```
import pandas as pd
import seaborn as sns
import plotly.express as px
import plotly.offline as py
import matplotlib.pyplot as plt

df = pd.read_csv('processed.cleveland.data',names=  ['age','sex','chest_pain','blood press
               'electrocardiographic','max_heart_rate','induced_angina','ST_depression','s
```

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

	age	sex	chest_pain	blood pressure	serum_cholestoral	fasting_blood_sugar	electroc
0	63.0	1.0	1.0	145.0	233.0	1.0	
1	67.0	1.0	4.0	160.0	286.0	0.0	
2	67.0	1.0	4.0	120.0	229.0	0.0	
3	37.0	1.0	3.0	130.0	250.0	0.0	
4	41.0	0.0	2.0	130.0	204.0	0.0	

```
df.describe()
```

	age	sex	chest_pain	blood pressure	serum_cholestoral	fasting_blo
count	303.000000	303.000000	303.000000	303.000000	303.000000	30
mean	54.438944	0.679868	3.158416	131.689769	246.693069	
std	9.038662	0.467299	0.960126	17.599748	51.776918	
min	29.000000	0.000000	1.000000	94.000000	126.000000	
25%	48.000000	0.000000	3.000000	120.000000	211.000000	
50%	56.000000	1.000000	3.000000	130.000000	241.000000	
75%	61.000000	1.000000	4.000000	140.000000	275.000000	
max	77.000000	1.000000	4.000000	200.000000	564.000000	

```
df.info()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 303 entries, 0 to 302
Data columns (total 14 columns):
 #   Column                Non-Null Count  Dtype
```

```
 ---  ------                --------------  -----
  0   age                   303 non-null    float64
  1   sex                   303 non-null    float64
  2   chest_pain            303 non-null    float64
  3   blood pressure        303 non-null    float64
  4   serum_cholestoral     303 non-null    float64
  5   fasting_blood_sugar   303 non-null    float64
  6   electrocardiographic  303 non-null    float64
  7   max_heart_rate        303 non-null    float64
  8   induced_angina        303 non-null    float64
  9   ST_depression         303 non-null    float64
  10  slope                 303 non-null    float64
  11  vessels               303 non-null    object
  12  thal                  303 non-null    object
  13  diagnosis             303 non-null    int64
dtypes: float64(11), int64(1), object(2)
memory usage: 33.3+ KB
```

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

```
age                   0
sex                   0
chest_pain            0
blood pressure        0
serum_cholestoral     0
fasting_blood_sugar   0
electrocardiographic  0
max_heart_rate        0
induced_angina        0
ST_depression         0
slope                 0
vessels               0
thal                  0
diagnosis             0
dtype: int64
```

```
(df == '?').sum()
```

```
age                   0
sex                   0
chest_pain            0
blood pressure        0
serum_cholestoral     0
fasting_blood_sugar   0
electrocardiographic  0
max_heart_rate        0
induced_angina        0
ST_depression         0
slope                 0
vessels               4
thal                  2
diagnosis             0
dtype: int64
```

Removing the '?' misssing values

```
df[df['vessels'] == '?']['vessels']
```

```
166    ?
192    ?
287    ?
302    ?
Name: vessels, dtype: object
```

```
df[df['thal'] == '?']['thal']
```

```
87     ?
266    ?
Name: thal, dtype: object
```

```
missing_vessels = df[df['vessels'] == '?']['vessels'].index
missing_thals = df[df['thal'] == '?']['thal'].index
```

```
df.drop(missing_vessels,inplace=True)
df.drop(missing_thals,inplace=True)
```

