null Count  Dtype  
---  ------                    --------------  -----  
 0   Pregnancies               768 non-null    int64  
 1   Glucose                   768 non-null    int64  
 2   BloodPressure             768 non-null    int64  
 3   SkinThickness             768 non-null    int64  
 4   Insulin                   768 non-null    int64  
 5   BMI                       768 non-null    float64
 6   DiabetesPedigreeFunction  768 non-null    float64
 7   Age                       768 non-null    int64  
 8   Outcome                   768 non-null    int64  
dtypes: float64(2), int64(7)
memory usage: 54.1 KB
```

```
df.head()
```

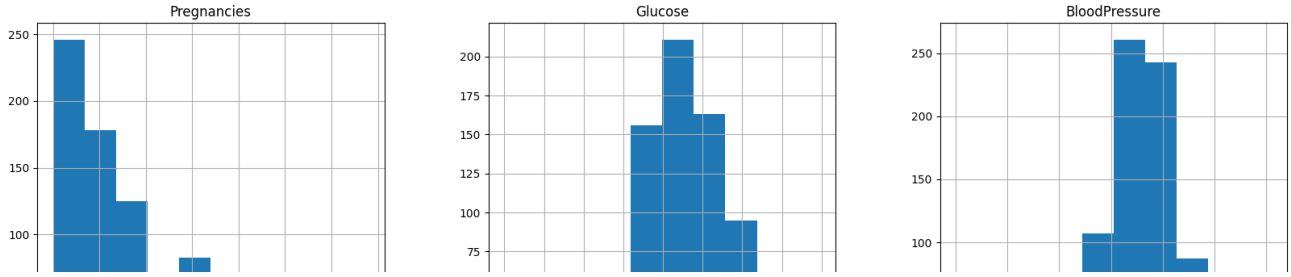
	Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	BMI	DiabetesPedigre
0	6	148	72	35	0	33.6	
1	1	85	66	29	0	26.6	
2	8	183	64	0	0	23.3	
3	1	89	66	23	94	28.1	
4	0	137	40	35	168	43.1	

```
df.columns
```

```
Index(['Pregnancies', 'Glucose', 'BloodPressure', 'SkinThickness', 'Insulin',
       'BMI', 'DiabetesPedigreeFunction', 'Age', 'Outcome'],
      dtype='object')
```

```
df.hist(figsize = (20,20))
```

```
array([[<Axes: title={'center': 'Pregnancies'}>,
        <Axes: title={'center': 'Glucose'}>,
        <Axes: title={'center': 'BloodPressure'}>],
       [<Axes: title={'center': 'SkinThickness'}>,
        <Axes: title={'center': 'Insulin'}>,
        <Axes: title={'center': 'BMI'}>],
       [<Axes: title={'center': 'DiabetesPedigreeFunction'}>,
        <Axes: title={'center': 'Age'}>,
        <Axes: title={'center': 'Outcome'}>]], dtype=object)
```



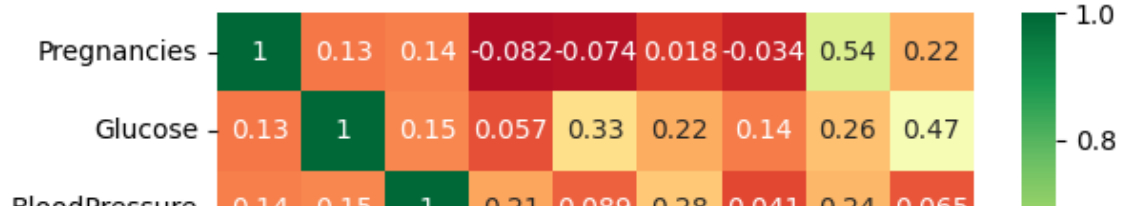
This command can be useful for quickly visualizing the distribution of each numeric feature in the dataset. For example, it can help identify any features that have a large number of values in a particular range or features that have many missing values. Additionally, it can be useful for identifying potential outliers or skewness in the distribution of a feature, which can be important considerations when building a predictive model.

