Predicting heart disease using machine learning

This notebook looks into using various python-based machine learning and data science libraries in an attempt to build a machine learning model capable of predicting whether or not someone has heart disease based on their medical attributes

We're going to take the following approach:

1. Problem definition
2. Data
3. Evaluation
4. Features
5. Modelling
6. Experimentation

1. Problem Definition

In our case, the problem we will be exploring is binary classification (a sample can only be one of two things).

This is because we're going to be using a number of differnet features (pieces of information) about a person to predict whether they have heart disease or not.

In a statement,

```
Given clinical parameters about a patient, can we predict whether or not they have heart disease?
```

2. Data

What you'll want to do here is dive into the data your problem definition is based on. This may involve, sourcing, defining different parameters, talking to experts about it and finding out what you should expect.

The original data came from the Cleveland database from UCI Machine Learning Repository

Howevever, we've downloaded it in a formatted way from Kaggle

The original database contains 76 attributes, but here only 14 attributes will be used. Attributes (also called features) are the variables what we'll use to predict our target variable.

Attributes and features are also referred to as independent variables and a target variable can be referred to as a dependent variable.

```
We use the independent variables to predict our dependent variable.
```

Or in our case, the independent variables are a patients different medical attributes and the dependent variable is whether or not they have heart disease.

3. Evaluation

The evaluation metric is something you might define at the start of a project.

Since machine learning is very experimental, you might say something like,

```
        If we can reach 95% accuracy at predicting whether or not a patient has
heart disease during the proof of concept, we'll pursure this project.
```

The reason this is helpful is it provides a rough goal for a machine learning engineer or data scientist to work towards.

However, due to the nature of experimentation, the evaluation metric may change over time.

4. Features

Features are different parts of the data. During this step, you'll want to start finding out what you can about the data.

This is where you'll get different information about each of the features in your data

One of the most common ways to do this, is to create a **data dictionary**.

Heart Disease Data Dictionary

A data dictionary describes the data you're dealing with. Not all datasets come with them so this is where you may have to do your research or ask a **subject matter expert** (someone who knows about the data) for more.

The following are the features we'll use to predict our target variable (heart disease or no heart disease).

1. age - age in years
2. sex - (1 = male; 0 = female)
3. chest pain type
    - 0: Typical angina: chest pain related decrease blood supply to the heart
    - 1: Atypical angina: chest pain not related to heart
    - 2: Non-anginal pain: typically esophageal spasms (non heart related)
    - 3: Asymptomatic: chest pain not showing signs of disease
4. trestbps - resting blood pressure (in mm Hg on admission to the hospital)
    - anything above 130-140 is typically cause for concern
5. chol - serum cholestoral in mg/dl
    - serum = LDL + HDL + .2 * triglycerides
    - above 200 is cause for concern
6. fbs - (fasting blood sugar > 120 mg/dl) (1 = true; 0 = false)
    - '>126' mg/dL signals diabetes
7. restecg - resting electrocardiographic results
    - 0: Nothing to note
    - 1: ST-T Wave abnormality
        - can range from mild symptoms to severe problems
        - signals non-normal heart beat

    - 2: Possible or definite left ventricular hypertrophy
        - Enlarged heart's main pumping chamber
8. thalach - maximum heart rate achieved
9. exang - exercise induced angina (1 = yes; 0 = no)
10. oldpeak - ST depression induced by exercise relative to rest
    - looks at stress of heart during excercise
    - unhealthy heart will stress more
11. slope - the slope of the peak exercise ST segment
    - 0: Upsloping: better heart rate with excercise (uncommon)
    - 1: Flatsloping: minimal change (typical healthy heart)
    - 2: Downslopins: signs of unhealthy heart
12. ca - number of major vessels (0-3) colored by flourosopy
    - colored vessel means the doctor can see the blood passing through
    - the more blood movement the better (no clots)
13.
    - thalium stress result
    - 1,3: normal
    - 6: fixed defect: used to be defect but ok now
    - 7: reversable defect: no proper blood movement when excercising
14. target - have disease or not (1=yes, 0=no) (= the predicted attribute) **Note**: No personal identifiable information (PPI) can be found in the dataset.

It's a good idea to save these to a Python dictionary or in an external file, so we can look at them later without coming back here.

Preparing the tools

We're going to use Pandas, Matplotlib and Numpy for Data Analysis anad manipulation.

At the start of any project, it's custom to see the required libraries imported in a big chunk like you can see below.

However, in practice, your projects may import libraries as you go. After you've spent a couple of hours working on your problem, you'll probably want to do some tidying up. This is where you may want to consolidate every library you've used at the top of your notebook (like the cell below).

The libraries you use will differ from project to project. But there are a few which will you'll likely take advantage of during almost every structured data project.

- pandas for data analysis.
- NumPy for numerical operations.
- Matplotlib/seaborn for plotting or data visualization(https://seaborn.pydata.org).
- Scikit-Learn for machine learning modelling and evaluation.

In [3]:
```
# Import all the tools we need

# Regular EDA (Exploratory Data Analysis) and plotting libraries
import numpy as np
import pandas as pd
import matplotlib.pyplot as plt
import seaborn as sns

# We want our plot to appear inside the notebook
```

```
%matplotlib inline

# Models from Scikit-learn
from sklearn.linear_model import LogisticRegression
from sklearn.neighbors import KNeighborsClassifier
from sklearn.ensemble import RandomForestClassifier

# Model Evaluations
from sklearn.model_selection import train_test_split, cross_val_score
from sklearn.model_selection import RandomizedSearchCV, GridSearchCV
from sklearn.metrics import confusion_matrix, classification_report
from sklearn.metrics import precision_score, recall_score, f1_score
from sklearn.metrics import plot_roc_curve
```

Load Data

There are many different kinds of ways to store data. The typical way of storing **tabular data**, data similar to what you'd see in an Excel file is in .csv format. .csv stands for comma seperated values.

Pandas has a built-in function to read .csv files called read_csv() which takes the file pathname of your .csv file. You'll likely use this a lot.

In [5]:
```
df = pd.read_csv('heart-disease.csv') # 'DataFrame' shortened to 'df'
df.shape  # (rows, columns)
```

Out[5]:
```
(303, 14)
```

Data Exploration (Exploratory Data Analysis or EDA)

Once you've imported a dataset, the next step is to explore. There's no set way of doing this. But what you should be trying to do is become more and more familiar with the dataset.

Compare different columns to each other, compare them to the target variable. Refer back to your **data dictionary** and remind yourself of what different columns mean.

Your goal is to become a subject matter expert on the dataset you're working with. So if someone asks you a question about it, you can give them an explanation and when you start building models, you can sound check them to make sure they're not performing too well (**overfitting**) or why they might be performing poorly (**underfitting**).

Since EDA has no real set methodolgy, the following is a short check list you might want to walk through:

1. What question(s) are you trying to solve (or prove wrong)?
2. What kind of data do you have and how do you treat different types?
3. What's missing from the data and how do you deal with it?
4. Where are the outliers and why should you care about them?
5. How can you add, change or remove features to get more out of your data?

Once of the quickest and easiest ways to check your data is with the head() function. Calling it on any dataframe will print the top 5 rows, tail() calls the bottom 5. You can also pass a number to them like head(10) to show the top 10 rows.

In [6]:
```
# Let's check the top 5 rows of our dataframe
```

```
df.head()
```

Out[6]:

	age	sex	cp	trestbps	chol	fbs	restecg	thalach	exang	oldpeak	slope	ca	thal	target
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

In [7]:
```
# To check the bottom 5 rows of our dataframe
df.tail()
```

Out[7]:

	age	sex	cp	trestbps	chol	fbs	restecg	thalach	exang	oldpeak	slope	ca	thal	target
298	57	0	0	140	241	0	1	123	1	0.2	1	0	3	0
299	45	1	3	110	264	0	1	132	0	1.2	1	0	3	0
300	68	1	0	144	193	1	1	141	0	3.4	1	2	3	0
301	57	1	0	130	131	0	1	115	1	1.2	1	1	3	0
302	57	0	1	130	236	0	0	174	0	0.0	1	1	2	0

In [8]:
```
# And the top 10
df.head(10)
```

Out[8]:

	age	sex	cp	trestbps	chol	fbs	restecg	thalach	exang	oldpeak	slope	ca	thal	target
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
5	57	1	0	140	192	0	1	148	0	0.4	1	0	1	1
6	56	0	1	140	294	0	0	153	0	1.3	1	0	2	1
7	44	1	1	120	263	0	1	173	0	0.0	2	0	3	1
8	52	1	2	172	199	1	1	162	0	0.5	2	0	3	1
9	57	1	2	150	168	0	1	174	0	1.6	2	0	2	1

value_counts() allows you to show how many times each of the values of a **categorical** column appear.

In [9]:
```
# Let's find out how many of each class there are
df['target'].value_counts()
```

Out[9]:
```
1    165
0    138
Name: target, dtype: int64
```

Since these two values are close to even, our target column can be considered **balanced**. An **unbalanced** target

column, meaning some classes have far more samples, can be harder to model than a balanced set. Ideally, all of your target classes have the same number of samples.

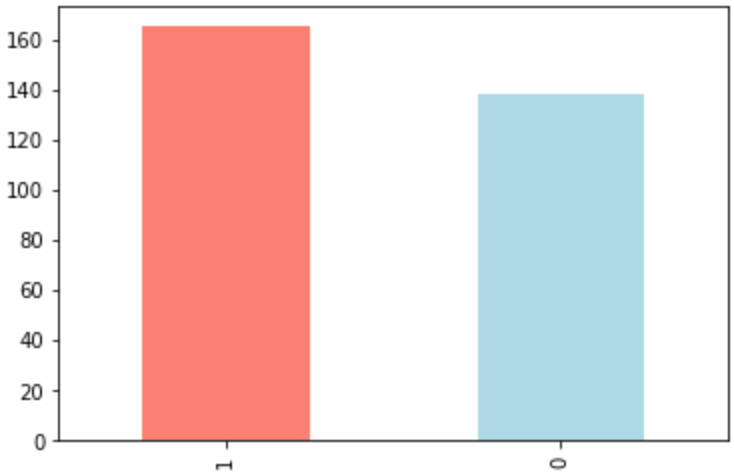
If you'd prefer these values in percentages, value_counts() takes a parameter, normalize which can be set to true.