After removing 6 missing values

```
df
```

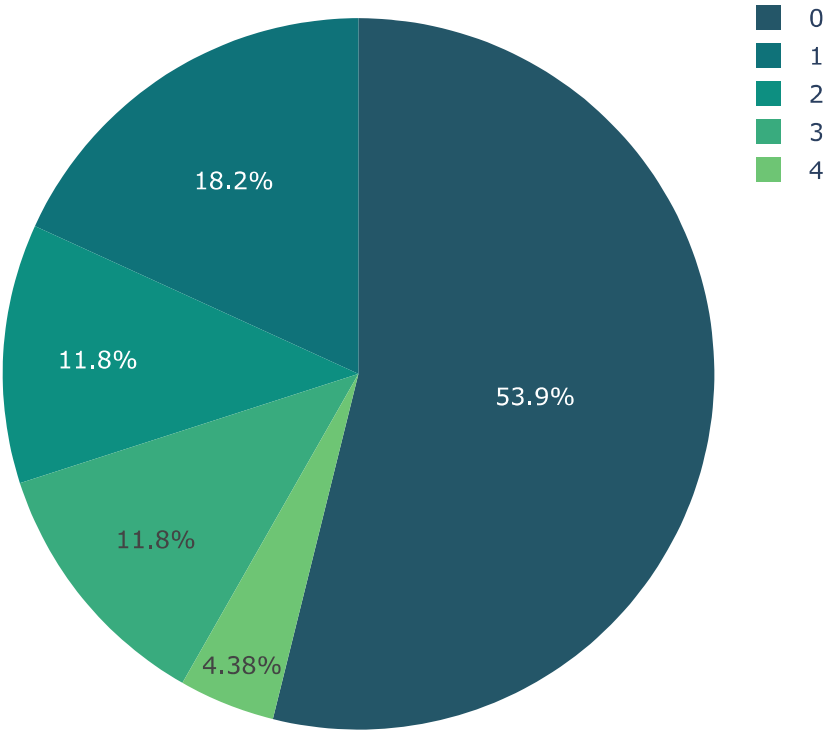
	age	sex	chest_pain	blood pressure	serum_cholestoral	fasting_blood_sugar	electr
0	63.0	1.0	1.0	145.0	233.0	1.0	
1	67.0	1.0	4.0	160.0	286.0	0.0	
2	67.0	1.0	4.0	120.0	229.0	0.0	
3	37.0	1.0	3.0	130.0	250.0	0.0	
4	41.0	0.0	2.0	130.0	204.0	0.0	
...	...	...	...	...	...	...	
297	57.0	0.0	4.0	140.0	241.0	0.0	
298	45.0	1.0	1.0	110.0	264.0	0.0	
299	68.0	1.0	4.0	144.0	193.0	1.0	
300	57.0	1.0	4.0	130.0	131.0	0.0	
301	57.0	0.0	2.0	130.0	236.0	0.0	

297 rows × 14 columns

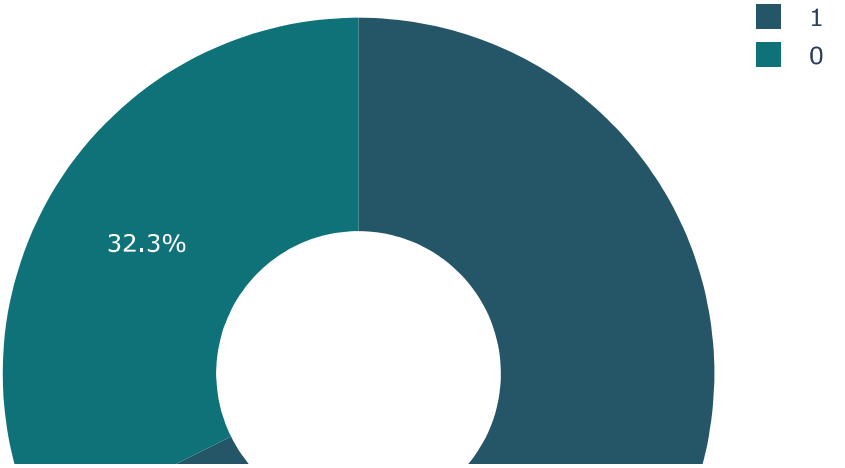
```
dfa=df.copy()
dfa['sex']=dfa['sex'].map({
```

```
    1:'Male',
    0:'Female'
})
```

```
px.pie(df, names='diagnosis',color_discrete_sequence=px.colors.sequential.Aggrnyl)
```




```
px.pie(df, names='sex',
       color_discrete_sequence=px.colors.sequential.Aggrnyl,
       hole=.4,

       )
```