```
df_copy=df
```

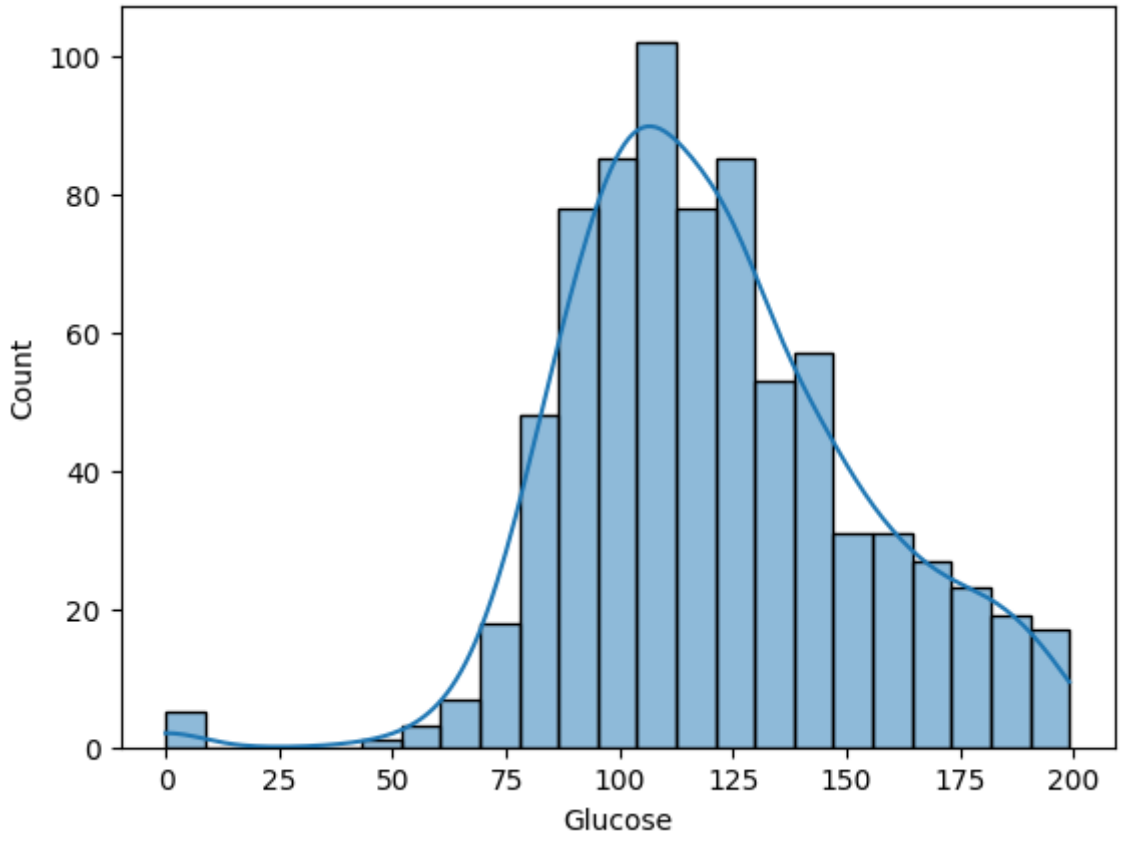


```
sns.heatmap(df_copy.corr(), annot=True,cmap ='RdYlGn')
```

```
<Axes: >
```

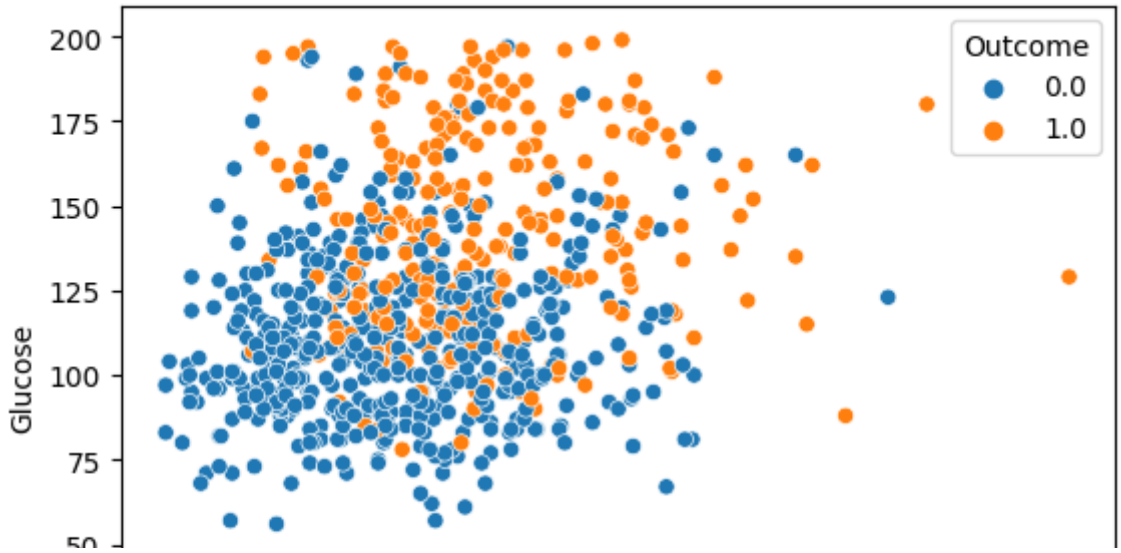



```
sns.histplot(data=df, x="Glucose", kde=True)
plt.show()
```



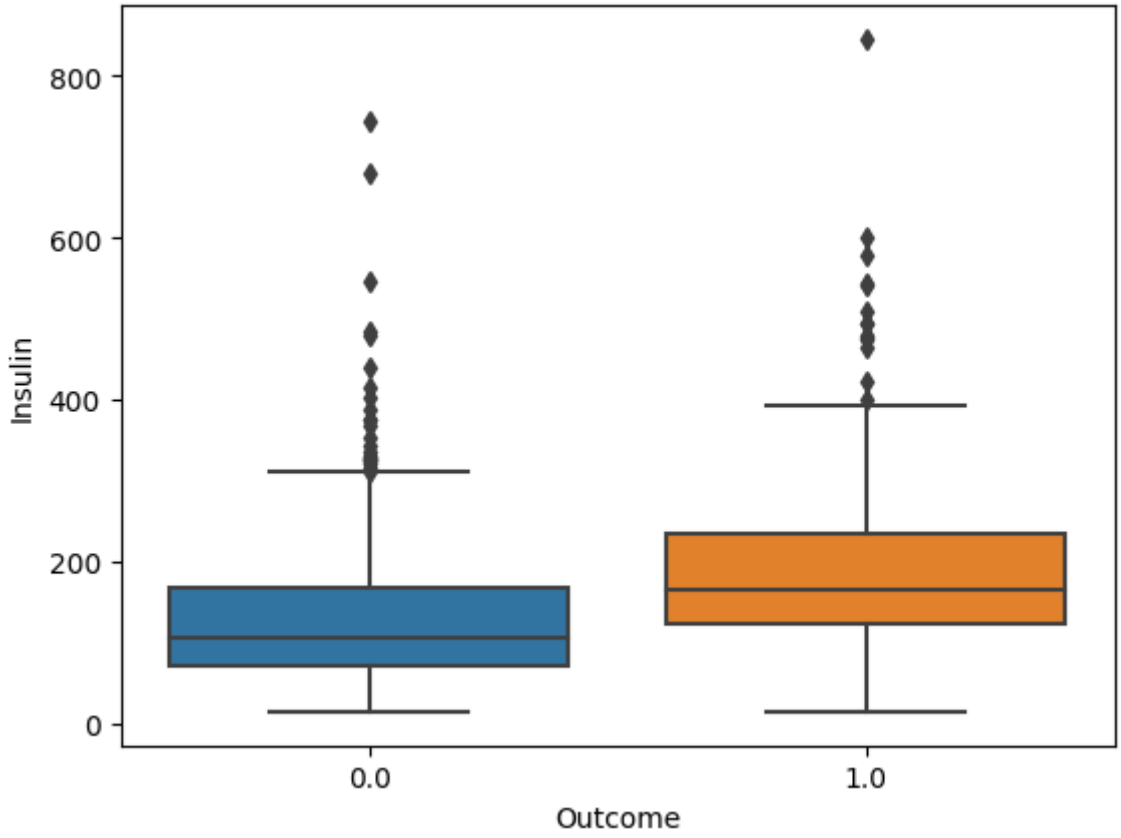
The histogram can give insights into the range of glucose values in the dataset and the number of observations in each range. The kernel density estimation plot can provide additional information about the shape of the distribution of the feature, indicating whether it is normally distributed or skewed, which can be an important consideration when selecting appropriate statistical methods for data analysis.

```
sns.scatterplot(data=df, x="BMI", y="Glucose", hue="Outcome")
plt.show()
```



The scatter plot can show any patterns or trends in the data, such as a positive or negative correlation between the two features, as well as how these patterns relate to the target variable.

```
sns.boxplot(data=df, x="Outcome", y="Insulin")
plt.show()
```



The box in the boxplot represents the interquartile range (IQR) of the data, with the lower and upper hinges representing the first and third quartiles, respectively. The horizontal line inside the box represents the median insulin level, while the whiskers extending from the box represent the range of the data, excluding outliers. The plot shows that the median insulin level is higher for diabetic patients (Outcome = 1) compared to non-diabetic patients (Outcome = 0). There are

also some outliers for both classes, with diabetic patients having more extreme values. Overall, this suggests that insulin levels may be a useful feature for predicting diabetes in this dataset.

```
df["Insulin"] = df["Insulin"].replace(0, np.nan)
df["SkinThickness"] = df["SkinThickness"].replace(0, np.nan)
df["BMI"] = df["BMI"].replace(0, np.nan)
```

```
from sklearn.impute import KNNImputer
# Create a copy of the dataset to impute missing values
dfc = df.copy()

# Fit and transform the KNN imputer on the entire dataset
imputer = KNNImputer(n_neighbors=3)
dfc.iloc[:, :] = imputer.fit_transform(dfc)
```

```
dfc.head()
```

	Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	BMI	DiabetesPedig
0	6.0	148.0	72.0	35.0	125.333333	33.6	
1	1.0	85.0	66.0	29.0	66.666667	26.6	
2	8.0	183.0	64.0	30.0	195.000000	23.3	
3	1.0	89.0	66.0	23.0	94.000000	28.1	
4	0.0	137.0	40.0	35.0	168.000000	43.1	

```
df=dfc
```

```
df.head()
```

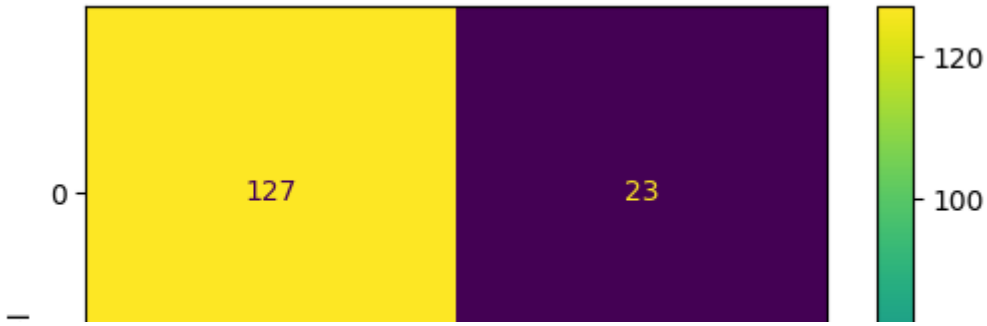
	Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	BMI	DiabetesPedig
0	6.0	148.0	72.0	35.0	125.333333	33.6	
1	1.0	85.0	66.0	29.0	66.666667	26.6	
2	8.0	183.0	64.0	30.0	195.000000	23.3	
3	1.0	89.0	66.0	23.0	94.000000	28.1	
4	0.0	137.0	40.0	35.0	168.000000	43.1	

```
from sklearn.model_selection import train_test_split
from sklearn.preprocessing import LabelEncoder
```

```
X = df.drop(['Outcome'], axis= 1)
y = df['Outcome']


X_train, X_test, y_train, y_test = train_test_split(X, y,test_size = 0.3,random_state=80)


from sklearn.preprocessing import StandardScaler
st_x= StandardScaler()
X_train= st_x.fit_transform(X_train)
X_test= st_x.transform(X_test)


from sklearn.metrics import (
    accuracy_score,
    confusion_matrix,
    ConfusionMatrixDisplay,
    f1_score,
    roc_curve,
    roc_auc_score
)


from sklearn.ensemble import RandomForestClassifier
# Initializing a Random Forest Classifier
c = RandomForestClassifier(n_estimators=300, random_state=10)

# Fitting the classifier to the training data
c.fit(X_train, y_train)

# Using the classifier to make predictions on the testing data
pred = c.predict(X_test)
```

To display the confusion matrix

```
labels = [0,1]
confusion_matrix_rf= confusion_matrix(y_test,pred, labels=labels)
disp = ConfusionMatrixDisplay(confusion_matrix=confusion_matrix_rf, display_labels=labels)
disp.plot();
```



Accuracy

