		AmirReza Azari 99101087												
	( t	In this notebook, we are looking for the diagnosis of heart disease among patients using the <a href="heart disease dataset">heart disease dataset</a> ( <a href="https://www.kaggle.com/johnsmith88/heart-disease-dataset">https://www.kaggle.com/johnsmith88/heart-disease-dataset</a> ). First, read the information about the different features, then answer the questions in each section using the attached data.						ad						
		Da	ata											
		lm	ро	rti	ng Li	bra	arie	es						
					ook, you orted be		not u	ıse scik	it learn	and ot	her libra	ries, e	exce	ept
	im im	port port	num mat	py plo	as pd as np tlib.pyp n as sns		as p	olt						
		Lo	ad	Da	atase	t								
	L	oad	data	ase	csv file	into	a da	ita fram	e.					
		<b>=</b> p .hea		ad_	csv( <b>"he</b> a	art.c	sv")	)						
_		age	sex	ср	trestbps	chol	fbs	restecg	thalach	exang	oldpeak	slope	ca	thal
		52	1	0	125	212		1	168	0	1.0	2	2	3
		53	1	0	140	203		0	155	1	3.1	0	0	3 z
		70 61	1	0	145 148	<ul><li>174</li><li>203</li></ul>	0	1	<ul><li>125</li><li>161</li></ul>	1	<ul><li>2.6</li><li>0.0</li></ul>	0	0	3
		62	0	0	138	294		1	106	0	1.9	1	3	2

[3]:  df.ta	nil()											
	age	sex	ср	trestbps	chol	fbs	restecg	thalach	exang	oldpeak	slope	ca
1020	59	1	1	140	221	0	1	164	1	0.0	2	0
1021	60	1	0	125	258	0	0	141	1	2.8	1	1
1022	47	1	0	110	275	0	0	118	1	1.0	1	1
1023	50	0	0	110	254	0	0	159	0	0.0	2	0
1024	54	1	0	120	188	0	1	113	0	1.4	1	1

# **EDA**

In statistics, exploratory data analysis (EDA) is an approach to analyzing data sets to summarize their main characteristics, often using statistical graphics and other data visualization methods. In this section, you should analyze the data. You can use the functions provided by the Pandas library. You can use analysis such as null checking of features, number of features and samples, and type of features. But don't stop there and search for it.

```
In [5]:
        df.info()
         <class 'pandas.core.frame.DataFrame'>
         RangeIndex: 1025 entries, 0 to 1024
         Data columns (total 14 columns):
              Column
                       Non-Null Count Dtype
              _____
                       -----
                      1025 non-null int64
          0
              age
          1
                      1025 non-null int64
             sex
          2
                      1025 non-null
                                    int64
             ср
          3
             trestbps 1025 non-null
                                    int64
             chol
                      1025 non-null
                                    int64
          4
          5
             fbs
                      1025 non-null int64
          6
             restecg 1025 non-null int64
          7
             thalach 1025 non-null
                                    int64
          8
                      1025 non-null int64
             exang
          9
              oldpeak 1025 non-null
                                    float64
          10 slope
                      1025 non-null
                                    int64
                                    int64
          11
             ca
                       1025 non-null
             thal
                                    int64
          12
                       1025 non-null
          13 target
                      1025 non-null
                                      int64
         dtypes: float64(1), int64(13)
         memory usage: 112.2 KB
```

, 6:02 PM				Heart_Disease	_Prediction	on - Jupyt	er Notebo	ook	
In [6]:	df.desc	ribe()	.Т						
		count	mean	std	min	25%	50%	75%	max
	age	1025.0	54.434146	9.072290	29.0	48.0	56.0	61.0	77.0
	sex	1025.0	0.695610	0.460373	0.0	0.0	1.0	1.0	1.0
	ср	1025.0	0.942439	1.029641	0.0	0.0	1.0	2.0	3.0
	trestbps	1025.0	131.611707	17.516718	94.0	120.0	130.0	140.0	200.0
	chol	1025.0	246.000000	51.592510	126.0	211.0	240.0	275.0	564.0
	fbs	1025.0	0.149268	0.356527	0.0	0.0	0.0	0.0	1.0
	restecg	1025.0	0.529756	0.527878	0.0	0.0	1.0	1.0	2.0
	thalach	1025.0	149.114146	23.005724	71.0	132.0	152.0	166.0	202.0
	exang	1025.0	0.336585	0.472772	0.0	0.0	0.0	1.0	1.0
	oldpeak	1025.0	1.071512	1.175053	0.0	0.0	0.8	1.8	6.2
	slope	1025.0	1.385366	0.617755	0.0	1.0	1.0	2.0	2.0
	ca	1025.0	0.754146	1.030798	0.0	0.0	0.0	1.0	4.0
	thal	1025.0	2.323902	0.620660	0.0	2.0	2.0	3.0	3.0
	target	1025.0	0.513171	0.500070	0.0	0.0	1.0	1.0	1.0
In [7]:	1.6	()							
-II [,].	df.nuni	.que()							
	age		41						
	sex		2						
	ср		4						
	trestb		49						
	chol		152						
	fbs		2						

fbs 3 restecg thalach 91 2 exang oldpeak 40 slope 3 5 ca thal target dtype: int64