In [10]:
```
df['target'].value_counts(normalize=True)
```

Out[10]:
```
1    0.544554
0    0.455446
Name: target, dtype: float64
```

We can plot the target column value counts by calling the plot() function and telling it what kind of plot we'd like, in this case, bar is good.

In [11]:
```
df['target'].value_counts().plot(kind='bar', color=['salmon', 'lightblue']);
```



df.info() shows a quick insight to the number of missing values you have and what type of data you're working with.

In our case, there are no missing values and all of our columns are numerical in nature.

In [12]:
```
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    int64  
 1   sex       303 non-null    int64  
 2   cp        303 non-null    int64  
 3   trestbps  303 non-null    int64  
 4   chol      303 non-null    int64  
 5   fbs       303 non-null    int64  
 6   restecg   303 non-null    int64  
 7   thalach   303 non-null    int64  
 8   exang     303 non-null    int64  
 9   oldpeak   303 non-null    float64
 10  slope     303 non-null    int64  
 11  ca        303 non-null    int64  
 12  thal      303 non-null    int64  
 13  target    303 non-null    int64  
dtypes: float64(1), int64(13)
memory usage: 33.3 KB
```

In [13]:
```
# Are there any missing values?
df.isna().sum()
```

Out[13]:
```
age         0
sex         0
cp          0
trestbps    0
chol        0
fbs         0
restecg     0
thalach     0
exang       0
oldpeak     0
slope       0
ca          0
thal        0
target      0
dtype: int64
```

Another way to get some quick insights on your dataframe is to use df.describe(). describe() shows a range of different metrics about your numerical columns such as mean, max and standard deviation.

In [14]:
```
df.describe()
```

Out[14]:

	age	sex	cp	trestbps	chol	fbs	restecg	thalach	exang
count	303.000000	303.000000	303.000000	303.000000	303.000000	303.000000	303.000000	303.000000	303.000000
mean	54.366337	0.683168	0.966997	131.623762	246.264026	0.148515	0.528053	149.646865	0.326733
std	9.082101	0.466011	1.032052	17.538143	51.830751	0.356198	0.525860	22.905161	0.469794
min	29.000000	0.000000	0.000000	94.000000	126.000000	0.000000	0.000000	71.000000	0.000000
25%	47.500000	0.000000	0.000000	120.000000	211.000000	0.000000	0.000000	133.500000	0.000000
50%	55.000000	1.000000	1.000000	130.000000	240.000000	0.000000	1.000000	153.000000	0.000000
75%	61.000000	1.000000	2.000000	140.000000	274.500000	0.000000	1.000000	166.000000	1.000000
max	77.000000	1.000000	3.000000	200.000000	564.000000	1.000000	2.000000	202.000000	1.000000

Heart Disease Frequency according to gender

If you want to compare two columns to each other, you can use the function pd.crosstab(column_1, column_2).

This is helpful if you want to start gaining an intuition about how your independent variables interact with your dependent variables.

Let's compare our target column with the sex column.

Remember from our data dictionary, for the target column, 1 = heart disease present, 0 = no heart disease. And for sex, 1 = male, 0 = female.

In [15]:
```
df.sex.value_counts()
```

Out[15]:
```
1    207
0     96
Name: sex, dtype: int64
```

In [16]:
```
# Compare target column with sex column
```

```
pd.crosstab(df.target, df.sex)
```

Out[16]:

target	sex 0	1
0	24	114
1	72	93

What can we infer from this? Let's make a simple heuristic.

Since there are about 100 women and 72 of them have a postive value of heart disease being present, we might infer, based on this one variable if the participant is a woman, there's a 75% chance she has heart disease.

As for males, there's about 200 total with around half indicating a presence of heart disease. So we might predict, if the participant is male, 50% of the time he will have heart disease.

Averaging these two values, we can assume, based on no other parameters, if there's a person, there's a 62.5% chance they have heart disease.

This can be our very simple **baseline**, we'll try to beat it with machine learning.

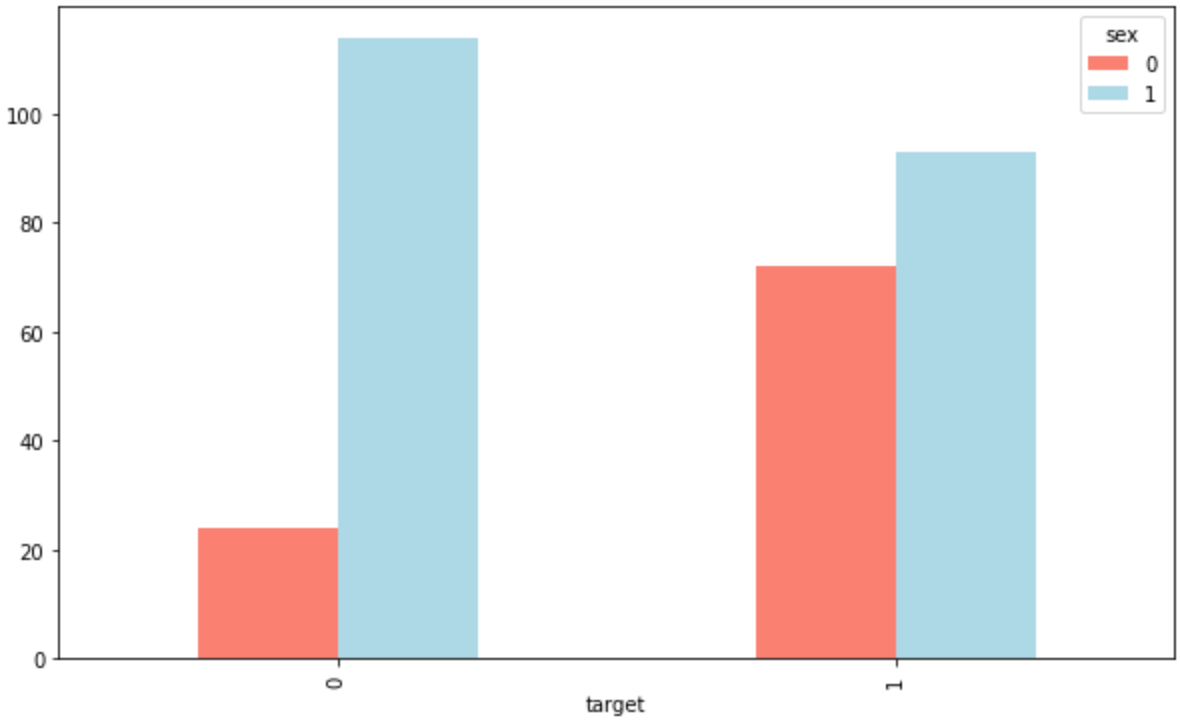
Making our crosstab visual

You can plot the crosstab by using the plot() function and passing it a few parameters such as, kind (the type of plot you want), figsize=(width, height) (how big you want it to be) and color=[colour_1, colour_2] (the different colours you'd like to use).

Different metrics are represented best with different kinds of plots. In our case, a bar graph is great. We'll see examples of more later. And with a bit of practice, you'll gain an intuition of which plot to use with different variables.

In [17]:

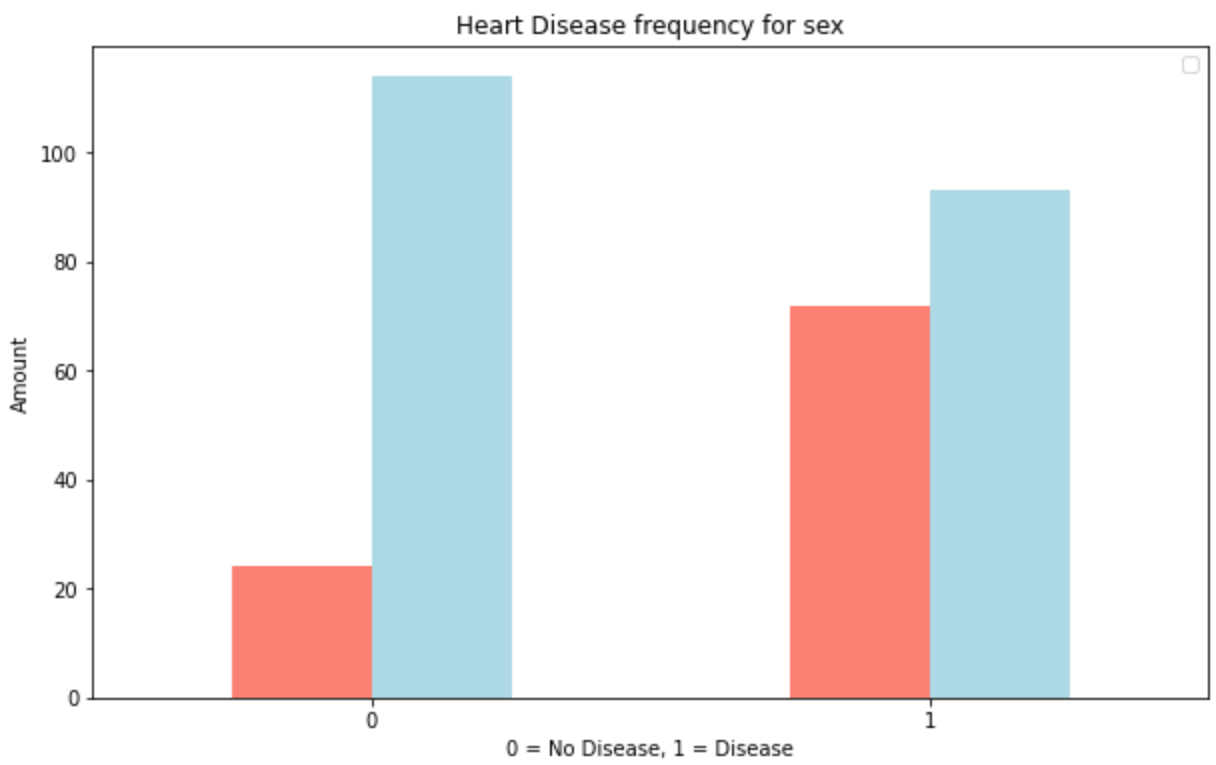
```
# Create a plot
pd.crosstab(df.target, df.sex).plot(kind='bar',
                                    figsize=(10, 6),
                                    color=['salmon', 'lightblue']);
```



In [18]:

```
# Create a plot
pd.crosstab(df.target, df.sex).plot(kind='bar',
                                    figsize=(10, 6),
                                    color=['salmon', 'lightblue']);

# Add some attributes
plt.title('Heart Disease frequency for sex')
plt.xlabel('0 = No Disease, 1 = Disease')
plt.ylabel('Amount')
plt.legend('Female', 'Male')
plt.xticks(rotation = 0); # keep the labels on the x-axis vertical
```