```
accuracy_score_rf= accuracy_score(y_test,pred)
accuracy_score_rf
```

```
0.7532467532467533
```

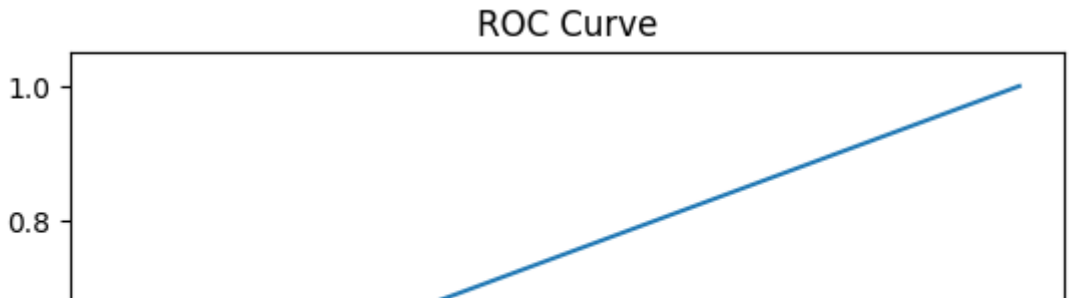
F1 score

```
f1_rf= f1_score(pred, y_test, average="weighted")
f1_rf
```

```
0.7578706508882612
```

ROC Curve and Area under the ROC curve

```
fpr_rf, tpr_rf, _ = roc_curve(y_test, pred)

#create ROC curve
plt.plot(fpr_rf,tpr_rf)
plt.title("ROC Curve")
plt.ylabel('True Positive Rate')
plt.xlabel('False Positive Rate')
plt.show()
```




```
score_rf= roc_auc_score(y_test, pred)
score_rf
```

```
0.7134567901234568
```

```
def DIABETES(c):
  ip1=float(input("Enter Number of pregnancies: "))
  ip2=float(input("Enter Glucose: "))
  ip3=float(input("Enter Blood Pressure: "))
  ip4=float(input("Enter Skin Thickness: "))
  ip5=float(input("Enter Insulin Levels: "))
  ip6=float(input("Enter BMI: "))
  ip7=float(input("Enter DiabetesPedigreeFunction: "))
  ip8=float(input("Enter Age: "))

  output=c.predict([[ip1,ip2,ip3,ip4,ip5,ip6,ip7,ip8]])
  if output[0]==0:
    print("Patient is not at risk of diabetes.")
  else:
    print("Patient is at risk of diabetes. Take Care!")
```

MATERNAL HEALTH CARE

```
import numpy as np
import pandas as pd
import matplotlib.pyplot as plt
import seaborn as sns
```

```
df= pd.read_csv("/content/Maternal Health Dataset.csv")
```

```
df.size
```

```
7098
```

```
df.shape
```

```
(1014, 7)
```

```
df.info()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 1014 entries, 0 to 1013
Data columns (total 7 columns):
 #   Column       Non-Null Count  Dtype  
---  ------       --------------  -----  
 0   Age          1014 non-null   int64  
 1   SystolicBP   1014 non-null   int64  
 2   DiastolicBP  1014 non-null   int64  
 3   BS           1014 non-null   float64
 4   BodyTemp     1014 non-null   float64
 5   HeartRate    1014 non-null   int64  
 6   RiskLevel    1014 non-null   object 
dtypes: float64(2), int64(4), object(1)
memory usage: 55.6+ KB
```

```
df.describe()
```

	Age	SystolicBP	DiastolicBP	BS	BodyTemp	HeartRate
count	1014.000000	1014.000000	1014.000000	1014.000000	1014.000000	1014.000000
mean	29.871795	113.198225	76.460552	8.725986	98.665089	74.301775
std	13.474386	18.403913	13.885796	3.293532	1.371384	8.088702
min	10.000000	70.000000	49.000000	6.000000	98.000000	7.000000
25%	19.000000	100.000000	65.000000	6.900000	98.000000	70.000000
50%	26.000000	120.000000	80.000000	7.500000	98.000000	76.000000
75%	39.000000	120.000000	90.000000	8.000000	98.000000	80.000000
max	70.000000	160.000000	100.000000	19.000000	103.000000	90.000000

```
df.head(5)
```

	Age	SystolicBP	DiastolicBP	BS	BodyTemp	HeartRate	RiskLevel
0	25	130	80	15.0	98.0	86	high risk
1	35	140	90	13.0	98.0	70	high risk
2	29	90	70	8.0	100.0	80	high risk
3	30	140	85	7.0	98.0	70	high risk
4	35	120	60	6.1	98.0	76	low risk

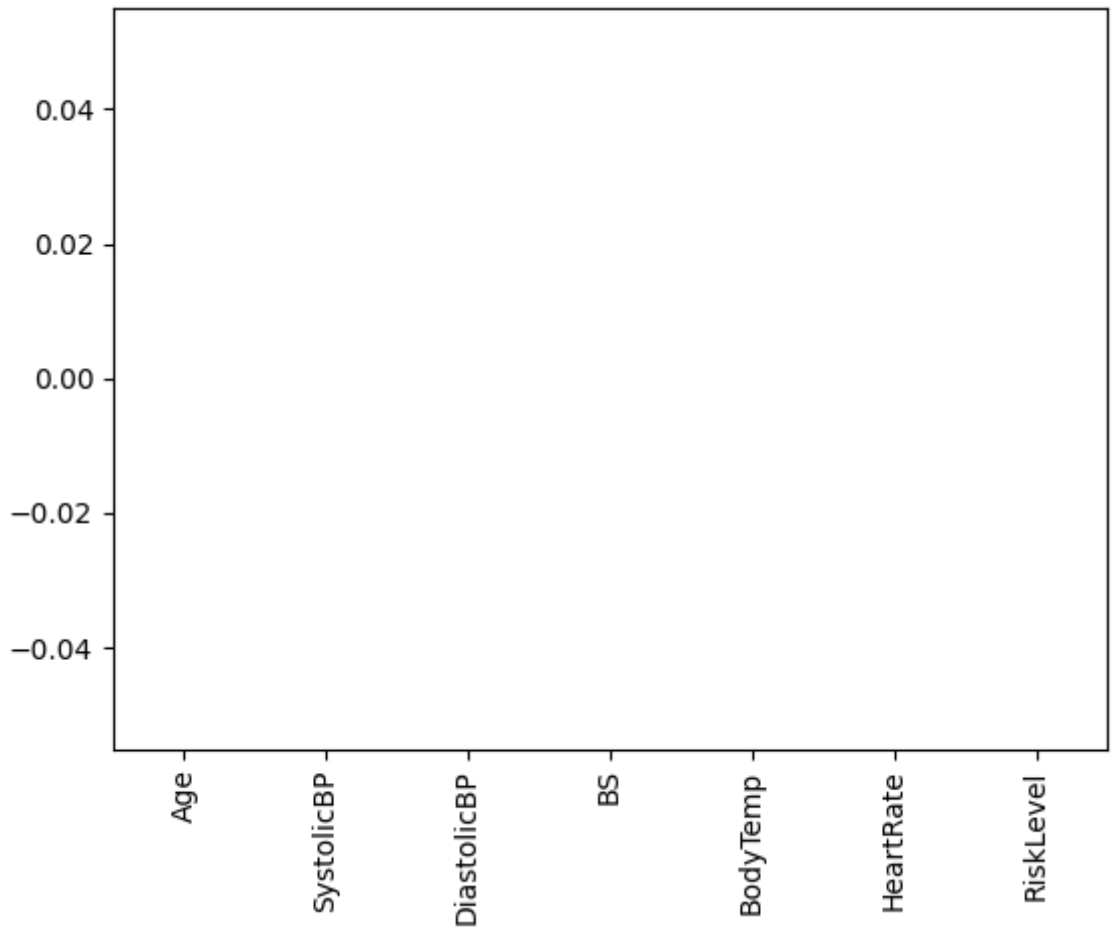
```
df.isnull().sum()
```