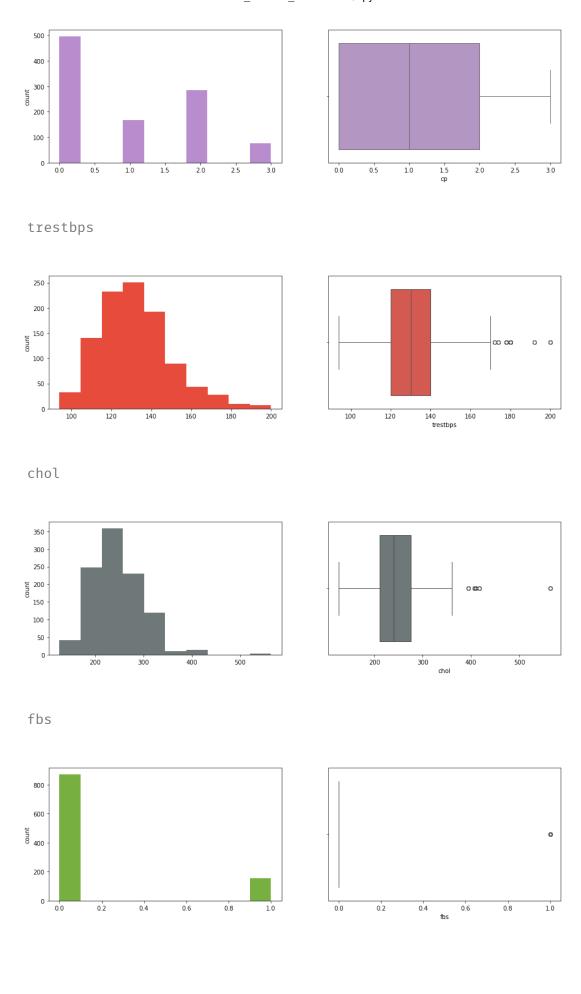
```
In [8]:
         df.age.value_counts()
           58
                  68
           57
                  57
           54
                  53
           59
                  46
           52
                  43
           51
                  39
           56
                  39
           62
                  37
           60
                  37
           44
                  36
           64
                  34
           41
                  32
           63
                  32
           67
                  31
           61
                  31
           55
                  30
           65
                  27
           43
                  26
           42
                  26
           53
                  26
           66
                  25
           45
                  25
           48
                  23
           46
                  23
           50
                  21
           47
                  18
           49
                  17
                  15
           35
           39
                  14
           70
                  14
           68
                  12
           38
                  12
           71
                  11
           40
                  11
           69
                   9
           37
                   6
           34
                   6
           29
                   4
           76
                   3
           77
                   3
                   3
           74
           Name: age, dtype: int64
```

```
df.sex.value_counts()
                713
           0
                312
           Name: sex, dtype: int64
In [10]: | df.cp.value_counts()
               497
           2
               284
           1
                167
                77
           Name: cp, dtype: int64
In [11]: | df.ca.value_counts()
                578
           0
           1
                226
           2
               134
           3
                69
                 18
           Name: ca, dtype: int64
In [12]:
         df.target.value_counts()
                526
                499
           Name: target, dtype: int64
```

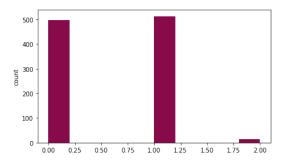
6:02 PM					Heart	_Disease	_Prediction	on - Jupyter	Notebook			
In [13]:	df.is	null(	)									
		age	sex	ср	trestbps	chol	fbs	restecg	thalach	exang	oldpeak	slo
	0	False	False	False	False	False	False	False	False	False	False	Fal
	1	False	False	False	False	False	False	False	False	False	False	Fal
	2	False	False	False	False	False	False	False	False	False	False	Fal
	3	False	False	False	False	False	False	False	False	False	False	Fal
	4	False	False	False	False	False	False	False	False	False	False	Fal
		•••	•••		•••	• • •	•••	•••	•••	•••	•••	•••
	1020	False	False	False	False	False	False	False	False	False	False	Fal
	1021	False	False	False	False	False	False	False	False	False	False	Fal
				False			False		False	False	False	Fal
				False			False		False	False	False	Fal
				False			False		False	False	False	Fal
	1024	Tatsc	Talsc	Talsc	Tatsc	Talsc	Tatsc	Tatsc	ratsc	Tatsc	Tatsc	rat
	1025	rows	× 14	colum	ns							
In [14]:	df.is	null(	).sum	()								
	age		0									
	sex		0									
	ср		0									
		stbps	0									
	chol	-	0									
	fbs		0									
	rest	- AC Ø	_									
			(°)									
	thal		0									
		ach	0									
	exar	ach ng	<ul><li>0</li><li>0</li></ul>									
	exar oldp	ach ng peak	<ul><li>0</li><li>0</li><li>0</li></ul>									
	exar oldp slop	ach ng peak	<ul><li>Θ</li><li>Θ</li><li>Θ</li></ul>									
	exar oldr slor ca	ach ng peak pe	<ul><li>0</li><li>0</li><li>0</li><li>0</li><li>0</li></ul>									
	exar oldp slop	ach ng peak pe	<ul><li>Θ</li><li>Θ</li><li>Θ</li></ul>									

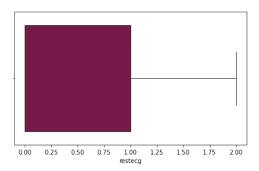
dtype: int64

```
In [15]:
          cols = df.select_dtypes(include=np.number).columns.tolist()
          colors = ["#F39C12", "#1ABC9C", "#BB8FCE", "#E74C3C", "#707B7C", "#1
          color_index = 0
          for col in cols:
              print(col)
              plt.figure(figsize = (15, 4))
              plt.subplot(1, 2, 1)
              df[col].hist(grid=False, color=colors[color_index])
              plt.ylabel('count')
              plt.subplot(1, 2, 2)
              sns.boxplot(x=df[col], color=colors[color_index])
              color_index += 1
              plt.show()
           age
            200
            150
            sex
            700
           400
00h
            300
            200
            100
                                                        0.2
           ср
```