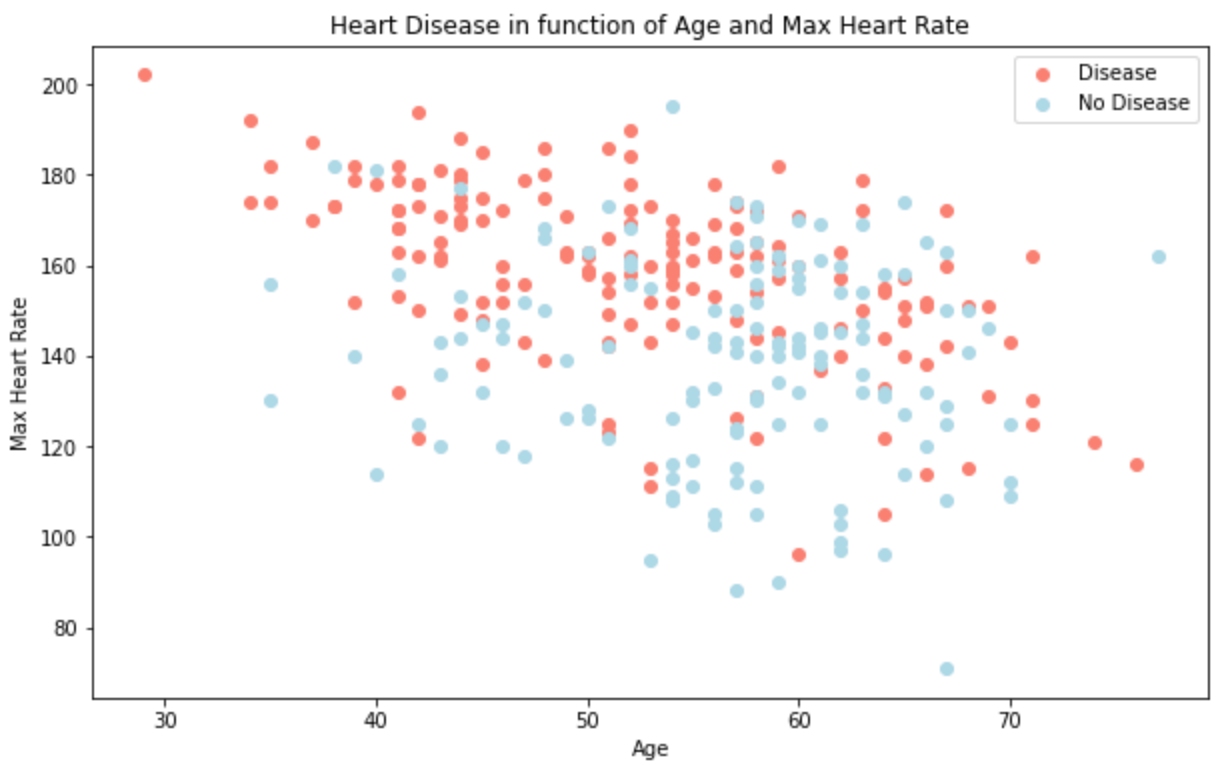
```
<ipython-input-18-5f5ac11fe86f>:10: UserWarning: Legend does not support 'F' instances.
A proxy artist may be used instead.
See: https://matplotlib.org/users/legend_guide.html#creating-artists-specifically-for-addi
ng-to-the-legend-aka-proxy-artists
  plt.legend('Female', 'Male')
<ipython-input-18-5f5ac11fe86f>:10: UserWarning: Legend does not support 'e' instances.
A proxy artist may be used instead.
See: https://matplotlib.org/users/legend_guide.html#creating-artists-specifically-for-addi
ng-to-the-legend-aka-proxy-artists
  plt.legend('Female', 'Male')
<ipython-input-18-5f5ac11fe86f>:10: UserWarning: Legend does not support 'm' instances.
A proxy artist may be used instead.
See: https://matplotlib.org/users/legend_guide.html#creating-artists-specifically-for-addi
ng-to-the-legend-aka-proxy-artists
  plt.legend('Female', 'Male')
<ipython-input-18-5f5ac11fe86f>:10: UserWarning: Legend does not support 'a' instances.
A proxy artist may be used instead.
See: https://matplotlib.org/users/legend_guide.html#creating-artists-specifically-for-addi
ng-to-the-legend-aka-proxy-artists
  plt.legend('Female', 'Male')
```



Age vs Max Heart rate for Heart Disease

In [19]:

```
# create another figure
plt.figure(figsize=(10, 6))

# Start with positive example
plt.scatter(df.age[df.target==1],
            df.thalach[df.target==1],
            color='salmon') # define it as a scatter figure

# Start with a negative example, we want them on the same plot so we call plt again
plt.scatter(df.age[df.target==0],
            df.thalach[df.target==0],
            color='lightblue') # Axis always comes as (x, y)

# Add some helpful info
plt.title('Heart Disease in function of Age and Max Heart Rate')
plt.xlabel('Age')
plt.ylabel('Max Heart Rate')
plt.legend(['Disease', 'No Disease']);
```



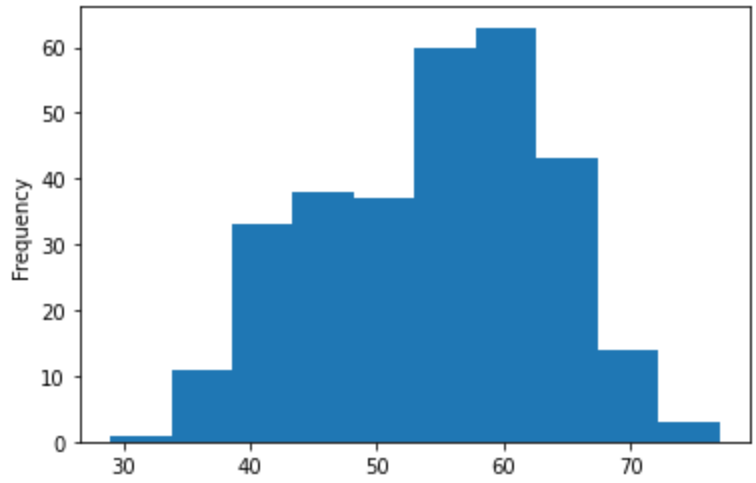
What can we infer from this?

It seems the younger someone is, the higher their max heart rate (dots are higher on the left of the graph) and the older someone is, the more green dots there are. But this may be because there are more dots all together on the right side of the graph (older participants).

Both of these are observational of course, but this is what we're trying to do, build an understanding of the data.

Let's check the age **distribution**.

In [20]:
```
# Check the distribution of the Age column with a Histogram
df.age.plot.hist();
```



Heart Disease Frequency per Chest Pain Type

1. chest pain type
    - 0: Typical angina: chest pain related decrease blood supply to the heart
    - 1: Atypical angina: chest pain not related to heart
    - 2: Non-anginal pain: typically esophageal spasms (non heart related)

- 3: Asymptomatic: chest pain not showing signs of disease

Let's try another independent variable. This time, cp (chest pain).

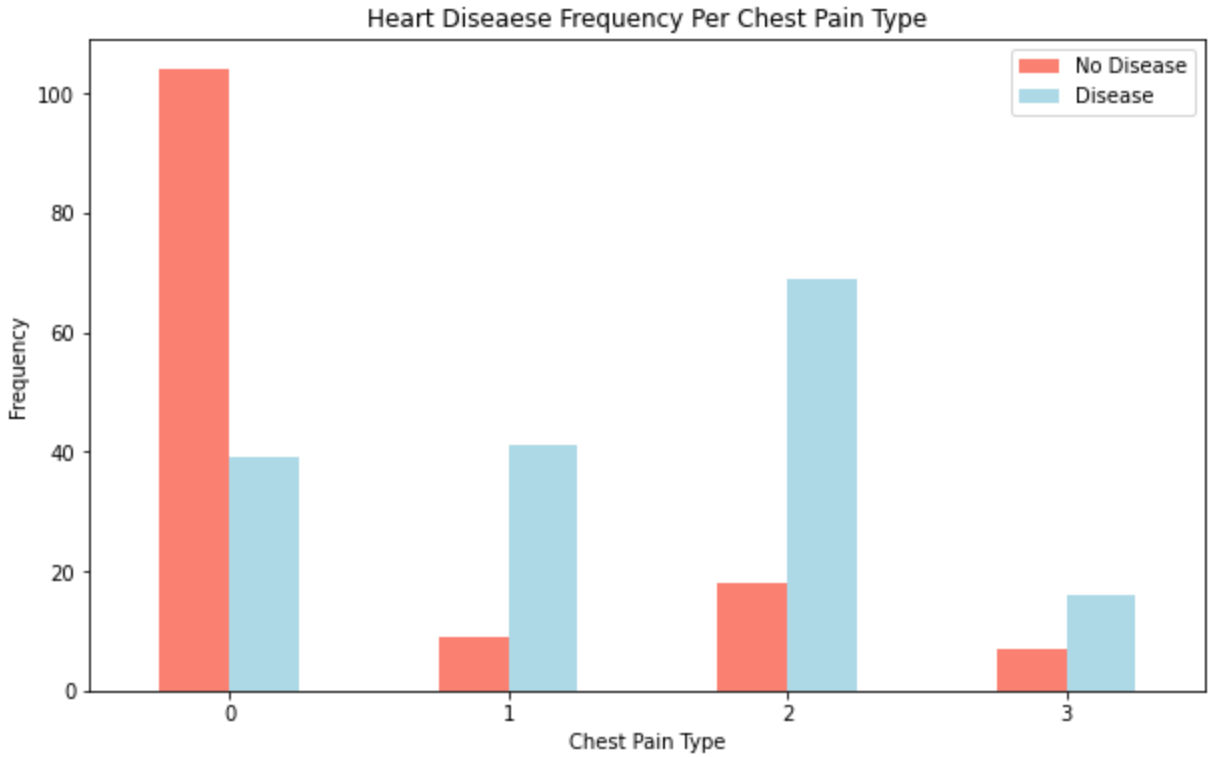
We'll use the same process as we did before with sex.