```
Age           0
SystolicBP    0
DiastolicBP   0
BS            0
```

```
BodyTemp       0
HeartRate      0
RiskLevel      0
dtype: int64
```

```
df.isnull().sum().plot.bar()
```

```
<Axes: >
```




```
df.columns
```

```
Index(['Age', 'SystolicBP', 'DiastolicBP', 'BS', 'BodyTemp', 'HeartRate',
       'RiskLevel'],
      dtype='object')
```

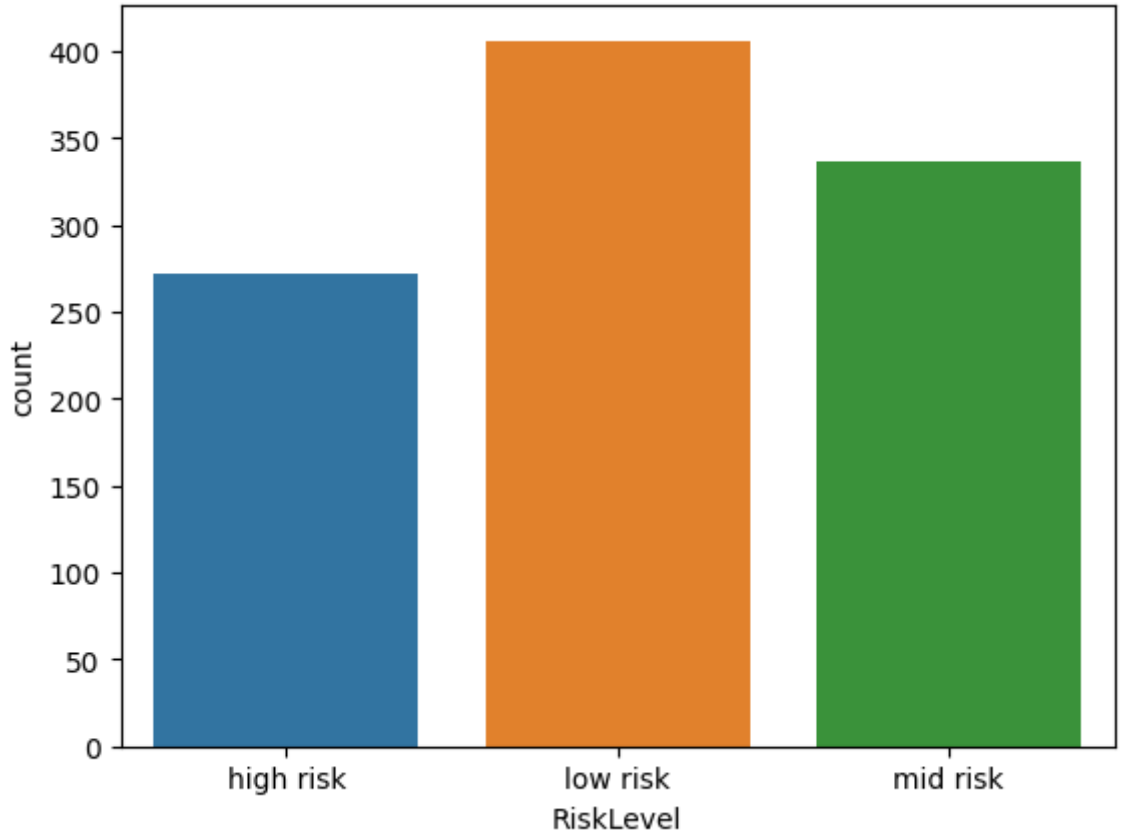
```
for i in df:
  print(i,np.unique(df[i]))
```

```
Age [10 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34
 35 36 37 38 39 40 41 42 43 44 45 46 48 49 50 51 54 55 56 59 60 62 63 65
 66 70]
SystolicBP [ 70  75  76  78  80  83  85  90  95  99 100 110 115 120 129 130 135 140
 160]
DiastolicBP [ 49  50  60  63  65  68  69  70  75  76  80  85  89  90  95 100]
BS [ 6.    6.1   6.3   6.4   6.5   6.6   6.7   6.8   6.9   7.    7.01  7.1
  7.2   7.5   7.6   7.7   7.8   7.9   8.    9.   10.   11.   12.   13.
 15.   16.   17.   18.   19.  ]
BodyTemp [ 98.   98.4  98.6  99.  100.  101.  102.  103. ]
```

```
HeartRate [ 7 60 65 66 67 68 70 75 76 77 78 80 82 86 88 90]
RiskLevel ['high risk' 'low risk' 'mid risk']
```

```
sns.countplot(x='RiskLevel', data=df)
```

```
<Axes: xlabel='RiskLevel', ylabel='count'>
```

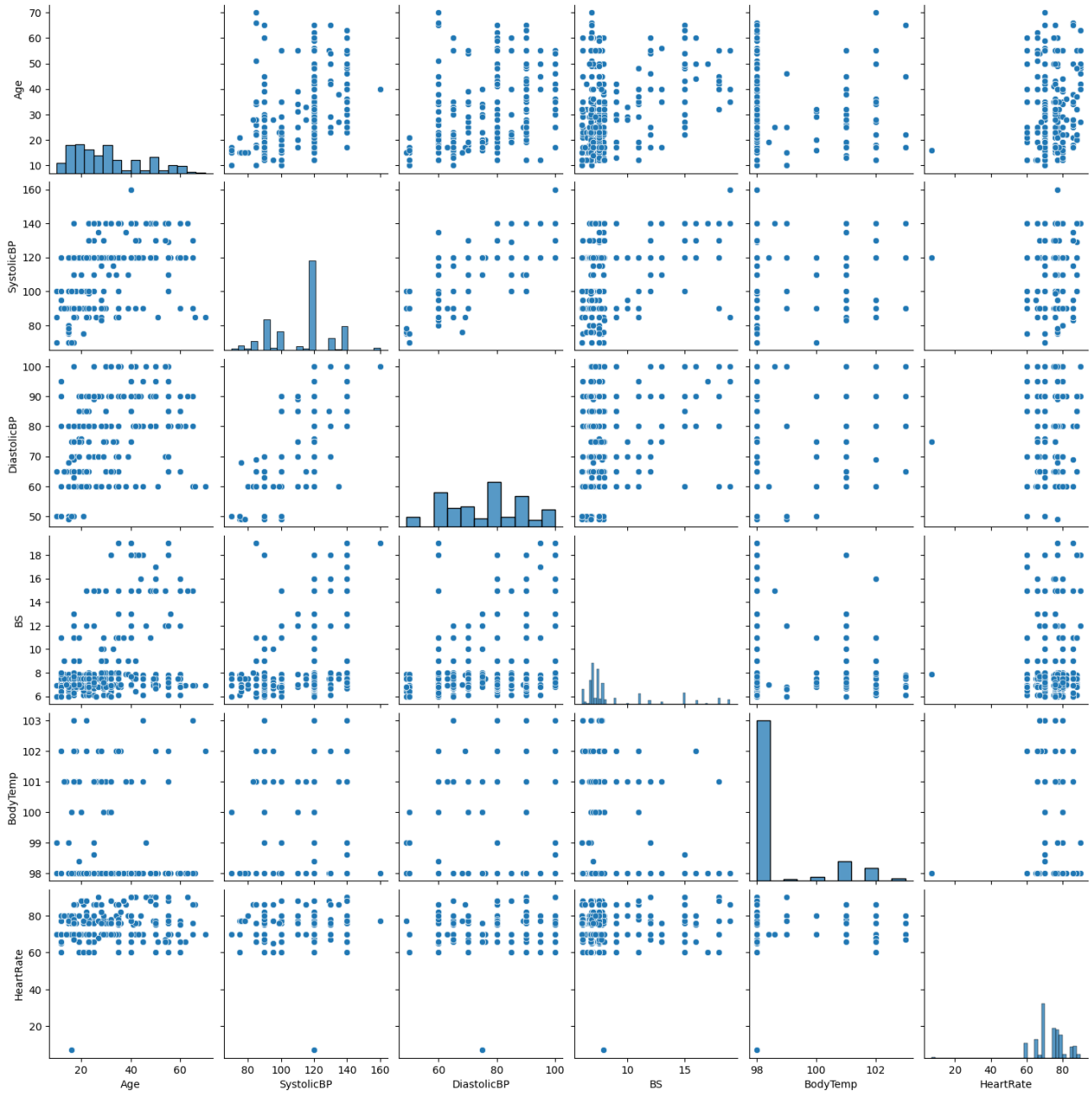