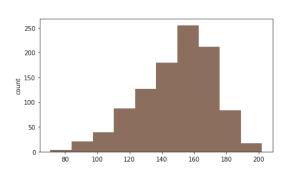


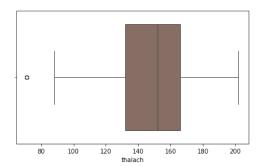




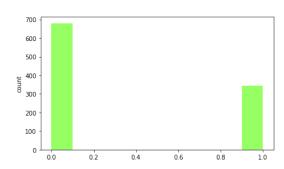


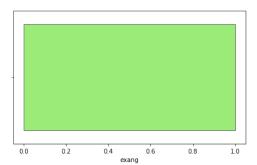
#### thalach



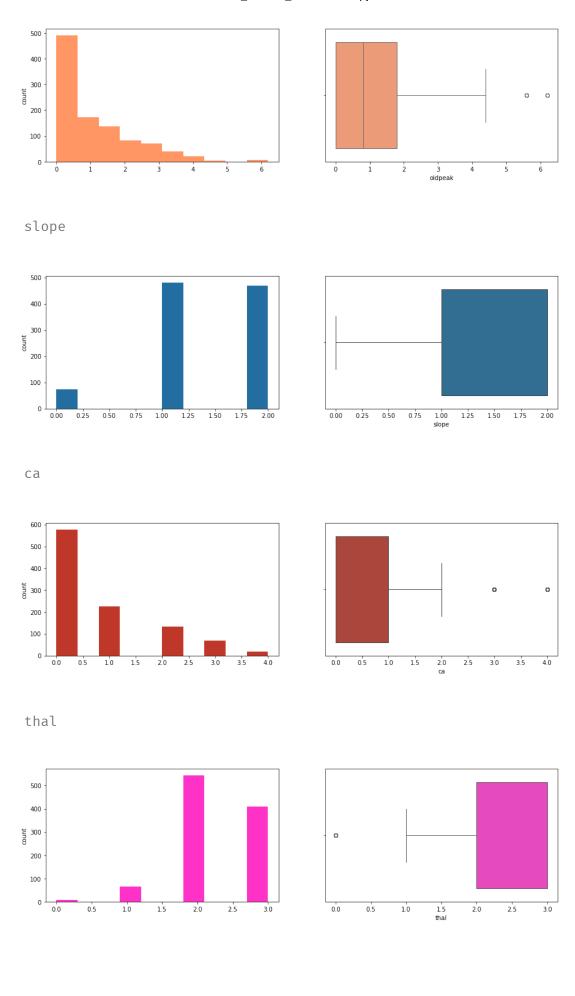


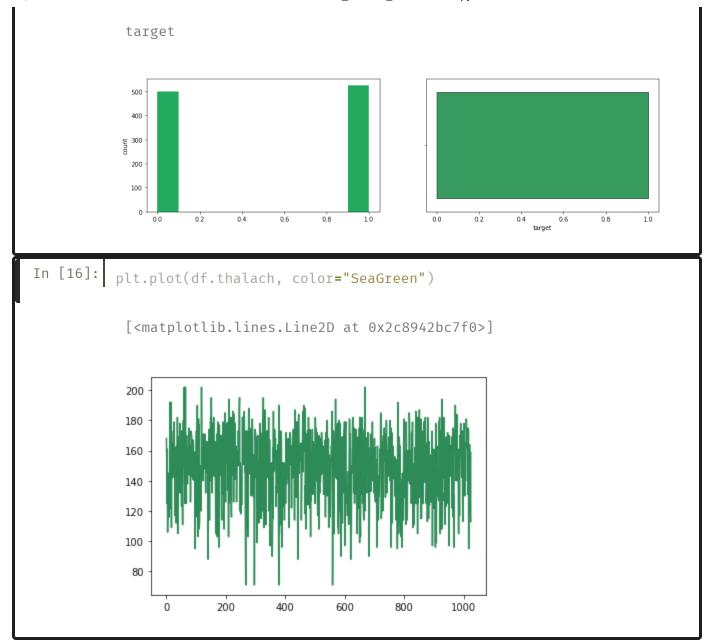
#### exang

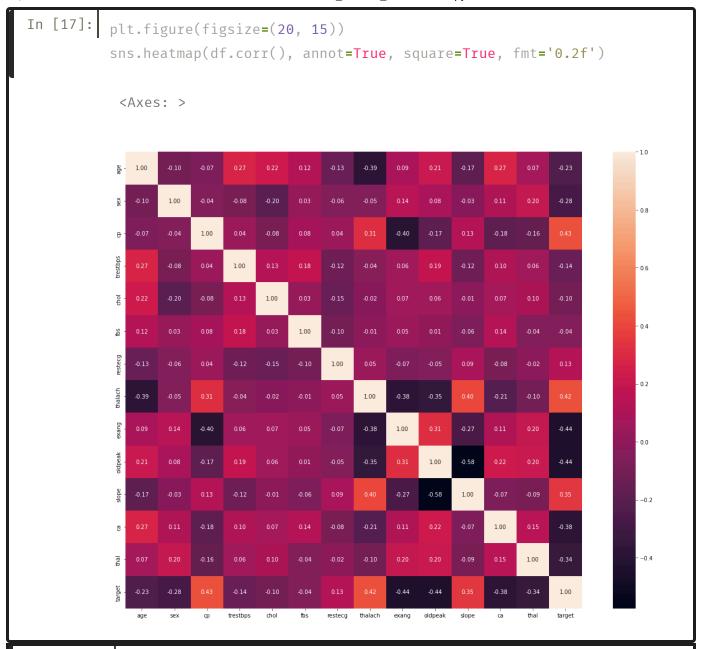




oldpeak







# **Analysis of Features**

As you have probably noticed, in the dataset that you checked, some features are discrete and the rest are continuous. The following code specifies continuous and discrete features for you. **Note**: In the cells below, df is the same dataframe that you loaded in the previous section. You can change its name according to your code.

There are 14 features found in the data

```
In [19]: #Print Discrete Feature Data
    discrete_feature=[feature for feature in feature_list if len(df[feature]))
    print("Discrete Variables Count: {}".format(len(discrete_feature)))
    print("Discrete features are ",discrete_feature)

#Print Continuous Feature Data
    cont_feature=[feature for feature in feature_list if len(df[feature]))
    print("Continuous Variables Count: {}".format(len(cont_feature)))
    print("Continuous features are ",cont_feature)

Discrete Variables Count: 9
    Discrete features are ['sex', 'cp', 'fbs', 'restecg', 'exang', 'slope', 'ca', 'thal', 'target']
    Continuous Variables Count: 5
    Continuous features are ['age', 'trestbps', 'chol', 'thalach', 'oldpeak']
```

# Perceptron

#### Stochastic Gradient Descent

We will implement the perceptron algorithm in python 3 and numpy. The perceptron will learn using the stochastic gradient descent algorithm (SGD). Gradient Descent minimizes a function by following the gradients of the cost function.

## Calculating the Error

To calculate the error of a prediction we first need to define the objective function of the perceptron.

#### Hinge Loss Function

To do this, we need to define the loss function, to calculate the prediction error. We will use hinge loss for our perceptron:

$$c(x, y, f(x)) = (1 - y * f(x))_{+}$$

c is the loss function, x the sample, y is the true label, f(x) the predicted label.