In [21]:
```
pd.crosstab(df.cp, df.target)
```

Out[21]:

target	0	1
cp		
0	104	39
1	9	41
2	18	69
3	7	16

In [22]:
```
# Make the crosstab more visual
pd.crosstab(df.cp, df.target).plot(kind='bar',
                                   figsize=(10, 6),
                                   color=['salmon', 'lightblue'])

# Add attributes to the plot to make it more readable
plt.title('Heart Diseaese Frequency Per Chest Pain Type')
plt.xlabel('Chest Pain Type')
plt.ylabel('Frequency')
plt.legend(['No Disease', 'Disease'])
plt.xticks(rotation=0);
```



What can we infer from this?

Remember from our data dictionary what the different levels of chest pain are.

1. cp - chest pain type

- 0: Typical angina: chest pain related decrease blood supply to the heart
- 1: Atypical angina: chest pain not related to heart
- 2: Non-anginal pain: typically esophageal spasms (non heart related)
- 3: Asymptomatic: chest pain not showing signs of disease

It's interesting the atypical agina (value 1) states it's not related to the heart but seems to have a higher ratio of participants with heart disease than not.

Wait...?

What does atypical agina even mean?

At this point, it's important to remember, if your data dictionary doesn't supply you enough information, you may want to do further research on your values. This research may come in the form of asking a **subject matter expert** (such as a cardiologist or the person who gave you the data) or Googling to find out more.

According to PubMed, it seems even some medical professionals are confused by the term.

> Today, 23 years later, “atypical chest pain” is still popular in medical circles. Its meaning, however, remains unclear. A few articles have the term in their title, but do not define or discuss it in their text. In other articles, the term refers to noncardiac causes of chest pain.

Although not conclusive, this graph above is a hint at the confusion of defintions being represented in data.

In [23]:
```
df.head()
```

Out[23]:

	age	sex	cp	trestbps	chol	fbs	restecg	thalach	exang	oldpeak	slope	ca	thal	target
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

Correlation between independent variables

Finally, we'll compare all of the independent variables in one hit.

Why?

Because this may give an idea of which independent variables may or may not have an impact on our target variable.

We can do this using df.corr() which will create a correlation matrix for us, in other words, a big table of numbers telling us how related each variable is the other.

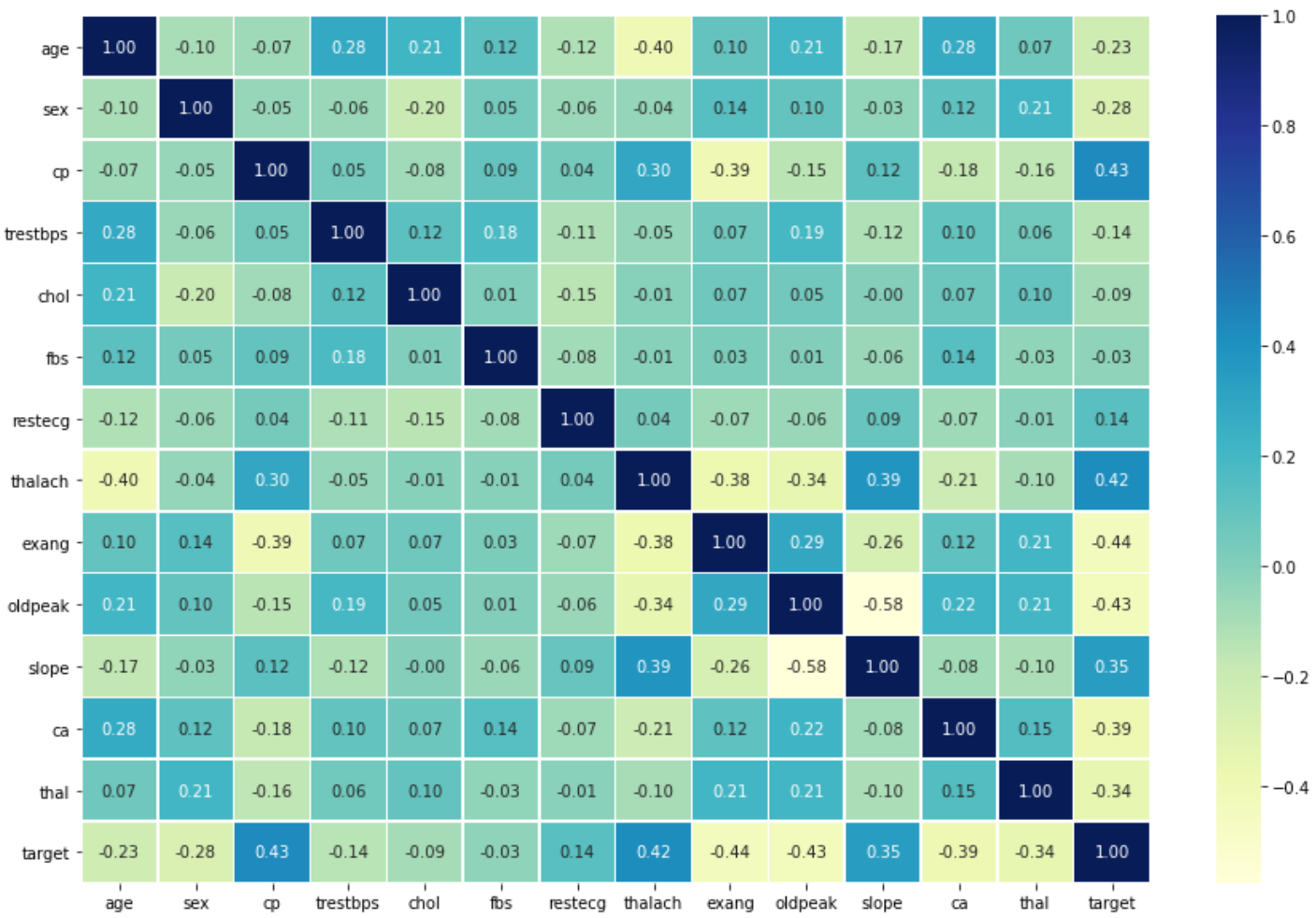
In [24]:
```
# Make a correlation matrix
corr_matrix= df.corr()
corr_matrix
```

Out[24]:

	age	sex	cp	trestbps	chol	fbs	restecg	thalach	exang	oldpeak
age	1.000000	-0.098447	-0.068653	0.279351	0.213678	0.121308	-0.116211	-0.398522	0.096801	0.210013
sex	-0.098447	1.000000	-0.049353	-0.056769	-0.197912	0.045032	-0.058196	-0.044020	0.141664	0.096093
cp	-0.068653	-0.049353	1.000000	0.047608	-0.076904	0.094444	0.044421	0.295762	-0.394280	-0.149230
trestbps	0.279351	-0.056769	0.047608	1.000000	0.123174	0.177531	-0.114103	-0.046698	0.067616	0.193216
chol	0.213678	-0.197912	-0.076904	0.123174	1.000000	0.013294	-0.151040	-0.009940	0.067023	0.053952
fbs	0.121308	0.045032	0.094444	0.177531	0.013294	1.000000	-0.084189	-0.008567	0.025665	0.005747
restecg	-0.116211	-0.058196	0.044421	-0.114103	-0.151040	-0.084189	1.000000	0.044123	-0.070733	-0.058770
thalach	-0.398522	-0.044020	0.295762	-0.046698	-0.009940	-0.008567	0.044123	1.000000	-0.378812	-0.344187
exang	0.096801	0.141664	-0.394280	0.067616	0.067023	0.025665	-0.070733	-0.378812	1.000000	0.288223
oldpeak	0.210013	0.096093	-0.149230	0.193216	0.053952	0.005747	-0.058770	-0.344187	0.288223	1.000000
slope	-0.168814	-0.030711	0.119717	-0.121475	-0.004038	-0.059894	0.093045	0.386784	-0.257748	-0.577537
ca	0.276326	0.118261	-0.181053	0.101389	0.070511	0.137979	-0.072042	-0.213177	0.115739	0.222682
thal	0.068001	0.210041	-0.161736	0.062210	0.098803	-0.032019	-0.011981	-0.096439	0.206754	0.210244
target	-0.225439	-0.280937	0.433798	-0.144931	-0.085239	-0.028046	0.137230	0.421741	-0.436757	-0.430696

In [25]:

```
# Let's make the correlation matrix look a little prettier
corr_matrix=df.corr()
plt.figure(figsize=(15, 10))
sns.heatmap(corr_matrix,
            annot=True,
            linewidth=0.5,
            fmt='.2f',
            cmap='YlGnBu');
```



5. Modelling

We've explored the data, now we'll try to use machine learning to predict our target variable based on the 13 independent variables.

Remember our problem?

> Given clinical parameters about a patient, can we predict whether or not they have heart disease?

That's what we'll be trying to answer.

And remember our evaluation metric?

> If we can reach 95% accuracy at predicting whether or not a patient has heart disease during the proof of concept, we'll pursure this project.

That's what we'll be aiming for.

But before we build a model, we have to get our dataset ready.

Let's look at it again.

In [26]:
```
df.head()
```

Out[26]:

	age	sex	cp	trestbps	chol	fbs	restecg	thalach	exang	oldpeak	slope	ca	thal	target
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

We're trying to predict our target variable using all of the other variables.

To do this, we'll split the target variable from the rest.

In [27]:

```
# Split the data into X(features) and y(labels)
X = df.drop('target', axis=1)
y = df['target']
```

In [28]:

```
# Independent variables (no target column)
X
```

Out[28]:

	age	sex	cp	trestbps	chol	fbs	restecg	thalach	exang	oldpeak	slope	ca	thal
0	63	1	3	145	233	1	0	150	0	2.3	0	0	1
1	37	1	2	130	250	0	1	187	0	3.5	0	0	2
2	41	0	1	130	204	0	0	172	0	1.4	2	0	2
3	56	1	1	120	236	0	1	178	0	0.8	2	0	2
4	57	0	0	120	354	0	1	163	1	0.6	2	0	2
...	...	...	...	...	...	...	...	...	...	...	...	...	...
298	57	0	0	140	241	0	1	123	1	0.2	1	0	3
299	45	1	3	110	264	0	1	132	0	1.2	1	0	3
300	68	1	0	144	193	1	1	141	0	3.4	1	2	3
301	57	1	0	130	131	0	1	115	1	1.2	1	1	3
302	57	0	1	130	236	0	0	174	0	0.0	1	1	2

303 rows × 13 columns

In [29]:

```
# Target
y
```

Out[29]:

```
0       1
1       1
2       1
3       1
4       1
       ..
298     0
299     0
300     0
301     0
```

```
302    0
Name: target, Length: 303, dtype: int64
```

Training and test split

Now comes one of the most important concepts in machine learning, the **training/test split**.