```
df.head(10)
```

	Age	SystolicBP	DiastolicBP	BS	BodyTemp	HeartRate	RiskLevel
0	25	130	80	15.00	98.0	86	high risk
1	35	140	90	13.00	98.0	70	high risk
2	29	90	70	8.00	100.0	80	high risk
3	30	140	85	7.00	98.0	70	high risk
4	35	120	60	6.10	98.0	76	low risk
5	23	140	80	7.01	98.0	70	high risk
6	23	130	70	7.01	98.0	78	mid risk
7	35	85	60	11.00	102.0	86	high risk
8	32	120	90	6.90	98.0	70	mid risk
9	42	130	80	18.00	98.0	70	high risk

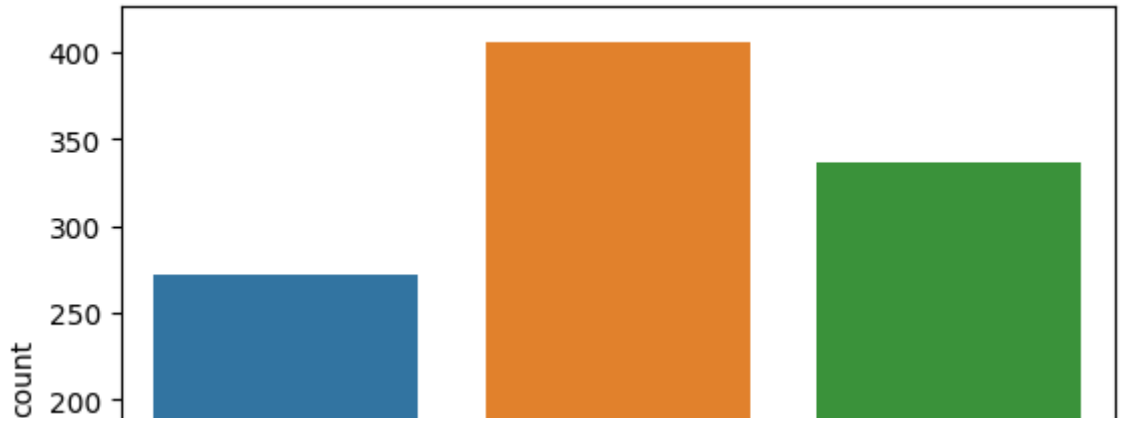
```
sns.pairplot(df, diag_kind="hist")
```

```
<seaborn.axisgrid.PairGrid at 0x7f10cba2be20>
```



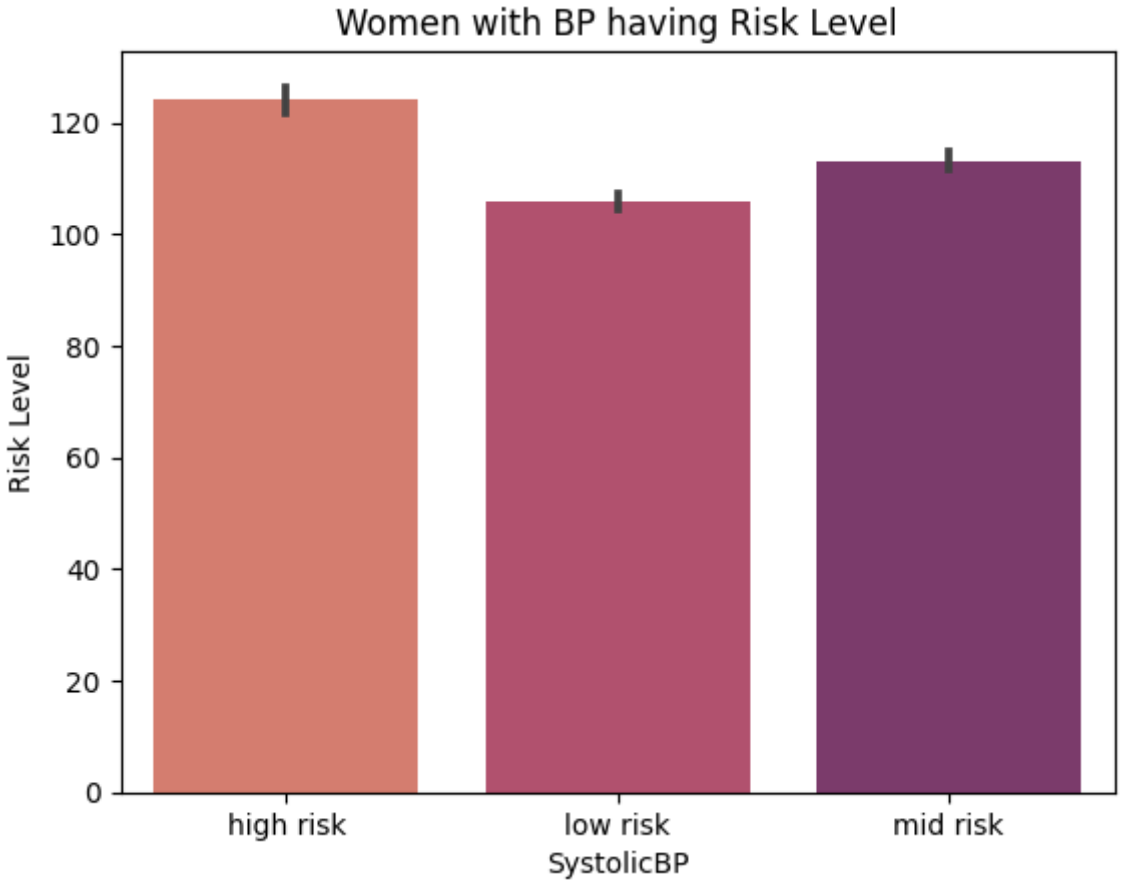

```
sns.countplot(x='RiskLevel', data=df)
```

```
<Axes: xlabel='RiskLevel', ylabel='count'>
```



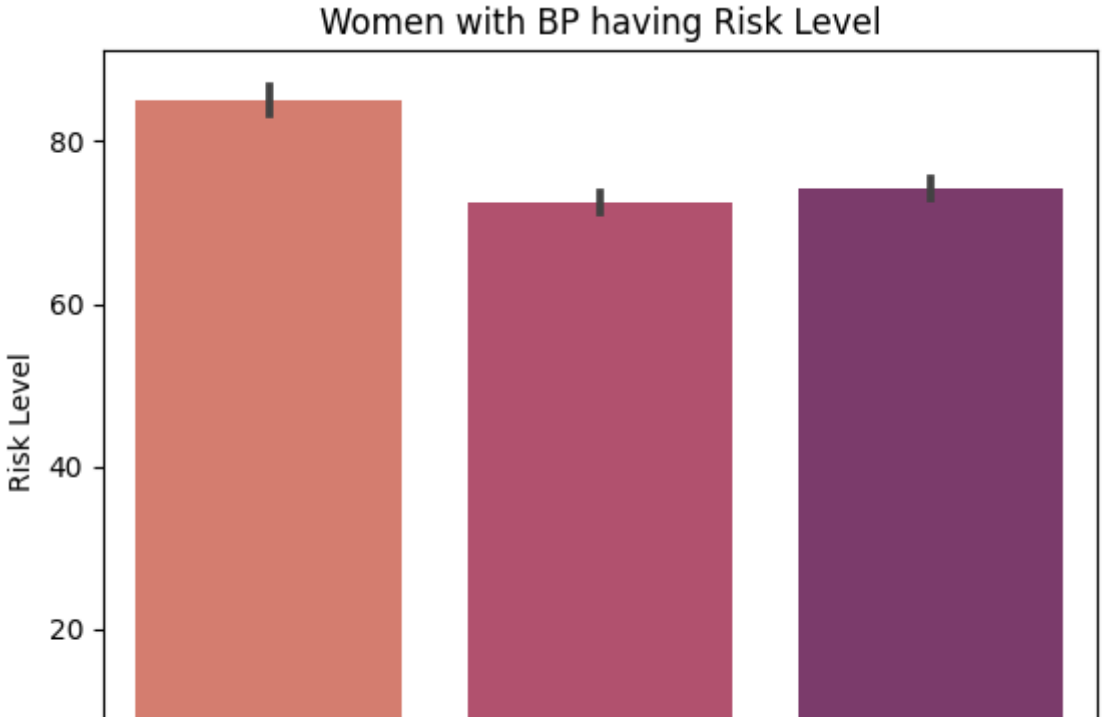

```
sns.barplot(y='SystolicBP', x='RiskLevel', data=df, palette="flare")
plt.title('Women with BP having Risk Level')
plt.xlabel('SystolicBP')
plt.ylabel('Risk Level')
```