This means the following:

$$c(x, y, f(x)) = \begin{cases} 0, & \text{if } y * f(x) \ge 1\\ 1 - y * f(x), & \text{else} \end{cases}$$

So consider, if y and f(x) are signed values (+1, -1):

- the loss is 0, if y \* f(x) are positive, respective both values have the same sign.
- loss is 1 y \* f(x) if y \* f(x) is negative

#### **Objective Function**

As we defined the loss function, we can now define the objective function for the perceptron:

$$l_i(w) = (-y_i\langle x_i, w\rangle)_+$$

We can write this without the dot product with a sum sign:

$$l_i(w) = (-y_i \sum_{i=1}^n x_i w)_+$$

So the sample  $x_i$  is misclassified, if  $y_i \langle x_i, w \rangle \leq 0$ . The general goal is, to find the global minima of this function, respectively find a parameter w, where the error is zero.

#### Derive the Objective Function

To do this we need the gradients of the objective function. The gradient of a function f is the vector of its partial derivatives. The gradient can be calculated by the partially derivative of the objective function.

$$\nabla l_i(w) = -y_i x_i$$

This means, if we have a misclassified sample  $x_i$ , respectively  $y_i\langle x_i,w\rangle\leq 0$ , update the weight vector w by moving it in the direction of the misclassified sample.

$$w = w + y_i x_i$$

With this update rule in mind, we can start writing our perceptron

## Model

Finally we can code our SGD algorithm using our update rule. To keep it simple, we will linearly loop over the sample set. For larger data sets it makes sence, to randomly pick a sample during each iteration in the forloop.

```
In [20]:
          def perceptron sgd(X, Y):
              # TODO: implement the below
              Initialize the weight vector for the perceptron with zeros
              Set the learning rate
              Set the number of epochs
              Iterate n times over the whole dataset.
              Iterate over each sample in the dataset
              Misclassification condition y_i * (x_i . w) <= 0
              Update rule for the weights w = w + y_i * x_i including the lear
              1.1.1
              w = np.zeros(X.shape[1])
              learning_rate = 0.1
              epochs = 130
              for epoch in range(epochs):
                  for idx, x in enumerate(X):
                      if (Y[idx] * np.dot(X[idx], w)) <= 0:
                          w = w + learning_rate * X[idx] * Y[idx]
              return w
```

# Let the Perceptron learn!

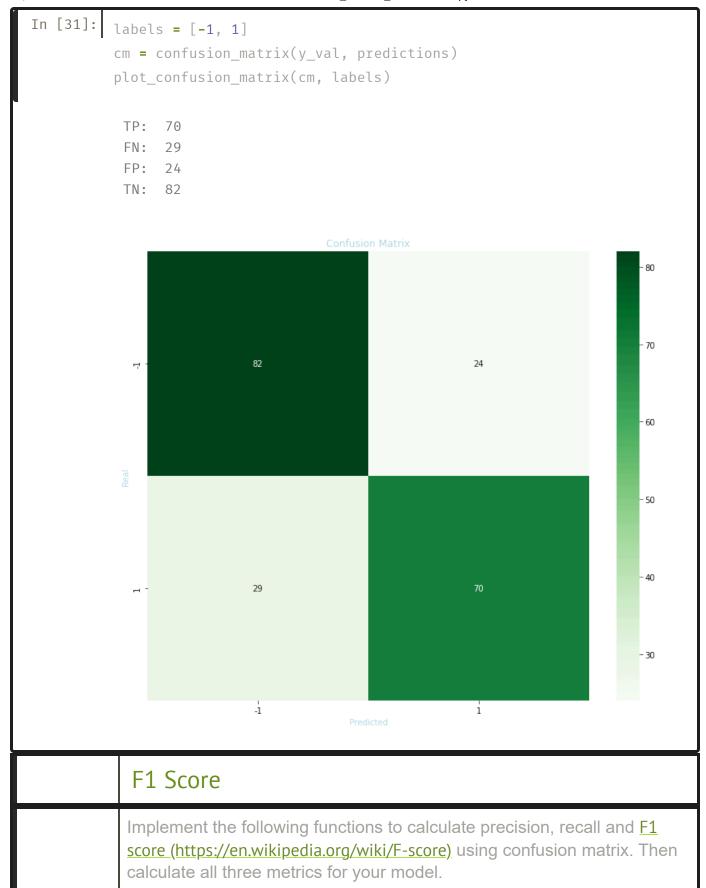
Next we can execute our code to train a classifier model. To see the learning progress of the perceptron, we add a plotting feature to our algorithm, counting the total error in each epoch.

```
In [21]:
          def perceptron_sgd_plot(X, Y):
              TODO: train perceptron and plot the total loss in each epoch. Yo
              :param X: data samples
              :param Y: data labels
              :return: weight vector as a numpy array
              w = np.zeros(X.shape[1])
              learning_rate = 0.1
              epochs = 130
              errors = []
              for epoch in range(epochs):
                  count = 0
                  for idx, x in enumerate(X):
                      if (Y[idx] * np.dot(X[idx], w)) <= 0:
                          count += (np.dot(X[idx], w) * Y[idx])
                          w = w + learning_rate * X[idx] * Y[idx]
                  errors.append(count * -1)
              plt.figure(figsize = (15, 4))
              plt.plot(errors)
              plt.xlabel('Epoch')
              plt.ylabel('Total Loss')
              return w
In [22]: | df = pd.read_csv("heart.csv")
          X = df[['sex', 'cp', 'fbs', 'restecg', 'exang', 'slope', 'ca', 'tha']
          v = df.loc[:, "target"].to numpy()
           array([0, 0, 0, ..., 0, 1, 0], dtype=int64)
```

```
In [23]: | for i in range(len(y)):
            if v[i] == 0:
                v[i] = -1
         У
          array([-1, -1, -1, ..., -1, 1, -1], dtype=int64)
In [24]: # TODO: Add a bias term -1 into the dataset. This is needed for the
         bias_column = np.full((X.shape[0], 1), -1)
         X = np.concatenate((X, bias_column), axis=1)
          array([[ 1., 0., 0., ..., 168., 1., -1.],
                [1., 0., 1., ..., 155., 3.1, -1.],
                [1., 0., 0., 125., 2.6, -1.],
                Γ 1.,
                         0., 0., ..., 118., 1., -1.],
                [ 0., 0., 0., 159., 0., -1. ],
                [1., 0., 0., 113., 1.4, -1.]
In [25]: # TODO: Split the data to train and test with a 0.2 ratio
         train_count = int(X.shape[0] * 0.8)
         X_train, X_val, y_train, y_val = X[:train_count], X[train_count:], \( \)
In [26]: | w = perceptron_sgd_plot(X_train,y_train)
           1.7
          S 1.4
         E 0
1.3
          1.2
           1.1
           Accuracy
          Implement the accuracy_score function by considering the predictions
          and true labels.
```

```
In [29]:
         def confusion_matrix(real, predicted):
              matrix = np.array([[0, 0], [0, 0]])
              count1 = 0
              count2 = 0
              count3 = 0
              count4 = 0
              for i in range(len(real)):
                  if real[i] == 1 and predicted[i] == 1:
                      matrix[1][1] += 1
                      count1 += 1
                  elif real[i] == -1 and predicted[i] == -1:
                      matrix[0][0] += 1
                      count4 += 1
                  elif real[i] == 1 and predicted[i] == -1:
                      matrix[1][0] += 1
                      count2 += 1
                  elif real[i] == -1 and predicted[i] == 1:
                      matrix[0][1] += 1
                      count3 += 1
              print("TP: ", count1)
              print("FN: ", count2)
              print("FP: ", count3)
              print("TN: ", count4)
              return matrix
           Implement the following function to plot the confusion matrix obtained
            from the previous part.
```