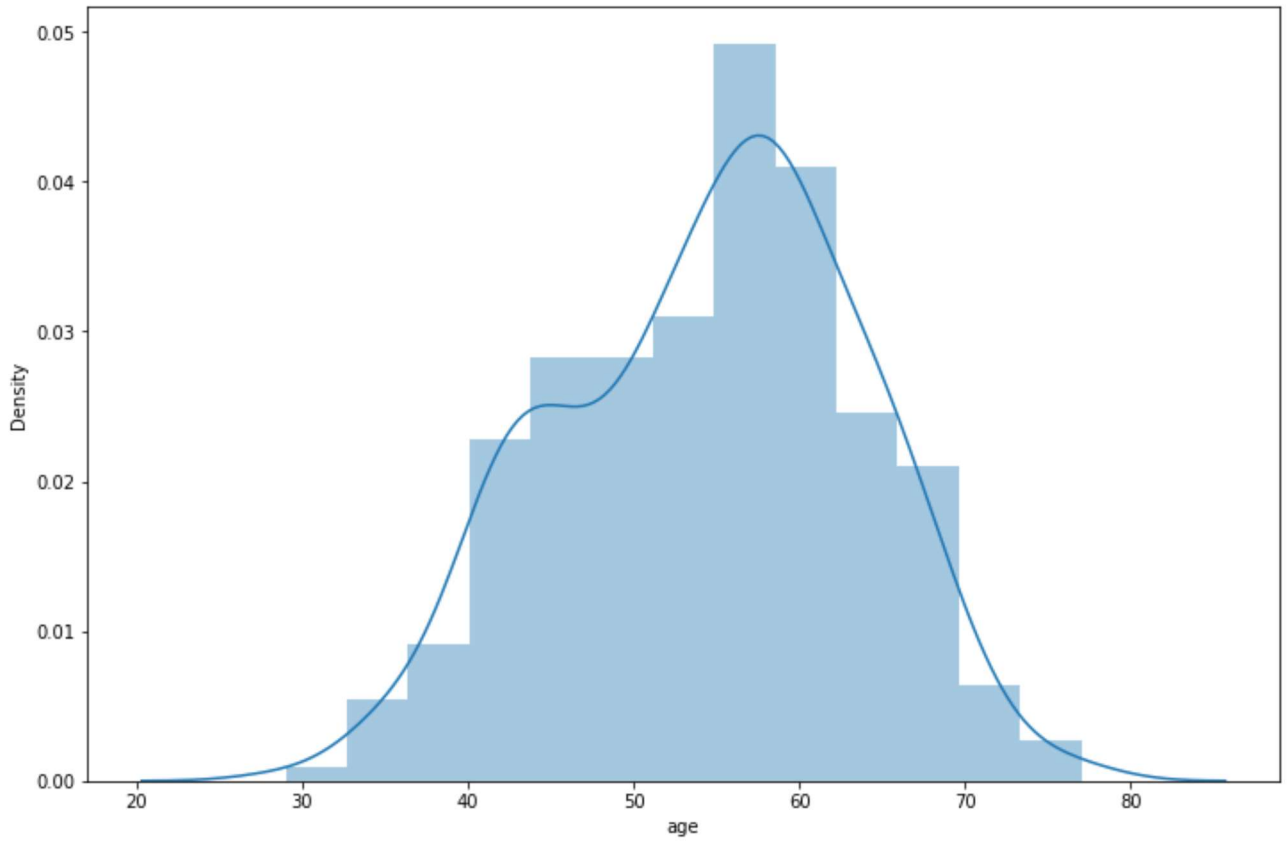
Blood Pressure vs Cholestrol

```
zero = df[df['diagnosis'] == 0]
one = df[df['diagnosis'] == 1]
two = df[df['diagnosis'] == 2]
three = df[df['diagnosis'] == 3]
four = df[df['diagnosis'] == 4]


plt.figure(figsize=(10,8))

plt.scatter(zero['blood pressure'], zero['serum_cholestoral'], c='green', alpha=0.5)
plt.scatter(one['blood pressure'], one['serum_cholestoral'], c='red', alpha=0.5)
plt.scatter(two['blood pressure'], two['serum_cholestoral'], c='blue', alpha=0.5)
plt.scatter(three['blood pressure'], three['serum_cholestoral'], c='purple', alpha=0.5)
plt.scatter(four['blood pressure'], four['serum_cholestoral'], c='black', alpha=0.5)
plt.show()
```