```
Text(0, 0.5, 'Risk Level')
```



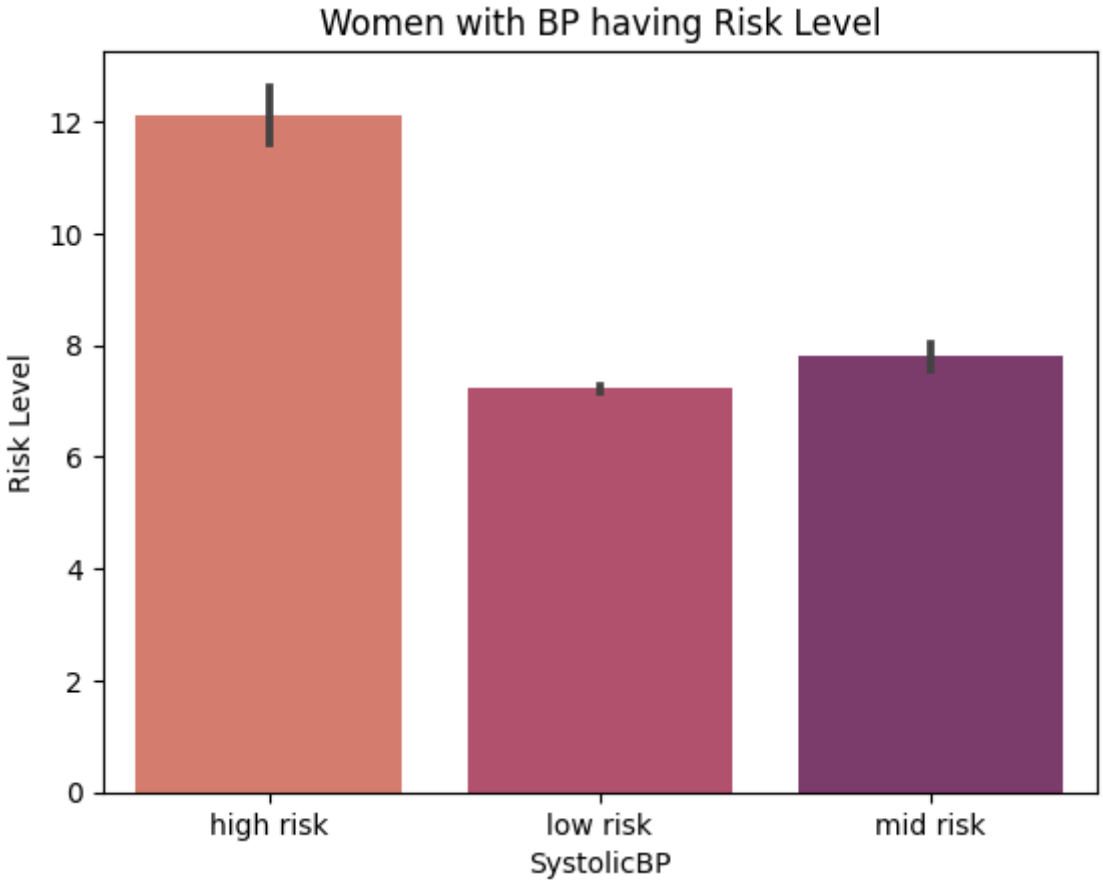

```
sns.barplot(y='DiastolicBP', x='RiskLevel', data=df, palette="flare")
plt.title('Women with BP having Risk Level')
plt.xlabel('SystolicBP')
plt.ylabel('Risk Level')
```

```
Text(0, 0.5, 'Risk Level')
```




```
sns.barplot(y='BS', x='RiskLevel', data=df, palette="flare")
plt.title('Women with BP having Risk Level')
plt.xlabel('SystolicBP')
plt.ylabel('Risk Level')
```

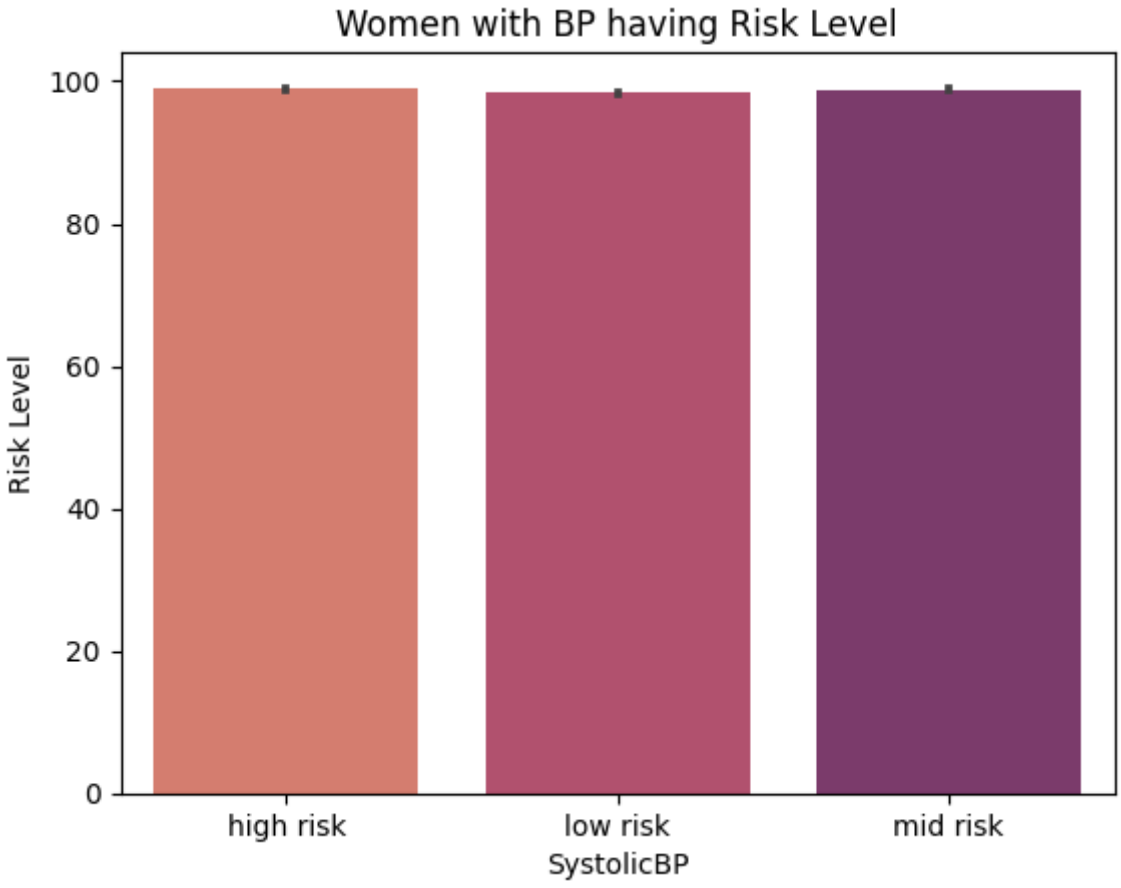
```
Text(0, 0.5, 'Risk Level')
```




```
sns.barplot(y='BodyTemp', x='RiskLevel', data=df, palette="flare")
plt.title('Women with BP having Risk Level')
plt.xlabel('SystolicBP')
```

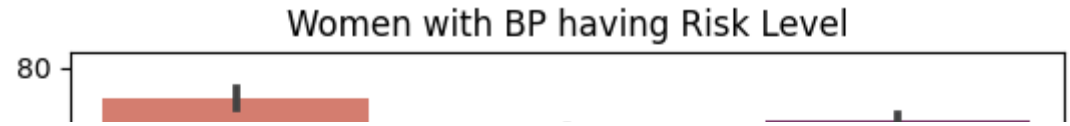
```
plt.xlabel('SystolicBP')
plt.ylabel('Risk Level')
```