Now plot the confusion matrix for your model:



```
In [32]:
         def recall_score(cm):
              return cm[1][1] / (cm[1][1] + cm[1][0])
          recall = recall_score(cm)
          recall
           0.7070707070707071
In [33]: | def precision_score(cm):
              return cm[1][1] / (cm[1][1] + cm[0][1])
          precision = precision_score(cm)
          precision
           0.7446808510638298
In [34]: def f1_score(cm):
              recall = cm[1][1] / (cm[1][1] + cm[1][0])
              precision = cm[1][1] / (cm[1][1] + cm[0][1])
              return (2 * recall * precision)/(precision + recall)
          f1_score(cm)
           0.7253886010362693
            Naive Bayes
            Model
           To predict the target column we want to use a Naive Bayes classifier. In
           this section, you must implement the functions of the MixedDataNB class.
```

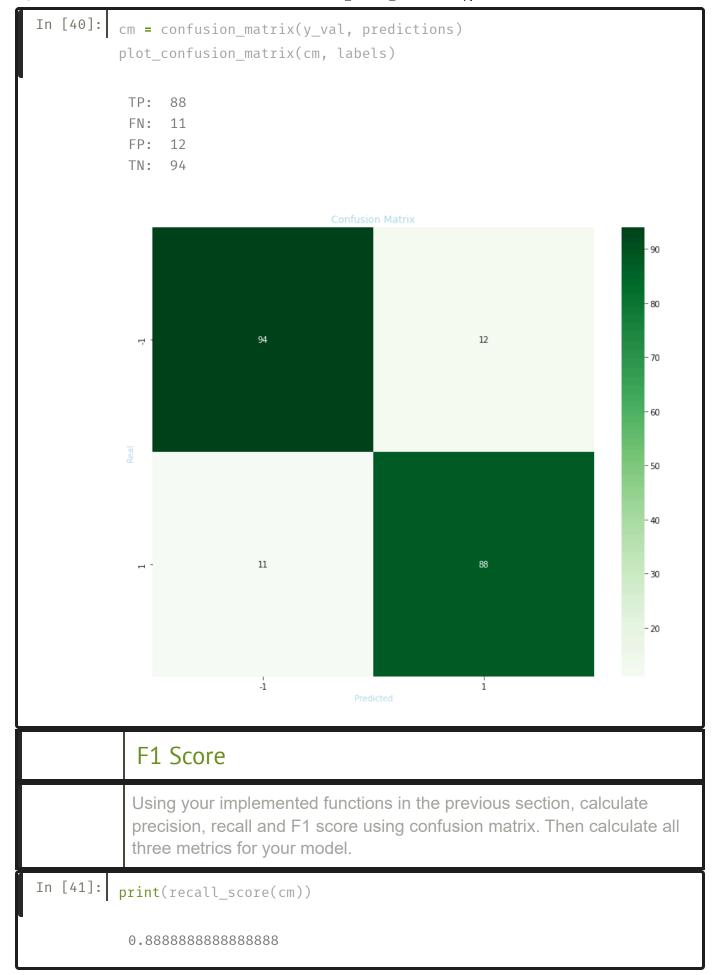
Assume continuous features follow a normal distribution. Hint: You need to train a Naive Bayes model that implements the likelihood function for categorical and continuous values in two different ways. Search for Gaussian NB and Multinomial NB. Note: Please feel free to modify the following class and its functions.

s/16/24, 6:02 PM	Heart_Disease_Prediction - Jupyter Notebook	

```
In [35]:
          class MixedDataNB:
              # Help a little from gpt and https://github.com/The-Swapster/Nat
              def init (self):
                  self.prior = None
                  self.countsss = None
                  self.category = {}
                  self.samples = None
                  self.features = None
                  self.mean data = {}
                  self.var_data = {}
              def fit(self, X, y):
                  self.samples = X.shape[0]
                  self.features = X.shape[1]
                  number_of_samps = X.shape[0]
                  number of feats = X.shape[1]
                  # self.countsss = np.zeros(n_classes)
                  # for i, c in enumerate(self.classes):
                        self.countsss[i] = np.sum(y == c) / n samples
                  self.types_of_cla = np.unique(y)
                  nums cla = len(self.types of cla)
                  self.prior = np.zeros(nums cla)
                  self.countsss = np.zeros(nums_cla)
                  all1 = np.all(np.array(X, dtype=float) == X, axis=0)
                  cont features = np.argmax(alll)
                  for i, classessse in enumerate(self.types_of_cla):
                      self.samples = X.shape[0]
                      self.features = X.shape[1]
                      X \text{ help} = X[y == classessse]
                      self.prior[i] = len(X_help) / number_of_samps
                      self.countsss[i] = len(X_help)
                      continuous_features = X_help[:, :cont_features]
                      self.category[classessse] = {}
                      categorical features = X help[:, cont features:]
                      for feat in range(cont_features, number_of_feats):
```