This is where you'll split your data into a **training set** and a **test set**.

You use your training set to train your model and your test set to test it.

The test set must remain separate from your training set.

Why not use all the data to train a model?

Let's say you wanted to take your model into the hospital and start using it on patients. How would you know how well your model goes on a new patient not included in the original full dataset you had?

This is where the test set comes in. It's used to mimic taking your model to a real environment as much as possible.

And it's why it's important to never let your model learn from the test set, it should only be evaluated on it.

To split our data into a training and test set, we can use Scikit-Learn's `train_test_split()` and feed it our independent and dependent variables (X & y).

In [30]:
```
# Random seed for reproducibility
np.random.seed(42)

# Split into training and test sets
X_train, X_test, y_train, y_test = train_test_split(X,   # Independent variable
                                                    y,   # Depenedent variable
                                                    test_size=0.2)   # Percentage of data t
```

In [31]:
```
X_train
```

Out[31]:

	age	sex	cp	trestbps	chol	fbs	restecg	thalach	exang	oldpeak	slope	ca	thal
132	42	1	1	120	295	0	1	162	0	0.0	2	0	2
202	58	1	0	150	270	0	0	111	1	0.8	2	0	3
196	46	1	2	150	231	0	1	147	0	3.6	1	0	2
75	55	0	1	135	250	0	0	161	0	1.4	1	0	2
176	60	1	0	117	230	1	1	160	1	1.4	2	2	3
...	...	...	...	...	...	...	...	...	...	...	...	...	...
188	50	1	2	140	233	0	1	163	0	0.6	1	1	3
71	51	1	2	94	227	0	1	154	1	0.0	2	1	3
106	69	1	3	160	234	1	0	131	0	0.1	1	1	2
270	46	1	0	120	249	0	0	144	0	0.8	2	0	3
102	63	0	1	140	195	0	1	179	0	0.0	2	2	2

242 rows × 13 columns

In [32]:
```
y_train, len(y_train)
```

Out[32]:
```
(132    1
 202    0
 196    0
 75     1
 176    0
       ..
 188    0
 71     1
 106    1
 270    0
 102    1
 Name: target, Length: 242, dtype: int64,
 242)
```

In [33]:
```
X_test
```

Out[33]:

	age	sex	cp	trestbps	chol	fbs	restecg	thalach	exang	oldpeak	slope	ca	thal
179	57	1	0	150	276	0	0	112	1	0.6	1	1	1
228	59	1	3	170	288	0	0	159	0	0.2	1	0	3
111	57	1	2	150	126	1	1	173	0	0.2	2	1	3
246	56	0	0	134	409	0	0	150	1	1.9	1	2	3
60	71	0	2	110	265	1	0	130	0	0.0	2	1	2
...	...	...	...	...	...	...	...	...	...	...	...	...	...
249	69	1	2	140	254	0	0	146	0	2.0	1	3	3
104	50	1	2	129	196	0	1	163	0	0.0	2	0	2
300	68	1	0	144	193	1	1	141	0	3.4	1	2	3
193	60	1	0	145	282	0	0	142	1	2.8	1	2	3
184	50	1	0	150	243	0	0	128	0	2.6	1	0	3

61 rows × 13 columns

In [34]:
```
y_test, len(y_test)
```

Out[34]:
```
(179    0
 228    0
 111    1
 246    0
 60     1
       ..
 249    0
 104    1
 300    0
 193    0
 184    0
 Name: target, Length: 61, dtype: int64,
 61)
```

Now we've got out data split into training and test sets, it's time to build our machine learning model.

We'll train it (find the patterns) on the training set.

And we'll test (use the patterns) on the test set.

We're going to try 3 different machine learning models;

1. Logistic Regression
2. K-Nearest Neighbors
3. RandomForestClassfier

In [35]:
```
# Put models in a dictionary
models = {'KNN': KNeighborsClassifier(),  # KNN, Logistic Regression, Random Forest are th
          'Logistic Regression': LogisticRegression(), # LogisticRegression(), RandomFores
          'Random Forest': RandomForestClassifier()}

# Create functions to fit and score the models
def fit_and_score(models, X_train, X_test, y_train, y_test):
    """
    fits and evaluate given machine learning model.
    models: a dict of different scikit-learn machine learning models
    X_train: training data
    X_test: testing data
    y_train: labels associated with training data
    y_test: label associated with test data
    """
    # Random seed for reproducible result
    np.random.seed(42)
    # Make a dictionary to keep model scores
    model_scores = {}
    # Loop through models
    for name, model in models.items():
        # Fit the model to the training data
        model.fit(X_train, y_train)

        # Evaluate the model and append its scores to model_scores
        model_scores[name] = model.score(X_test, y_test)
    return model_scores
```

In [36]:
```
model_scores =  fit_and_score(models=models,
                              X_train=X_train,
                              X_test=X_test,
                              y_train=y_train,
                              y_test=y_test)
model_scores
```

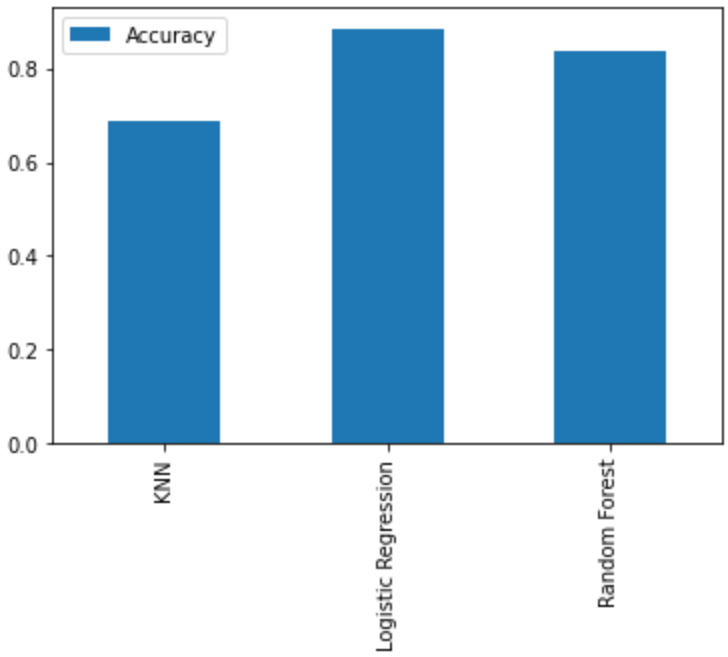
```
C:\Users\HP\Desktop\sample_project_1\env\lib\site-packages\sklearn\linear_model\_logistic.
py:763: ConvergenceWarning: lbfgs failed to converge (status=1):
STOP: TOTAL NO. of ITERATIONS REACHED LIMIT.

Increase the number of iterations (max_iter) or scale the data as shown in:
    https://scikit-learn.org/stable/modules/preprocessing.html
Please also refer to the documentation for alternative solver options:
    https://scikit-learn.org/stable/modules/linear_model.html#logistic-regression
  n_iter_i = _check_optimize_result(
```

Out[36]:
```
{'KNN': 0.6885245901639344,
 'Logistic Regression': 0.8852459016393442,
 'Random Forest': 0.8360655737704918}
```

Model Comparison

Since we've saved our models scores to a dictionary, we can plot them by first converting them to a DataFrame.

In [37]:
```
model_compare= pd.DataFrame(model_scores,  index=['Accuracy'])
model_compare.T.plot.bar();
```



Now we've got a baseline model... and we know that a model's first prediction aren't always what we should base our next step off. What should we do??

Alright, there were a few words in there which could sound made up to someone who's not a budding data scientist like yourself. But being the budding data scientist you are, you know data scientists make up words all the time.

Let's look at the following before we see them in action(These are some of the things we should pay attention to when working on a classification model).

1. **Hyperparameter tuning** - Each model you use has a series of dials you can turn to dictate how they perform. Changing these values may increase or decrease model performance.
2. **Feature importance** - If there are a large amount of features we're using to make predictions, do some have more importance than others? For example, for predicting heart disease, which is more important, sex or age?
3. **Confusion matrix** - Compares the predicted values with the true values in a tabular way, if 100% correct, all values in the matrix will be top left to bottom right (diagnol line).
4. **Cross-validation** - Splits your dataset into multiple parts and train and tests your model on each part and evaluates performance as an average.
5. **Precision** - Proportion of true positives over total number of samples. Higher precision leads to less false positives.
6. **Recall** - Proportion of true positives over total number of true positives and false negatives. Higher recall leads to less false negatives.
7. **F1 score** - Combines precision and recall into one metric. 1 is best, 0 is worst.

8. **Classification report** - Sklearn has a built-in function called classification_report() which returns some of the main classification metrics such as precision, recall and f1-score.
9. **ROC Curve** - Receiver Operating Characterisitc is a plot of true positive rate versus false positive rate.
10. **Area Under Curve (AUC)** - The area underneath the ROC curve. A perfect model achieves a score of 1.0.

Hyperparameter tuning and cross-validation

We'll be using this setup to tune the hyperparameters of some of our models and then evaluate them. We'll also get a few more metrics like precision, recall, F1-score and ROC at the same time.

Here's the game plan:

1. Tune model hyperparameters, see which performs best
2. Perform cross-validation
3. Plot ROC curves
4. Make a confusion matrix
5. Get precision, recall and F1-score metrics
6. Find the most important model features

Tune KNeighborsClassifier (K-Nearest Neighbors or KNN) by hand

There's one main hyperparameter we can tune for the K-Nearest Neighbors (KNN) algorithm, and that is number of neighbours. The default is 5 (n_neigbors=5).

What are neighbours?

Imagine all our different samples on one graph like the scatter graph we have above. KNN works by assuming dots which are closer together belong to the same class. If n_neighbors=5 then it assume a dot with the 5 closest dots around it are in the same class.

We've left out some details here like what defines close or how distance is calculated but I encourage you to research them.

For now, let's try a few different values of n_neighbors.