```
Text(0, 0.5, 'Risk Level')
```

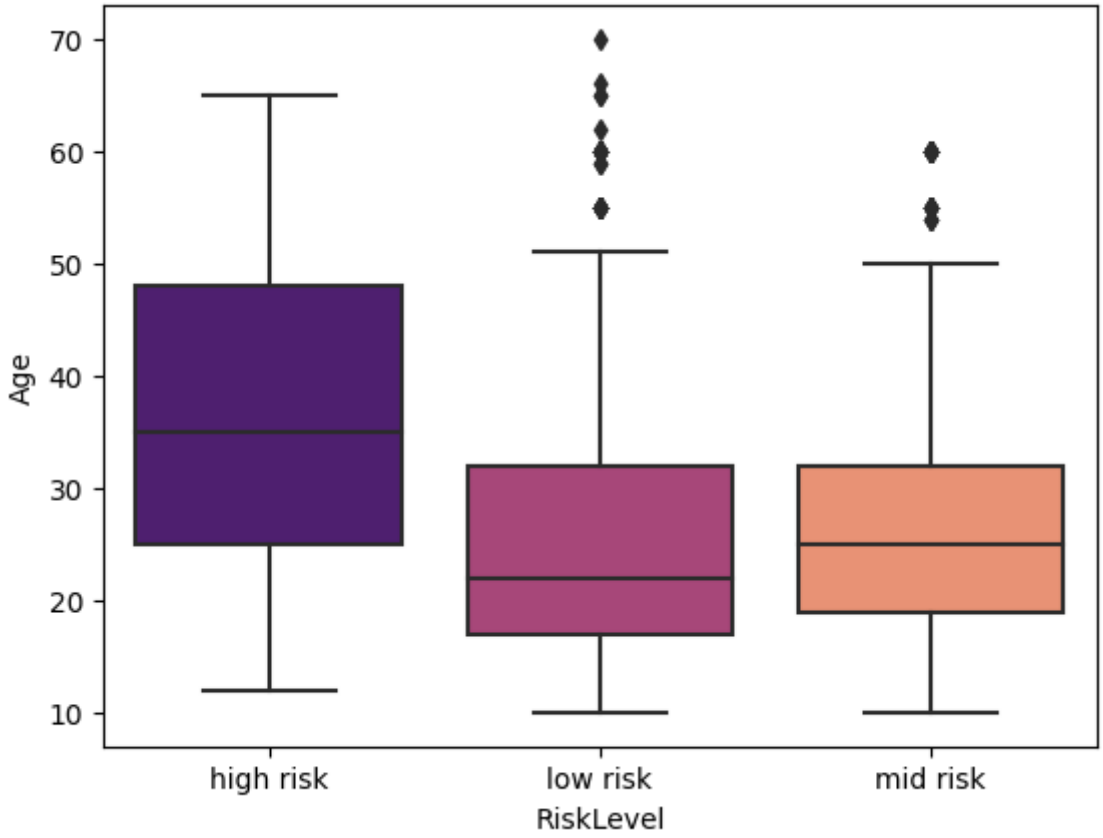



```
sns.barplot(y='HeartRate', x='RiskLevel', data=df, palette="flare")
plt.title('Women with BP having Risk Level')
plt.xlabel('SystolicBP')
plt.ylabel('Risk Level')
```

```
Text(0, 0.5, 'Risk Level')
```

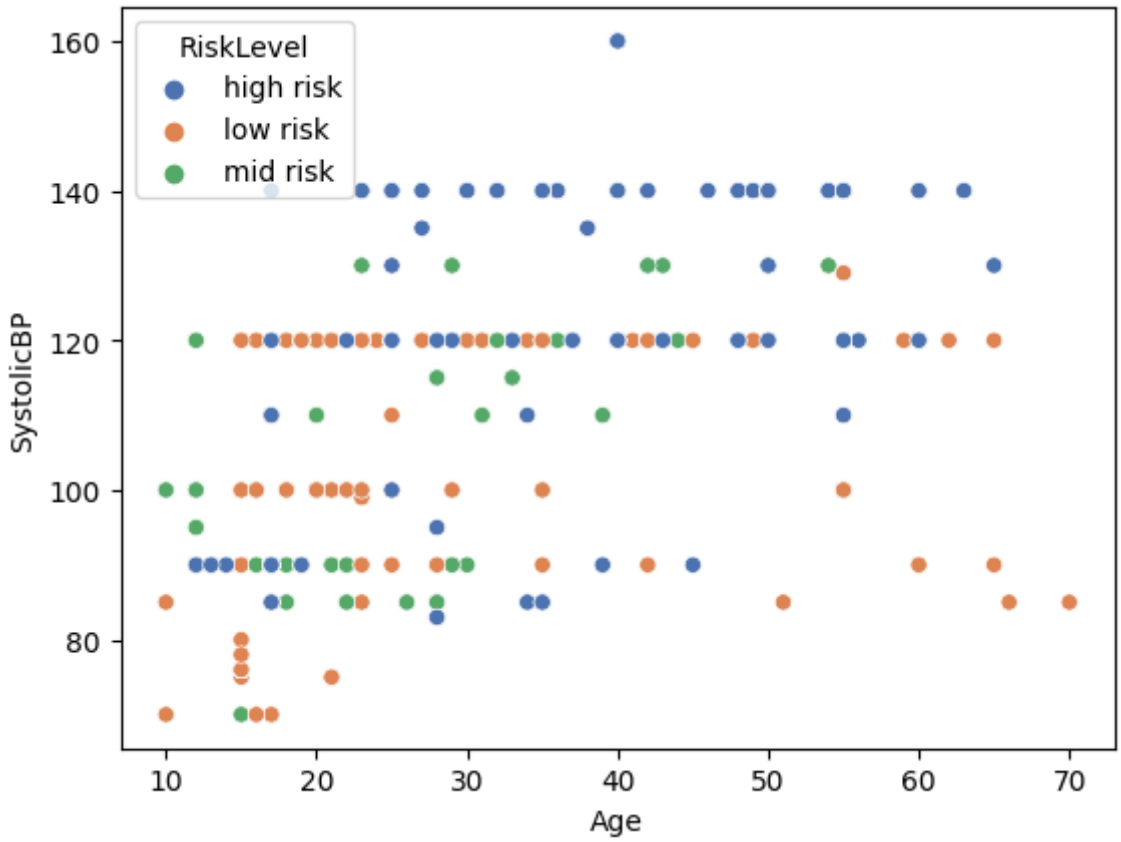



```
sns.boxplot(data=df, x='RiskLevel', y='Age', palette="magma")
plt.show()
```




```
sns.histplot(data=df, x='Age', bins=20)
plt.show()
```

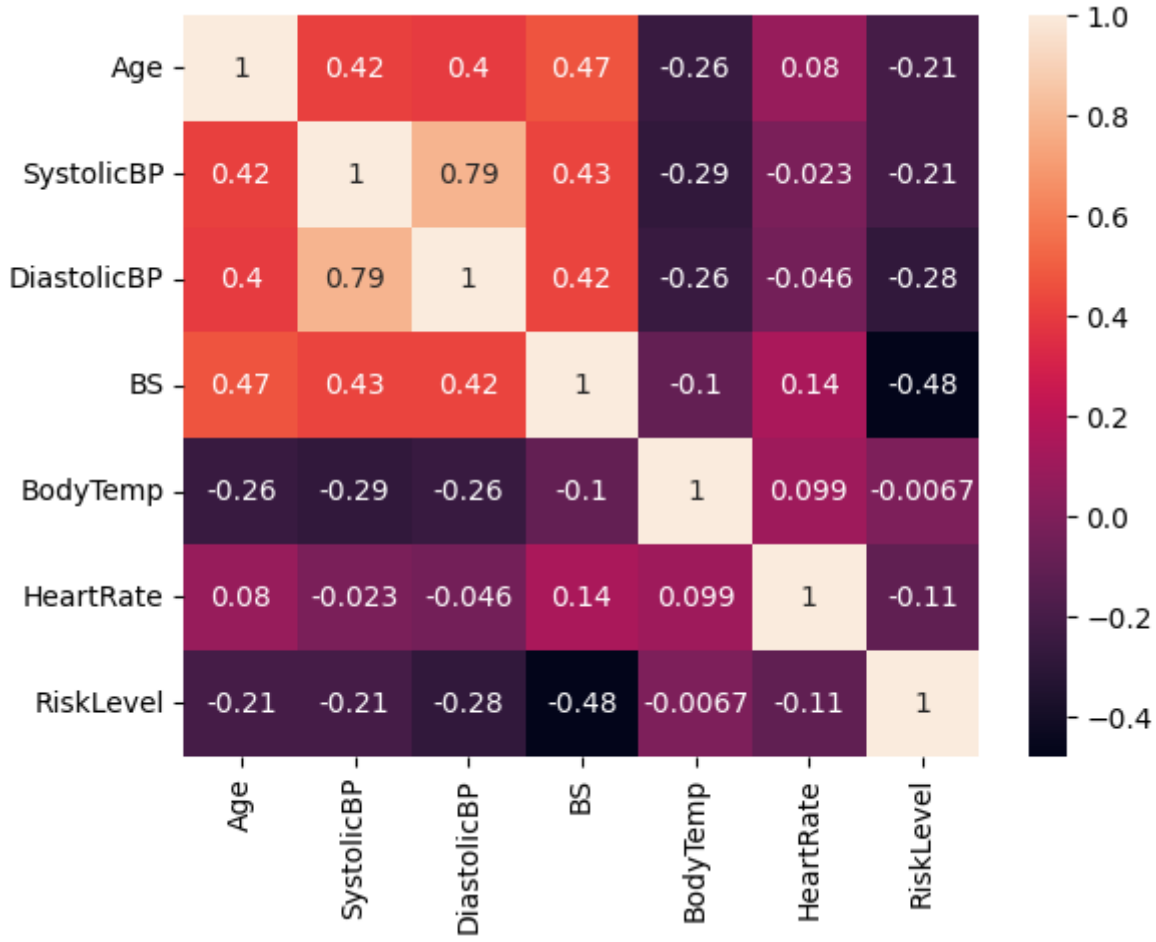