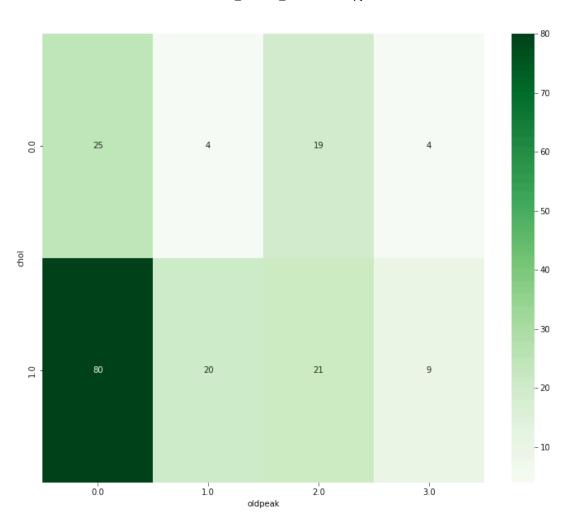
```
feature values, counts = np.unique(categorical feature)
                                               return counts=Tru
            self.category[classessse][feat] = dict(zip(feature__)
        # for i in range(len(X)):
              if y[i] == 1:
                  for j in range(self.numberOfFeature):
                      self.var 1[j] += ((X[i][j + 8] - self.miu
        self.mean_data[classessse] = np.mean(continuous_features)
        self.var_data[classessse] = np.var(continuous_features,
def predict(self, X):
    self.samples = X.shape[0]
    self.features = X.shape[1]
    n_samples, n_features = X.shape
    utilss = np.zeros((n samples, len(self.types of cla)))
    for i, cla in enumerate(self.types_of_cla):
        cont = len(self.mean_data[cla])
        likelihood1 = np.zeros(X.shape[0])
            likelihood1 = np.sum(np.log(self._pdf(i, j, x[j]))
        for i in range(cont):
            likelihood1 += -0.5 * np.log(2 * np.pi * self.var_da
                    (X[:, i] - self.mean_data[cla][i]) ** 2 / se
        cont = len(self.mean_data[cla])
        n features = X.shape[1]
        likelihood2 = np.zeros(X.shape[0])
        for j in range(cont, n features):
            likelihood2 += np.log([self.category[cla][j].get(x,
        # for i, c in enumerate(self.classes):
              prior = np.log(self.class_probabilities[i])
              likelihood = np.sum(np.log(self._pdf(i, j, x[j]))
             posterior = prior + likelihood
              posteriors.append(posterior)
        utilss[:, i] = np.log(self.prior[i]) + likelihood1 + lil
    return self.types_of_cla[np.argmax(utilss, axis=1)]
```

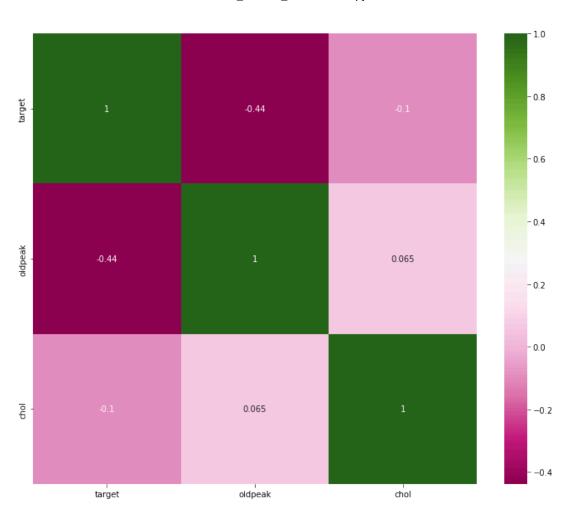
Train and Validation
Data splitting
Split the training and validation data. Separate 20% of the data for validation.
<pre>In [36]: #np.random.shuffle(X)  X = df[['sex', 'cp', 'fbs', 'restecg', 'exang', 'slope', 'ca', 'thai y = df.loc[:, "target"].to_numpy() y = np.array([1 if i == 1 else -1 for i in y]) train_count = int(X.shape[0] * 0.8) X_train, X_val, y_train, y_val = X[:train_count], X[train_count:], y</pre>
Model training
<pre>In [37]: model = MixedDataNB()</pre>
Make predictions
<pre>In [38]: predictions = model.predict(X_val)</pre>
Accuracy
Get the accuracy of your model using the function you implemented.
<pre>In [39]: print(accuracy_score(y_val, predictions))</pre>
0.8878048780487805
Confusion Matrix
Now, using the functions you wrote, plot the confusion matrix for the model you trained.