In [38]:

```
# Create a list of train scores
train_scores = []

# Create a list of test scores
test_scores = []

# Create a list of different values for n_neighbors
neighbors = range(1, 21) # 1 to 20

# Setup Algorithm(model)
knn = KNeighborsClassifier()

# Loop through different n_neighbors values
for i in neighbors:
    knn.set_params(n_neighbors=i)  # set neighbors value

    # Fit the algorithm(model)
    knn.fit(X_train, y_train)
```

```
    # Update the training scores list
    train_scores.append(knn.score(X_train, y_train))

    # Update the test scores list
    test_scores.append(knn.score(X_test, y_test))
```

In [39]:
```
train_scores
```

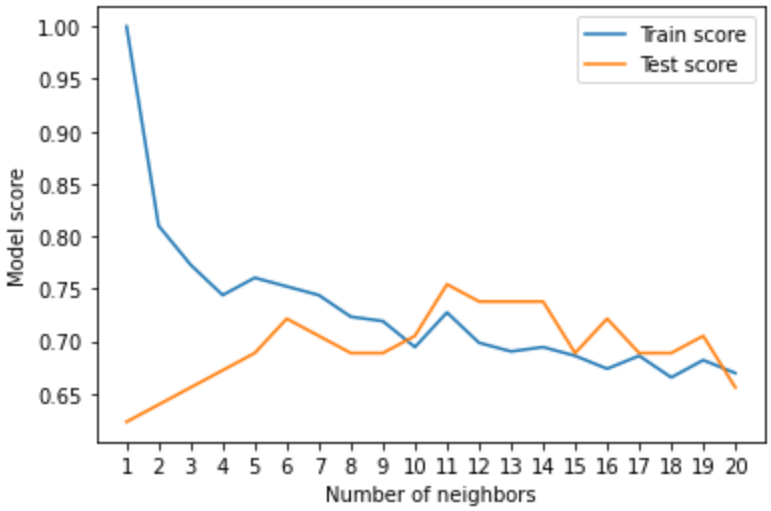
Out[39]:
```
[1.0,
 0.8099173553719008,
 0.7727272727272727,
 0.743801652892562,
 0.7603305785123967,
 0.7520661157024794,
 0.743801652892562,
 0.7231404958677686,
 0.71900826446281,
 0.6942148760330579,
 0.7272727272727273,
 0.6983471074380165,
 0.6900826446280992,
 0.6942148760330579,
 0.6859504132231405,
 0.6735537190082644,
 0.6859504132231405,
 0.6652892561983471,
 0.6818181818181818,
 0.6694214876033058]
```

In [40]:
```
test_scores
```

Out[40]:
```
[0.6229508196721312,
 0.639344262295082,
 0.6557377049180327,
 0.6721311475409836,
 0.6885245901639344,
 0.7213114754098361,
 0.7049180327868853,
 0.6885245901639344,
 0.6885245901639344,
 0.7049180327868853,
 0.7540983606557377,
 0.7377049180327869,
 0.7377049180327869,
 0.7377049180327869,
 0.6885245901639344,
 0.7213114754098361,
 0.6885245901639344,
 0.6885245901639344,
 0.7049180327868853,
 0.6557377049180327]
```

In [41]:
```
plt.plot(neighbors, train_scores, label='Train score')
plt.plot(neighbors, test_scores, label='Test score')
plt.xticks(np.arange(1, 21, 1))
plt.xlabel('Number of neighbors')
plt.ylabel('Model score')
plt.legend()

print(f'Maximum KNN score on the test data: {max(test_scores)*100:.2f}%')
```

```
Maximum KNN score on the test data: 75.41%
```



Looking at the graph, n_neighbors = 11 seems best.

Even knowing this, the KNN's model performance didn't get near what `LogisticRegression` or the `RandomForestClassifier` did.

Because of this, we'll discard KNN and focus on the other two.

We've tuned KNN by hand but let's see how we can tune `LogisticsRegression` and `RandomForestClassifier` using `RandomizedSearchCV`.

Instead of us having to manually try different hyperparameters by hand, `RandomizedSearchCV` tries a number of different combinations, evaluates them and saves the best.

Tuning models(hyperparameter) with RandomizedSearchCV

Reading the Scikit-Learn documentation for LogisticRegression, we find there's a number of different hyperparameters we can tune.

The same for RandomForestClassifier.

Let's create a hyperparameter grid (a dictionary of different hyperparameters) for each and then test them out.

In [42]:
```
# Different LogisticRegression hyperparameters
log_reg_grid = {'C': np.logspace(-4, 4, 20),
                'solver': ['liblinear']}

# Different RandomForestClassifier hyperparameters
rf_grid = {'n_estimators': np.arange(10, 1000, 50),
           'max_depth': [None, 3, 5, 10],
           'min_samples_split': np.arange(2, 20, 2),
           'min_samples_leaf': np.arange(1, 20, 2)}
```

Now let's use `RandomizedSearchCV` to try and tune our `LogisticRegression` model.

We'll pass it the different hyperparameters from `log_reg_grid` as well as set `n_iter = 20`. This means, `RandomizedSearchCV` will try 20 different combinations of hyperparameters from `log_reg_grid` and save the best ones.

In [43]:
```
# Tune LogisticRegression

# Setup Random seed
```

```
np.random.seed(42)

# Setup random hyperparameter search for LogisticRegression
rs_log_reg = RandomizedSearchCV(LogisticRegression(),
                                param_distributions = log_reg_grid,
                                cv = 5,
                                n_iter = 20,
                                verbose =  True)
# Fit random hyperparameter search model for LogisticRegression
rs_log_reg.fit(X_train, y_train)
```

Out[43]:
```
Fitting 5 folds for each of 20 candidates, totalling 100 fits
RandomizedSearchCV(cv=5, estimator=LogisticRegression(), n_iter=20,
                   param_distributions={'C': array([1.00000000e-04, 2.63665090e-04, 6.9519
2796e-04, 1.83298071e-03,
       4.83293024e-03, 1.27427499e-02, 3.35981829e-02, 8.85866790e-02,
       2.33572147e-01, 6.15848211e-01, 1.62377674e+00, 4.28133240e+00,
       1.12883789e+01, 2.97635144e+01, 7.84759970e+01, 2.06913808e+02,
       5.45559478e+02, 1.43844989e+03, 3.79269019e+03, 1.00000000e+04]),
                                        'solver': ['liblinear']},
                   verbose=True)
```

In [44]:
```
# Check the best parameter
rs_log_reg.best_params_
```

Out[44]:
```
{'solver': 'liblinear', 'C': 0.23357214690901212}
```

In [45]:
```
# Evaluate the model
rs_log_reg.score(X_test, y_test)
```

Out[45]:
```
0.8852459016393442
```

Now we've tuned `LogisticRegression` using `RandomizedSearchCV`, we'll do the same for `RandomForestClassifier`.

In [53]:
```
# Tune RandomForestClassifier

# Setup Random seed
np.random.seed(42)

# Setup random hyperparameter search for RandomForestClassifier
rs_rf = RandomizedSearchCV(RandomForestClassifier(),
                           param_distributions = rf_grid,
                           cv = 5,
                           n_iter = 20,
                           verbose = True)

# Fit random hyperparameter search model for RandomForestClassifier
rs_rf.fit(X_train, y_train)
```

Out[53]:
```
Fitting 5 folds for each of 20 candidates, totalling 100 fits
RandomizedSearchCV(cv=5, estimator=RandomForestClassifier(), n_iter=20,
                   param_distributions={'max_depth': [None, 3, 5, 10],
                                        'min_samples_leaf': array([ 1,  3,  5,  7,  9, 11,
13, 15, 17, 19]),
                                        'min_samples_split': array([ 2,  4,  6,  8, 10, 1
2, 14, 16, 18]),
                                        'n_estimators': array([ 10,  60, 110, 160, 210, 26
0, 310, 360, 410, 460, 510, 560, 610,
       660, 710, 760, 810, 860, 910, 960])},
                   verbose=True)
```

In [56]:
```
# Check the best parameter
rs_rf.best_params_
```

Out[56]:
```
{'n_estimators': 210,
 'min_samples_split': 4,
 'min_samples_leaf': 19,
 'max_depth': 3}
```

In [57]:
```
# Evaluate the model
rs_rf.score(X_test, y_test)
```

Out[57]:
```
0.8688524590163934
```

Excellent! Tuning the hyperparameters for each model saw a slight performance boost in both the `RandomForestClassifier` and `LogisticRegression`.

This is akin to tuning the settings on your oven and getting it to cook your favourite dish just right.

But since LogisticRegression is pulling out in front, we'll try tuning it further with `GridSearchCV`.

Tuning a model with GridSearchCV

The difference between `RandomizedSearchCV` and `GridSearchCV` is where `RandomizedSearchCV` searches over a grid of hyperparameters performing n_iter combinations, `GridSearchCV` will test every single possible combination.

In short:

- RandomizedSearchCV - tries n_iter combinations of hyperparameters and saves the best.
- GridSearchCV - tries every single combination of hyperparameters and saves the best.

Let's see it in action.

In [49]:
```
# Different LogisticRegression hyperparameters
log_reg_grid = {'C': np.logspace(-4, 4, 20),
                'solver': ['liblinear']}

# Setup grid hyperparameter search for LogisticRegression
gs_log_reg = GridSearchCV (LogisticRegression(),
                           param_grid = log_reg_grid,
                           cv = 5,
                           verbose = True)
# Fit grid hyperparamater search model
gs_log_reg.fit(X_train, y_train)
```

Out[49]:
```
Fitting 5 folds for each of 20 candidates, totalling 100 fits
GridSearchCV(cv=5, estimator=LogisticRegression(),
             param_grid={'C': array([1.00000000e-04, 2.63665090e-04, 6.95192796e-04, 1.832
98071e-03,
       4.83293024e-03, 1.27427499e-02, 3.35981829e-02, 8.85866790e-02,
       2.33572147e-01, 6.15848211e-01, 1.62377674e+00, 4.28133240e+00,
       1.12883789e+01, 2.97635144e+01, 7.84759970e+01, 2.06913808e+02,
       5.45559478e+02, 1.43844989e+03, 3.79269019e+03, 1.00000000e+04]),
                         'solver': ['liblinear']},
             verbose=True)
```

In [50]:
```
# Check the best hyperparameter
gs_log_reg.best_params_
```

Out[50]:
```
{'C': 0.23357214690901212, 'solver': 'liblinear'}
```

In [51]:
```
# Evaluate the grid search LogisticRegression model
gs_log_reg.score(X_test, y_test)
```

Out[51]:
```
0.8852459016393442
```

In [58]:
```
model_scores
```

Out[58]:
```
{'KNN': 0.6885245901639344,
 'Logistic Regression': 0.8852459016393442,
 'Random Forest': 0.8360655737704918}
```

In this case, we get the same results as before since our grid only has a maximum of 20 different hyperparameter combinations.