```
sns.scatterplot(data=df, x='Age', y='SystolicBP', hue='RiskLevel', palette="deep")
plt.show()
```




```
from sklearn import preprocessing
le = preprocessing.LabelEncoder()


x=list(df['RiskLevel'].unique())
le.fit(x)
df['RiskLevel']=le.transform(df.RiskLevel)


df
```

	Age	SystolicBP	DiastolicBP	BS	BodyTemp	HeartRate	RiskLevel
0	25	130	80	15.0	98.0	86	0
1	35	140	90	13.0	98.0	70	0
2	29	90	70	8.0	100.0	80	0
3	30	140	85	7.0	98.0	70	0
4	35	120	60	6.1	98.0	76	1

```
sns.heatmap(df.corr(), annot=True)
plt.show()
```




```
from sklearn.model_selection import train_test_split
from sklearn.preprocessing import LabelEncoder
from sklearn.svm import SVC


X = df.drop(['RiskLevel'], axis= 1)
y = df['RiskLevel']



X_train, X_test, y_train, y_test = train_test_split(X, y,test_size = 0.1,random_state=42)


from sklearn.preprocessing import StandardScaler
st_x= StandardScaler()
```

```
X_train= st_x.fit_transform(X_train)
X_test= st_x.transform(X_test)
```

Support Vector Machine(SVM)

```
from sklearn.svm import SVC # "Support vector classifier"
classifier = SVC(kernel='linear', random_state=0)
classifier.fit(X_train, y_train)
y_pred = classifier.predict(X_test)
```

Importing necessary performance metrics

```
from sklearn.metrics import (
    accuracy_score,
    confusion_matrix,
    ConfusionMatrixDisplay,
    f1_score,
    roc_curve,
    roc_auc_score
)
```

To display the confusion matrix for the model

```
labels = [0,1]
confusion_matrix_svm= confusion_matrix(y_test, y_pred, labels=labels)
disp = ConfusionMatrixDisplay(confusion_matrix=confusion_matrix_svm, display_labels=labels
disp.plot();
```

Accuracy of the model

```
accuracy_score_svm= accuracy_score(y_test, y_pred)
accuracy_score_svm
```

```
0.7254901960784313
```

F1 score of the model

```
f1_svm= f1_score(y_pred, y_test, average="weighted")
f1_svm
```

```
0.7430885544475808
```

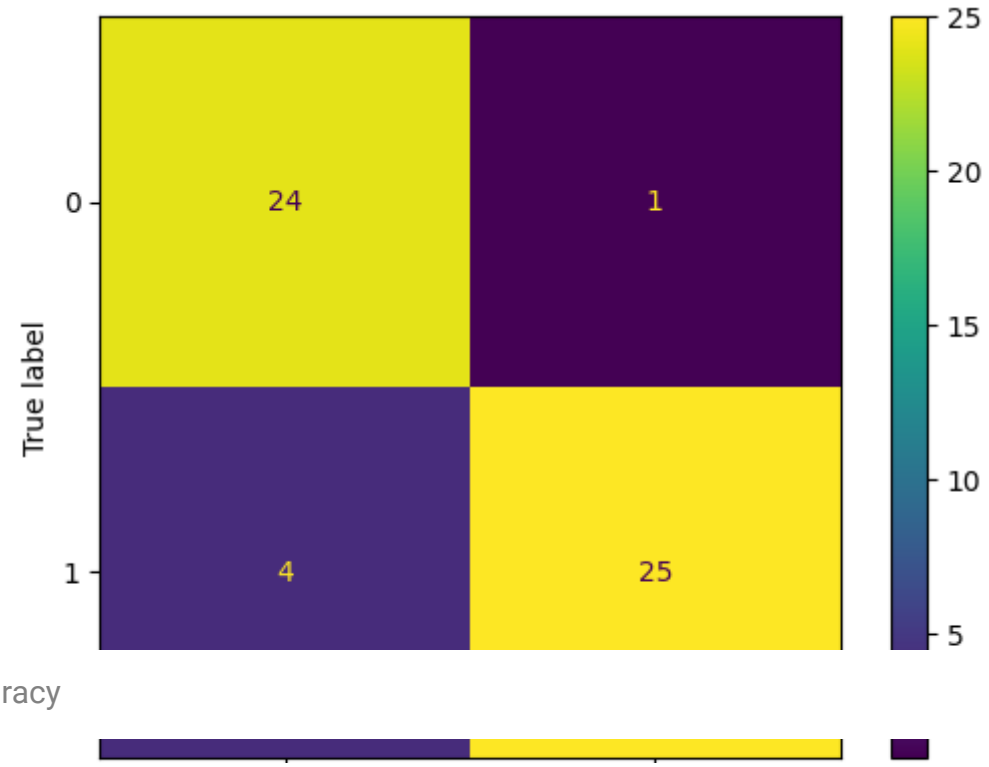
0 1

Random Forest

```
from sklearn.ensemble import RandomForestClassifier
# Initializing a Random Forest Classifier
clf = RandomForestClassifier(n_estimators=100, random_state=42)

# Fitting the classifier to the training data
clf.fit(X_train, y_train)

# Using the classifier to make predictions on the testing data
pred = clf.predict(X_test)
```

To display the confusion matrix

```
labels = [0,1]
confusion_matrix_rf= confusion_matrix(y_test,pred, labels=labels)
disp = ConfusionMatrixDisplay(confusion_matrix=confusion_matrix_rf, display_labels=labels)
disp.plot();
```



Accuracy

```
accuracy_score_rf= accuracy_score(y_test,pred)
accuracy_score_rf
```

```
0.7941176470588235
```

F1 score

```
f1_rf= f1_score(y_pred, y_test, average="weighted")
f1_rf
```

```
0.7430885544475808
```

```
df.columns
```

```
Index(['Age', 'SystolicBP', 'DiastolicBP', 'BS', 'BodyTemp', 'HeartRate',
       'RiskLevel'],
      dtype='object')
```

```
x=list(df['RiskLevel'].unique())
le.fit(x)
df['RiskLevel']=le.transform(df.RiskLevel)
```

```
df.head(10)
```

	Age	SystolicBP	DiastolicBP	BS	BodyTemp	HeartRate	RiskLevel
0	25	130	80	15.00	98.0	86	0
1	35	140	90	13.00	98.0	70	0
2	29	90	70	8.00	100.0	80	0
3	30	140	85	7.00	98.0	70	0
4	35	120	60	6.10	98.0	76	1
5	23	140	80	7.01	98.0	70	0

Taking inputs

```
def MHRP(clf):
  ip1=int(input("Enter age: "))
  ip2=int(input("Enter SystolicBP: "))
  ip3=int(input("Enter DiastolicBP: "))
  ip4=int(input("Enter Blood Sugar Level: "))
  ip5=int(input("Enter BodyTemp: "))
  ip6=int(input("Enter HeartRate: "))

  output=clf.predict([[ip1,ip2,ip3,ip4,ip5,ip6]])
  if output[0]==0:
    print("High Risk")
  elif output[0]==1:
    print("Low Risk")
  else:
    print("Mid Risk")
```

```
MHRP(clf)
```

```
Enter age: 52
Enter SystolicBP: 120
Enter DiastolicBP: 80
Enter Blood Sugar Level: 110
Enter BodyTemp: 98
Enter HeartRate: 100
High Risk
```

HEALTHCARE CENTRE

```
while True:
  print('Welcome to the Mini Health Care Centre!')
  print('Choose from the following predictors:')
```

```
··print('1.·Heart·Stroke·Predictor··\n2.·Diabetes·Predictor(Females)·\n3.·Maternal·Healthc
··opt·=·int(input('Enter·your·predictor·choice·number:·'))

··if·opt·==·1:
····predicter(clf)
··elif·opt·==·2:
····DIABETES(c)
  elif opt == 3:
    MHRP(clf)
  else:
    print('Invalid Option!')
  choice = input('Do you want to continue? (y/n) ')
  if choice.lower() == 'n':
    break
```

```
Welcome to the Mini Health Care Centre!
Choose from the following predictors:
1. Heart Stroke Predictor
2. Diabetes Predictor(Females)
3. Maternal Healthcare Predictor
Enter your predictor choice number: 4
Invalid Option!
Do you want to continue? (y/n) n
```