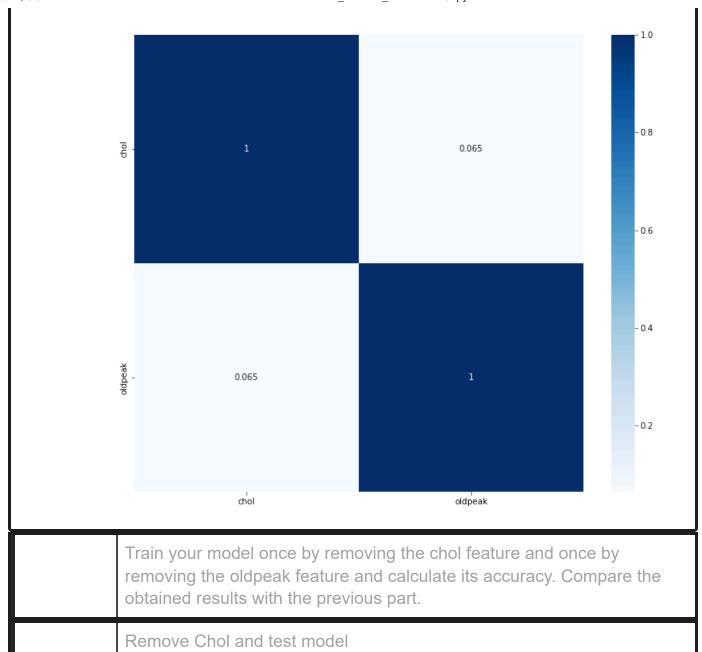


In [42]:	<pre>print(precision_score(cm))</pre>
	0.88
In [43]:	<pre>print(f1_score(cm))</pre>
	0.8844221105527638
	Heatmap
	By ploting the heatmap obtained for chol and oldpeak features from your model, compare the usefulness of these two features.

```
In [44]:
          # First:
          # Help from GPT
          df1 = pd.DataFrame({'Real': y_val, 'Predicted': predictions, 'chol'
          df2 = df1[df1['Real'] == df1['Predicted']]
          heatmap = df2.groupby(['chol', 'oldpeak']).size().unstack(fill_value
          plt.figure(figsize=(12, 10))
          sns.heatmap(heatmap, annot=True, cmap='Greens')
          plt.show()
          # Second:
          datas = df[['target' , 'oldpeak' , 'chol']]
          correlation_matrix = datas.corr()
          plt.figure(figsize=(12, 10))
          heatmap = sns.heatmap(correlation matrix, annot=True, cmap="PiYG")
          plt.show()
          # Third:
          columns = ['chol', 'oldpeak']
          correlation_matrix = df[columns].corr()
          plt.figure(figsize=(12, 10))
          sns.heatmap(correlation_matrix, annot=True, cmap='Blues')
          plt.show()
```







```
In [45]:
          # print(X)
          idx = feature list.index('chol')
          new_X = np.delete(X, idx, 1)
          # print(new_X)
          train count = int(new X.shape[0] * 0.8)
          X_train, X_val, y_train, y_val = new_X[:train_count], new_X[train_count]
         model2 = MixedDataNB()
          model2.fit(X_train, y_train)
          predictions = model2.predict(X val)
          print("Accuracy: ", round(accuracy_score(y_val, predictions) * 100,
          cm = confusion_matrix(y_val, predictions)
          print("\nrecall: ", round(recall score(cm), 4))
          print("precision: ", round(precision_score(cm), 4))
          print("f1_scores: ", round(f1_score(cm), 4))
           Accuracy: 87.805
           TP: 85
           FN: 14
           FP: 11
           TN: 95
           recall: 0.8586
           precision: 0.8854
           f1 scores:
                       0.8718
```

Remove oldpeak and test model

```
In [46]:
          # print(X)
          idx = feature list.index('oldpeak')
          new_X = np.delete(X, idx, 1)
          # print(new X)
          train count = int(new X.shape[0] * 0.8)
          X_train, X_val, y_train, y_val = new_X[:train_count], new_X[train_count]
          model2 = MixedDataNB()
          model2.fit(X train, y train)
          predictions = model2.predict(X val)
          print("Accuracy: ", round(accuracy_score(y_val, predictions) * 100,
          cm = confusion_matrix(y_val, predictions)
          print("\nrecall: ", round(recall_score(cm), 4))
          print("precision: ", round(precision_score(cm), 4))
          print("f1_scores: ", round(f1_score(cm), 4))
           Accuracy: 86.829
           TP: 85
           FN: 14
           FP: 13
           TN: 93
           recall: 0.8586
           precision: 0.8673
           f1 scores: 0.8629
            Comparison
            Answer:
            همانطور که مشخص است از لحاظ دقت، با حذف هر دو مقداری کم شده است اما این مقدار تغییر
            برای oldpeak بیشتر بوده است.
            اما به طور کلی هر دو تاثیر کمی داشته اند.
             Comparison
            Which model did better: the perceptron or the Naive Bayes model? What
            factors do you think influenced the difference in their performance?
```

#### Answer:

دقت برای perceptron حدود 74 درصد و برای Naive Bayes حدود 148 درصد بوده است. بنابراین Naive Bayes عملکرد بهتری داشته است.

لازم بود که فضای فرضیه پیچیده تری داشته باشیم و برای همین با پیچده تر کردن فضای فرضیه و الازم بود که فضای استفاده از مدل Naive Bayes دیدیم ک دقت زیاد شد.

همچنین به کمک کوررلیشن دیدیم ک داده ها تقریبا و relativly مستقل هستند که این با منطق و عملکرد Naive Bayes بیشتر همخوانی دارد ولی بایاس بیشتری برای Naive Bayes ایجاد میکند که باعث شد دقت کمتری داشته باشد.

دلیل دیگر این بود که 2 دسته داده داشتیم و طبیعتا Naive Bayes بهتر عمل مینماید.

# **Imbalanced Data**

By using the model you designed and the functions you implemented, train your model on the three imbalanced data sets provided to you and calculate accuracy, recall, precision, and F1 score metrics for it each time. The confusion matrix should also be plotted each time. Finally, analyze based on the obtained results which accuracy and F1 score metrics are most appropriate for evaluating the model in imbalanced datasets. **Note:** In order to prevent code duplication, you are free to define functions and only use them with different datasets.

### First dataset

#### Load data

In [47]: | df = pd.read\_csv("Imbalanced\_Datasets/1.csv")

#### Find the distribution

Find the number of samples from each target label.

In [48]: df['target'].value counts()