Note: If there are a large amount of hyperparameters combinations in your grid, `GridSearchCV` may take a long time to try them all out. This is why it's a good idea to start with `RandomizedSearchCV`, try a certain amount of combinations and then use `GridSearchCV` to refine them.

Evaluating our tuned machine learning classifier beyond accuracy

Now we've got a tuned model, let's get some of the metrics we discussed before.

We want:

- ROC curve and AUC score - `plot_roc_curve()`
- Confusion matrix - `confusion_matrix()`
- Classification report - $ication_rep$ or $t()$`
- Precision - `precision_score()`
- Recall - `recall_score()`
- F1-score - `f1_score()`

Luckily, Scikit-Learn has these all built-in.

To access them, we'll have to use our model to make predictions on the test set. You can make predictions by calling `predict()` on a trained model and passing it the data you'd like to predict on. To make comparisons and evaluate our trained model, first we need to make predictions

We'll make predictions on the test data.

In [59]:
```
# Making predictions on the test data
y_preds = gs_log_reg.predict(X_test)
```

In [60]:
```
y_preds
```

Out[60]:
```
array([0, 1, 1, 0, 1, 1, 1, 0, 0, 1, 1, 0, 1, 0, 1, 1, 1, 0, 0, 0, 1, 0,
       0, 1, 1, 1, 1, 1, 0, 1, 0, 0, 0, 0, 1, 0, 1, 1, 1, 1, 1, 1, 1, 1,
       1, 0, 1, 1, 0, 0, 0, 0, 1, 1, 0, 0, 0, 1, 0, 0, 0], dtype=int64)
```

In [61]:
```
y_test
```

Out[61]:
```
179    0
228    0
111    1
246    0
60     1
      ..
249    0
104    1
300    0
193    0
184    0
Name: target, Length: 61, dtype: int64
```

Since we've got our prediction values we can find the metrics we want.

Let's start with the ROC curve and AUC scores.

ROC Curve and AUC Scores

What's a ROC curve?

It's a way of understanding how your model is performing by comparing the true positive rate to the false positive rate.

In our case...

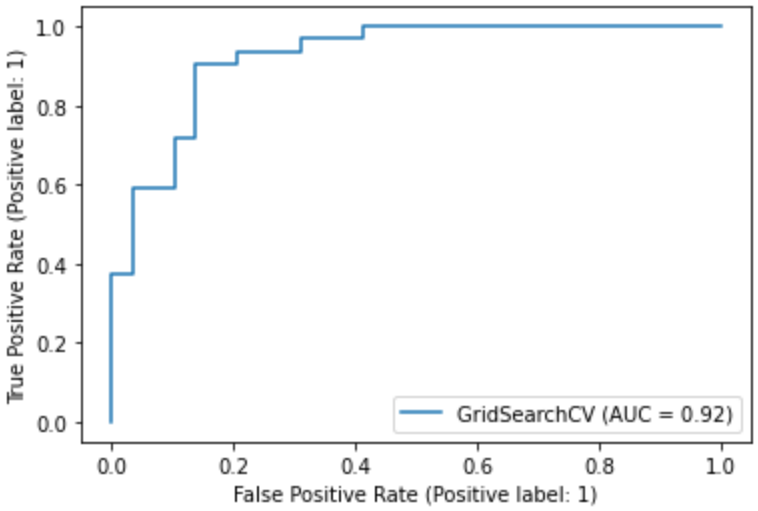
> To get an appropriate example in a real-world problem, consider a diagnostic test that seeks to determine whether a person has a certain disease. A false positive in this case occurs when the person tests positive, but does not actually have the disease. A false negative, on the other hand, occurs when the person tests negative, suggesting they are healthy, when they actually do have the disease.

Scikit-Learn implements a function `plot_roc_curve` which can help us create a ROC curve as well as calculate the area under the curve (AUC) metric.

Reading the documentation on the `plot_roc_curve` function we can see it takes (estimator, X, y) as inputs. Where estimator is a fitted machine learning model and X and y are the data you'd like to test it on.

In our case, we'll use the `GridSearchCV` version of our `LogisticRegression` estimator, `gs_log_reg` as well as the test data, `X_test` and `y_test`.

In [63]:
```
# Import ROC curve function from metrics module
from sklearn.metrics import plot_roc_curve

# Plot ROC curve and calculate AUC metric
plot_roc_curve(gs_log_reg, X_test, y_test);
```



This is great, our model does far better than guessing which would be a line going from the bottom left corner to the top right corner, AUC = 0.5. But a perfect model would achieve an AUC score of 1.0, so there's still room for improvement.

Confusion Matrix

confusion matrix is a visual way to show where your model made the right predictions and where it made the wrong predictions (or in other words, got confused).

Scikit-Learn allows us to create a confusion matrix using confusion_matrix() and passing it the true labels and predicted labels.

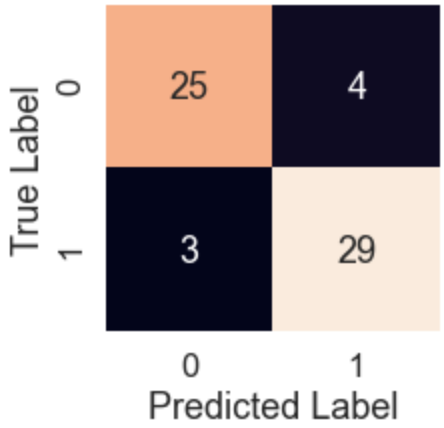
In [64]:
```
# Display Confusion Matrix
print(confusion_matrix(y_test, y_preds))
```

```
[[25  4]
 [ 3 29]]
```

As you can see, Scikit-Learn's built-in confusion matrix is a bit bland. For a presentation you'd probably want to make it visual.

Let's create a function which uses `Seaborn's heatmap()` for doing so.

In [67]:
```
# Import Seaborn
sns.set(font_scale=1.5)

def plot_conf_mat(y_test, y_preds):
    """
    plot conusion matrix using seaborn's heatmap().
    """
    fig, ax = plt.subplots(figsize=(3, 3))
    ax =  sns.heatmap(confusion_matrix(y_test, y_preds),
                      annot = True, # Annotate the boxes
                      cbar = False)
    plt.xlabel('Predicted Label')
    plt.ylabel('True Label')
plot_conf_mat(y_test, y_preds)
```



Now we've got a ROC curve, an AUC metric and a confusion matrix, let's get a classification report as well as cross-validated precision, recall and f1-score

Classification Report

We can make a classification report using `classification_report()` and passing it the true labels as well as our models predicted labels.

A classification report will also give us information of the precision and recall of our model for each class.

In [68]:
```
# Show classification report
print(classification_report(y_test, y_preds))
```

```
              precision    recall  f1-score   support

           0       0.89      0.86      0.88        29
           1       0.88      0.91      0.89        32

    accuracy                           0.89        61
   macro avg       0.89      0.88      0.88        61
weighted avg       0.89      0.89      0.89        61
```

What's going on here?

Let's get a refresh.

- Precision - Indicates the proportion of positive identifications (model predicted class 1) which were actually correct. A model which produces no false positives has a precision of 1.0.
- Recall - Indicates the proportion of actual positives which were correctly classified. A model which produces no false negatives has a recall of 1.0.
- F1 score - A combination of precision and recall. A perfect model achieves an F1 score of 1.0.
- Support - The number of samples each metric was calculated on.
- Accuracy - The accuracy of the model in decimal form. Perfect accuracy is equal to 1.0.
- Macro avg - Short for macro average, the average precision, recall and F1 score between classes. Macro avg doesn't class imbalance into effort, so if you do have class imbalances, pay attention to this metric.
- Weighted avg - Short for weighted average, the weighted average precision, recall and F1 score between classes. Weighted means each metric is calculated with respect to how many samples there are in each class. This metric will favour the majority class (e.g. will give a high value when one class out performs another due to having more samples).

Ok, now we've got a few deeper insights on our model. But these were all calculated using a single training and test set.

What we'll do to make them more solid is calculate them using cross-validation.

How?

We'll take the best model along with the best hyperparameters and use `cross_val_score()` along with various scoring parameter values.

`cross_val_score()` works by taking an estimator (machine learning model) along with data and labels. It then evaluates the machine learning model on the data and labels using cross-validation and a defined scoring parameter.

Let's remind ourselves of the best hyperparameters and then see them in action.

Check evaluation metrics using cross-validation

We're going to calculate precision, recall and f1-score of our model using cross-validation and to do so, we'll be using `cross_val_score()`.

In [69]:
```
# Check best hyperparameters
gs_log_reg.best_params_
```

Out[69]:
```
{'C': 0.23357214690901212, 'solver': 'liblinear'}
```

In [70]:
```
# Import cross_val_score
from sklearn.model_selection import cross_val_score

# Instantiate logisticRegression model with best hyperparameters (found with GridSearchCV)
clf = LogisticRegression(C=0.23357214690901212,
                         solver="liblinear")
```

Now we've got an instantiated classifier, let's find some cross-validated metrics.

In [72]:
```
# Cross-validated accuracy score
cv_acc = cross_val_score(clf,
                         X,
                         y,
                         cv = 5, # 5 fold cross-validation
                         scoring='accuracy')
cv_acc
```

Out[72]:
```
array([0.81967213, 0.90163934, 0.8852459 , 0.88333333, 0.75      ])
```

Since there are 5 metrics here, we'll take the average.

In [74]:
```
cv_acc = np.mean(cv_acc)
cv_acc
```

Out[74]:
```
0.8479781420765027
```

Now we'll do the same for other classification metrics.