Checking for age distribution

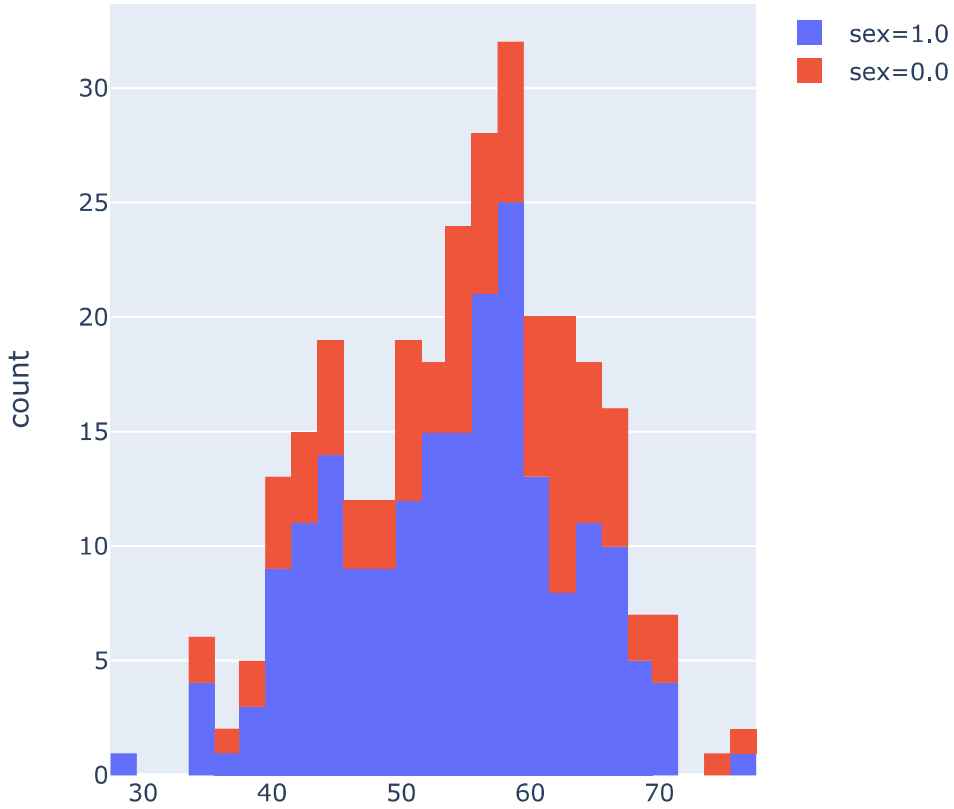
```
plt.figure(figsize=(12,8))
sns.distplot(df['age'])
```

```
/usr/local/lib/python3.7/dist-packages/seaborn/distributions.py:2619: FutureWarning:

`distplot` is a deprecated function and will be removed in a future version. Please

<matplotlib.axes._subplots.AxesSubplot at 0x7fe8b5230050>
```



Age range of people with their gender 1: Male 0: Female

```
plt.figure(figsize=(10,6))
px.histogram(df,'age',color='sex')
```




```
df['Target'] = df['diagnosis'].apply(lambda x : 1 if x >= 1 else 0)
```

```
df
```

	age	sex	chest_pain	blood pressure	serum_cholestoral	fasting_blood_sugar	electr
0	63.0	1.0	1.0	145.0	233.0	1.0	
1	67.0	1.0	4.0	160.0	286.0	0.0	
2	67.0	1.0	4.0	120.0	229.0	0.0	
3	37.0	1.0	3.0	130.0	250.0	0.0	
4	41.0	0.0	2.0	130.0	204.0	0.0	
...	...	...	...	...	...	...	
297	57.0	0.0	4.0	140.0	241.0	0.0	
298	45.0	1.0	1.0	110.0	264.0	0.0	
299	68.0	1.0	4.0	144.0	193.0	1.0	
300	57.0	1.0	4.0	130.0	131.0	0.0	
301	57.0	0.0	2.0	130.0	236.0	0.0	

297 rows × 15 columns

Training test Split

```
from sklearn.model_selection import train_test_split
from sklearn.tree import DecisionTreeClassifier
from sklearn.linear_model import LogisticRegression
from sklearn.neighbors import KNeighborsClassifier
from sklearn.ensemble import RandomForestClassifier


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


X_train, X_test, y_train, y_test = train_test_split(X, y, test_size=0.2)
```

Taking average of 10 training examples

```
from sklearn.metrics import classification_report, confusion_matrix,accuracy_score,log_los


dt_avg = []
for i in range(10):
    X_train, X_test, y_train, y_test = train_test_split(X, y, test_size=0.2)
    clf1 = DecisionTreeClassifier()
    dt_model = clf1.fit(X_train,y_train)
    dt_pred = dt_model.predict(X_test)
    dt_avg.append(accuracy_score(y_test,dt_pred))

print('Average Decision Tree Test accuracy:',sum(dt_avg)/10)
```

```
Average Decision Tree Test accuracy: 0.72
```

```
print(classification_report(y_test,dt_pred))

print(confusion_matrix(y_test,dt_pred))
```

```
                  precision    recall  f1-score   support

               0       0.74      0.80      0.77        35
               1       0.68      0.60      0.64        25

        accuracy                           0.72        60
       macro avg       0.71      0.70      0.70        60
    weighted avg       0.71      0.72      0.71        60

    [[28  7]
     [10 15]]
```

```
print('Log loss for Decision Tree model:',log_loss(y_test,dt_pred))
```

```
Log loss for Decision Tree model: 9.78607993159155
```

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