0 499

1 226

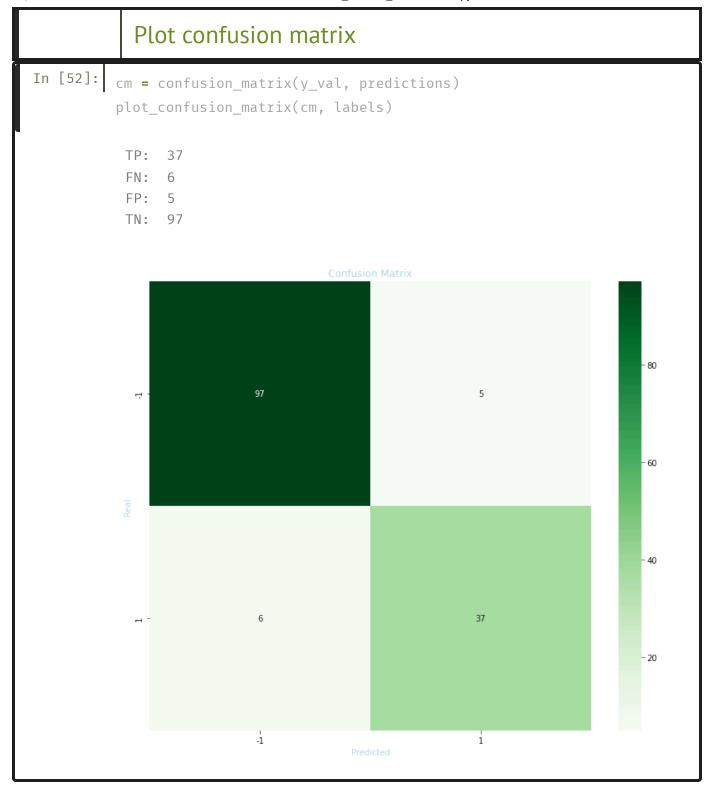
Name: target, dtype: int64

```
In [49]:
          df.head()
             age sex cp trestbps chol fbs restecg thalach exang oldpeak slope ca thal
          0 52
                                                        0
                                                                      2
                                                                           2
                                                                               3
                 1
                        125
                                212 0
                                         1
                                                168
                                                              1.0
          1 53
                        140
                                                155
                                                                      0
                1
                                203 1
                                         0
                                                        1
                                                              3.1
                                                                              3
                                                                           0
          2 70 1
                     0 145
                               174 0
                                                125
                                                              2.6
                                                                              3
          3 61 1
                                                        0
                                                                      2
                        148
                                203 0
                                                161
                                                              0.0
                                                                           1
                                                                               3
          4 62 0
                                                106
                                                                           3
                        138
                                294 1
                                                              1.9
                                                                               2
```

## Split data

# Train model and make predictions

```
In [51]: model.fit(X_train, y_train)
    predictions = model.predict(X_val)
```



#### Calculate metrics

# Second dataset

#### Load data

```
In [54]: | df = pd.read csv("Imbalanced Datasets/2.csv")
```

#### Find the distribution

Find the number of samples from each target label.

```
In [55]: | df['target'].value_counts()

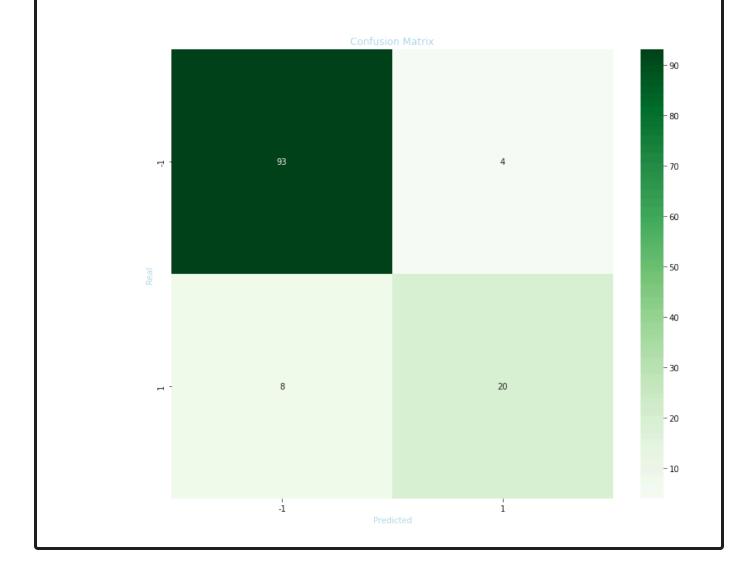
0     499
     1     126
     Name: target, dtype: int64
```

# Split data

# Train model and make predictions

# Plot confusion matrix

> TP: 20 FN: 8 FP: 4 TN: 93



#### Calculate metrics

# Third dataset

#### Load data

```
In [60]: | df = pd.read csv("Imbalanced Datasets/3.csv")
```

#### Find the distribution

Find the number of samples from each target label.

```
In [61]: | df['target'].value_counts()

0     499
1     26
Name: target, dtype: int64
```

## Split data

# 3/16/24, 6:02 PM Heart\_Disease\_Prediction - Jupyter Notebook Train model and make predictions In [63]: | model.fit(X\_train, y\_train) predictions = model.predict(X\_val) Plot confusion matrix In [64]: cm = confusion\_matrix(y\_val, predictions) plot\_confusion\_matrix(cm, labels) TP: 3 FN: FP: TN: 102 - 60 - 40

- 20

#### Calculate metrics

# Comparison

Based on the obtained results which accuracy and F1 score metrics are most appropriate for evaluating the model in imbalanced datasets?

#### Answer:

به دلیل اینکه منظور سوال را به طور درست متوجه نشدهام، یکبار جوابهای 3تا دیتاست را مقایسه accuracy و f1\_scores و

در دیتاست آخر، به دلیل کم بودن اطلاعات و مقدار زیاد imbalanced بودن آن، طبیعتا به نتیجه قابل توجه و درستی نرسیدهایم . قابل توجه و درستی نرسیدهایم اول به دیتاست اول به دیتاست اول به دلیل داشتن سمیل بیشتر، عملکرد بهتری داشته است.

در اینجا به تفاوت میان f1\_scores و در اینجا به تفاوت میان accuracy و عیردازیم. به طور کلی، مقدار f1\_scores مخصوصا برای توزیع کلاس نامتعادل مفیدتر و قابل اعتناتر میباشد.

accuracy ممکن است مناسب ترین متریک برای ارزیابی عملکرد مدل نباشد. زیرا که یک طبقه بندی کننده می تواند با پیش بینی کلاس اکثریت برای همه نمونه ها، به دقت بالایی برسد ، که لزوما نشان دهنده توانایی آن در طبقه بندی صحیح نمونه های کلاس اقلیت نیست. به مثال زیر توجه فرمایید:

Imagine we have a classification model for detecting a specific disease, where only 10% of the population actually has the disease and the rest are healthy.

If we have a very simple model that classifies everyone as healthy, our accuracy will be very high (around 90%) because most of the data is healthy. However, this model is not useful at all since it fails to detect any cases of the disease, so its F1 score will be very low.

On the other hand, if we have a more sophisticated model that is powerful enough to detect many cases of the disease, but may misclassify some healthy individuals as diseased, it might have slightly lower accuracy (say 75%), but its F1 score will be much higher because it detects more cases of the disease and also correctly identifies a large number of healthy individuals.

Therefore, the F1 score helps us evaluate a model's performance better in situations where classes are imbalanced and helps us consider how well precision and recall are balanced. In cases where precision and recall have equal importance, accuracy as a general metric may be sufficient.