In [75]:
```
# Cross-validated precision score
cv_precision = np.mean(cross_val_score(clf,
                                       X,
                                       y,
                                       cv = 5,
```

```
                                        scoring = 'precision'))
cv_precision
```

Out[75]:
```
0.8215873015873015
```

In [76]:
```
# Cross-validated Recall score
cv_recall = np.mean(cross_val_score(clf,
                                    X,
                                    y,
                                    cv=5,
                                    scoring='recall'))
cv_recall
```

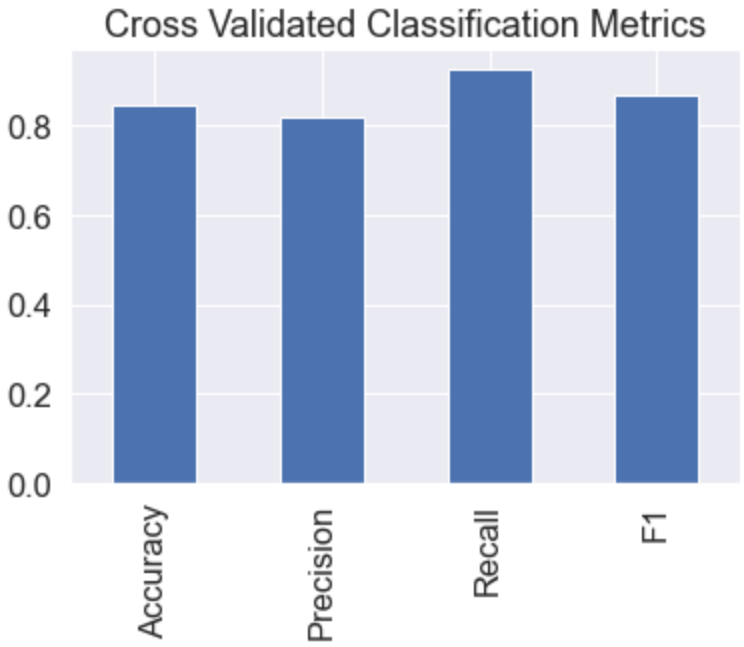
Out[76]:
```
0.9272727272727274
```

In [77]:
```
# cross-validated f1 score
cv_f1 =  np.mean(cross_val_score(clf,
                                 X,
                                 y,
                                 cv=5,
                                 scoring='f1'))
cv_f1
```

Out[77]:
```
0.8705403543192143
```

Let's visualize them.

In [81]:
```
# Visualizing cross-validated metrics
cv_metrics = pd.DataFrame({'Accuracy': cv_acc,
                           'Precision': cv_precision,
                           'Recall': cv_recall,
                           'F1': cv_f1},
                          index=[0])
cv_metrics.T.plot.bar(title='Cross Validated Classification Metrics', legend=False);
```



Feature importance

Feature importance is another way of asking, "which features contributing most to the outcomes of the model and how did they contribute?"

Or for our problem, trying to predict heart disease using a patient's medical characterisitcs, which charateristics contribute most to a model predicting whether someone has heart disease or not? Finding feature importance is different for each machine learning model.

Unlike some of the other functions we've seen, because how each model finds patterns in data is slightly different, how a model judges how important those patterns are is different as well. This means for each model, there's a slightly different way of finding which features were most important.

You can usually find an example via the Scikit-Learn documentation or via searching for something like "[MODEL TYPE] feature importance", such as, "random forest feature importance".

Since we're using `LogisticRegression`, we'll look at one way we can calculate feature importance for it.

To do so, we'll use the coef_ attribute. Looking at the Scikit-Learn documentation for LogisticRegression, the `coef_ attribute` is the coefficient of the features in the decision function.

We can access the `coef_ attribute` after we've fit an instance of `LogisticRegression`.

In [90]:
```
df.head()
```

Out[90]:

	age	sex	cp	trestbps	chol	fbs	restecg	thalach	exang	oldpeak	slope	ca	thal	target
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

In [82]:
```
# Fit an instance of LogisticRegression (taken from above)
clf.fit(X_train, y_train)
```

Out[82]:
```
LogisticRegression(C=0.23357214690901212, solver='liblinear')
```

In [83]:
```
# Check coef_
clf.coef_
```

Out[83]:
```
array([[ 0.00369922, -0.90424085,  0.67472828, -0.0116134 , -0.00170364,
         0.04787689,  0.33490184,  0.02472939, -0.63120401, -0.57590906,
         0.47095113, -0.65165351, -0.699842  ]])
```

Looking at this it might not make much sense. But these values are how much each feature contributes to how a model makes a decision on whether patterns in a sample of patients health data leans more towards having heart disease or not.

Even knowing this, in it's current form, this coef_ array still doesn't mean much. But it will if we combine it with the columns (features) of our dataframe.

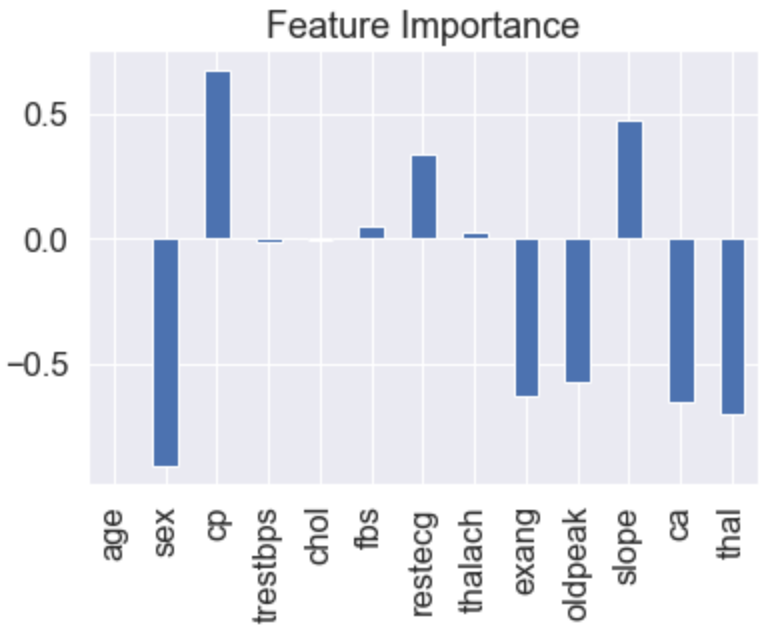
In [84]:
```
# Match coef of features to columns
features_dict = dict(zip(df.columns, list(clf.coef_[0])))
```

```
features_dict
```

Out[84]:
```
{'age': 0.003699218314634231,
 'sex': -0.9042408481315317,
 'cp': 0.6747282826858118,
 'trestbps': -0.011613404239724763,
 'chol': -0.0017036448048050072,
 'fbs': 0.04787689050301493,
 'restecg': 0.33490183888358416,
 'thalach': 0.024729385199310817,
 'exang': -0.6312040056168838,
 'oldpeak': -0.5759090611742839,
 'slope': 0.47095113183576787,
 'ca': -0.6516535125690047,
 'thal': -0.6998419969792693}
```

Now we've match the feature coefficients to different features, let's visualize them.

In [87]:
```
# Visualize feature importance
features_df = pd.DataFrame(features_dict, index=[0])
features_df.T.plot.bar(title='Feature Importance', legend=False);
```



You'll notice some are negative and some are positive.

The larger the value (bigger bar), the more the feature contributes to the models decision.

If the value is negative, it means there's a negative correlation. And vice versa for positive values.

For example, the sex attribute has a negative value of -0.904, which means as the value for sex increases, the target value decreases.

We can see this by comparing the sex column to the target column.

In [88]:
```
pd.crosstab(df['sex'], df['target'])
```

Out[88]:

target	0	1
sex		
0	24	72
1	114	93

You can see, when sex is 0 (female), there are almost 3 times as many (72 vs. 24) people with heart disease (target = 1) than without.

And then as sex increases to 1 (male), the ratio goes down to almost 1 to 1 (114 vs. 93) of people who have heart disease and who don't.

What does this mean?

It means the model has found a pattern which reflects the data. Looking at these figures and this specific dataset, it seems if the patient is female, they're more likely to have heart disease.

How about a positive correlation?

In [89]:
```
# Contrast slope (positive coefficient) with target
pd.crosstab(df['slope'], df['target'])
```

Out[89]:

target	0	1
slope		
0	12	9
1	91	49
2	35	107

Looking back the data dictionary, we see slope is the "slope of the peak exercise ST segment" where:

- 0: Upsloping: better heart rate with exercise (uncommon)
- 1: Flatsloping: minimal change (typical healthy heart)
- 2: Downslopins: signs of unhealthy heart

According to the model, there's a positive correlation of 0.470, not as strong as sex and target but still more than 0.

This positive correlation means our model is picking up the pattern that as slope increases, so does the target value.

Is this true?

When you look at the contrast (pd.crosstab(df["slope"], df["target"]) it is. As slope goes up, so does target.

What can you do with this information?

This is something you might want to talk to a subject matter expert about. They may be interested in seeing where machine learning model is finding the most patterns (highest correlation) as well as where it's not (lowest correlation).

Doing this has a few benefits:

1. **Finding out more** - If some of the correlations and feature importances are confusing, a subject matter expert may be able to shed some light on the situation and help you figure out more.
2. **Redirecting efforts** - If some features offer far more value than others, this may change how you collect data for different problems. See point 3.

3. **Less but better** - Similar to above, if some features are offering far more value than others, you could reduce the number of features your model tries to find patterns in as well as improve the ones which offer the most. This could potentially lead to saving on computation, by having a model find patterns across less features, whilst still achieving the same performance levels.

6. Experimentation

Well we've completed all the metrics your boss requested. You should be able to put together a great report containing a confusion matrix, a handful of cross-valdated metrics such as precision, recall and F1 as well as which features contribute most to the model making a decision.

But after all this you might be wondering where step 6 in the framework is, experimentation.

Well the secret here is, as you might've guessed, the whole thing is experimentation.

From trying different models, to tuning different models to figuring out which hyperparameters were best.

What we've worked through so far has been a series of experiments.

And the truth is, we could keep going. But of course, things can't go on forever.

So by this stage, after trying a few different things, we'd ask ourselves did we meet the evaluation metric?

Remember we defined one in step 3.

```
If we can reach 95% accuracy at predicting whether or not a patient has heart
disease during the proof of concept, we'll pursure this project.
```

In this case, we didn't. The highest accuracy our model achieved was below 90%.

What next?

You might be wondering, what happens when the evaluation metric doesn't get hit?

Is everything we've done wasted?

No.

It means we know what doesn't work. In this case, we know the current model we're using (a tuned version of LogisticRegression) along with our specific data set doesn't hit the target we set ourselves.

This is where step 6 comes into its own.

A good next step would be to discuss with your team or research on your own different options of going forward.

- Could you collect more data?
- Could you try a better model? If you're working with structured data, you might want to look into CatBoost or XGBoost.
- Could you improve the current models (beyond what we've done so far)?

- If your model is good enough, how would you export it and share it with others? Hint: check out Scikit-Learn's documentation on model persistance The key here is to remember, your biggest restriction will be time. Hence, why it's paramount to minimise your times between experiments.

The more you try, the more you figure out what doesn't work, the more you'll start to get a hang of what does.

In [ ]: