IMPORTING LIBARIES

In [1]:

```
import numpy as np
import pandas as pd
import seaborn as sns
import matplotlib.pyplot as plt
import warnings
warnings.filterwarnings("ignore")
import sklearn
```

IMPORTING THE DATA FILE

In [2]:

```
data = pd.read_csv(r"C:\Users\Biggest\Downloads\heart.csv")
```

In [3]:

```
data
```

Out[3]:

	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
...	...	...	...	...	...	...	...	...	...	...	...	...	...	...
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

303 rows × 14 columns

Variable and Description

age - Age of the patient in years

sex - Gender of the patient (0 = male, 1 = female)

cp - Chest pain type: 0: Typical angina 1: Atypical angina 2: Non-anginal pain 3: Asymptomatic trestbps - Resting blood pressure in mm Hg

chol - Serum cholesterol in mg/di

fbs - Fasting blood sugar level, categorized as above 120 mg/di (1 = true, 0 = false)

restecg - Resting electrocardiographic results: 0: Normal 1: Having ST-T wave abnormality 2: Showing probable or definite left ventricular hypertrophy

thalach - Maximum heart rate achieved during a stress test

exang - Exercise-induced angina (1 = yes, 0 = no)

oldpeak - ST depression induced by exercise relative to rest

slope - Slope of the peak exercise ST segment: 0: Upsloping 1: Flat 2: Downsloping

ca - Number of major vessels (0-4) colored by fluoroscopy

thai - Thalium stress test result: 0: Normal 1: Fixed defect 2: Reversible defect 3: Not described

target - Heart disease status (0 = no disease, 1 = presence of disease)

Checking for null value and exploring basic statistic

In [4]:
```
data.isnull().sum()
```

Out[4]:
```
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
```

In [5]:
```
data.describe().T
```

Out[5]:

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

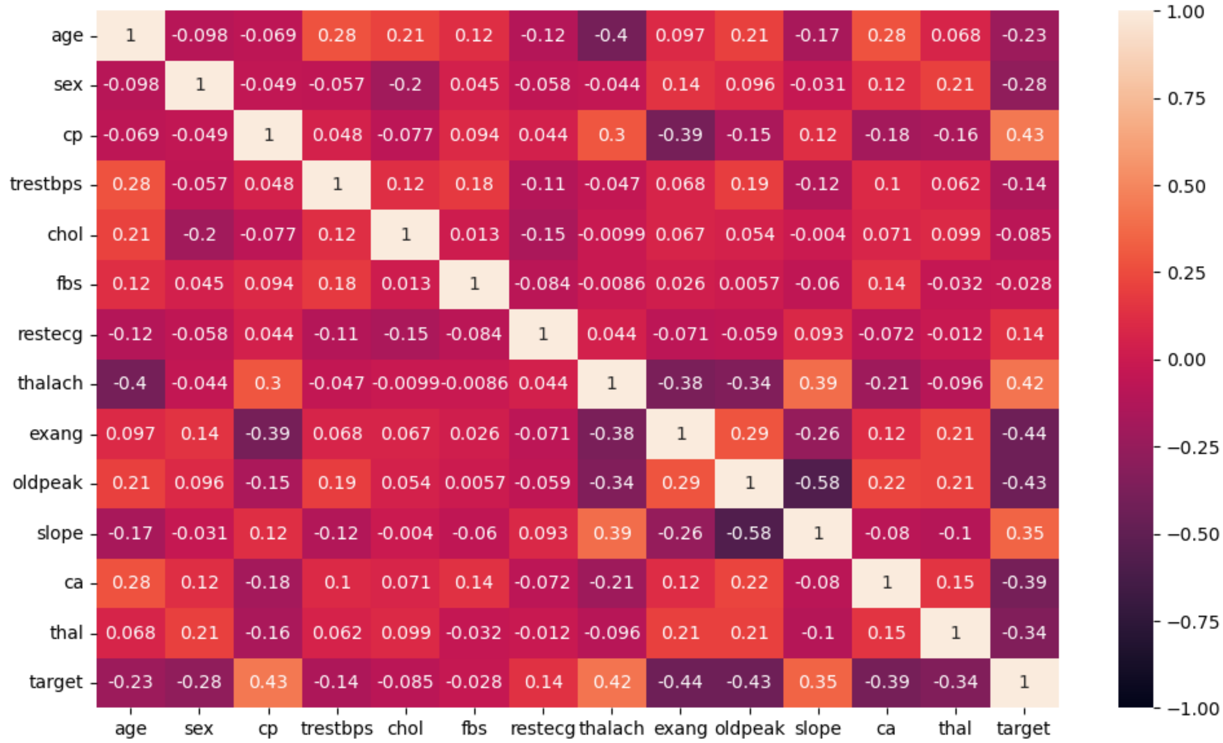
To identify the most relevant factors contributing to heart disease prediction, we can use:

- Corelleation map(Since all our data is numerical)
- BiVariate analysis- Using Scattered plot.

In [6]:

```
# Checking for correlation, using correlation map.

plt.figure(figsize=(12, 7))
sns.heatmap(data.corr(), annot = True, vmin = -1, vmax = 1)
plt.show()
```



OBSERVATIONS :

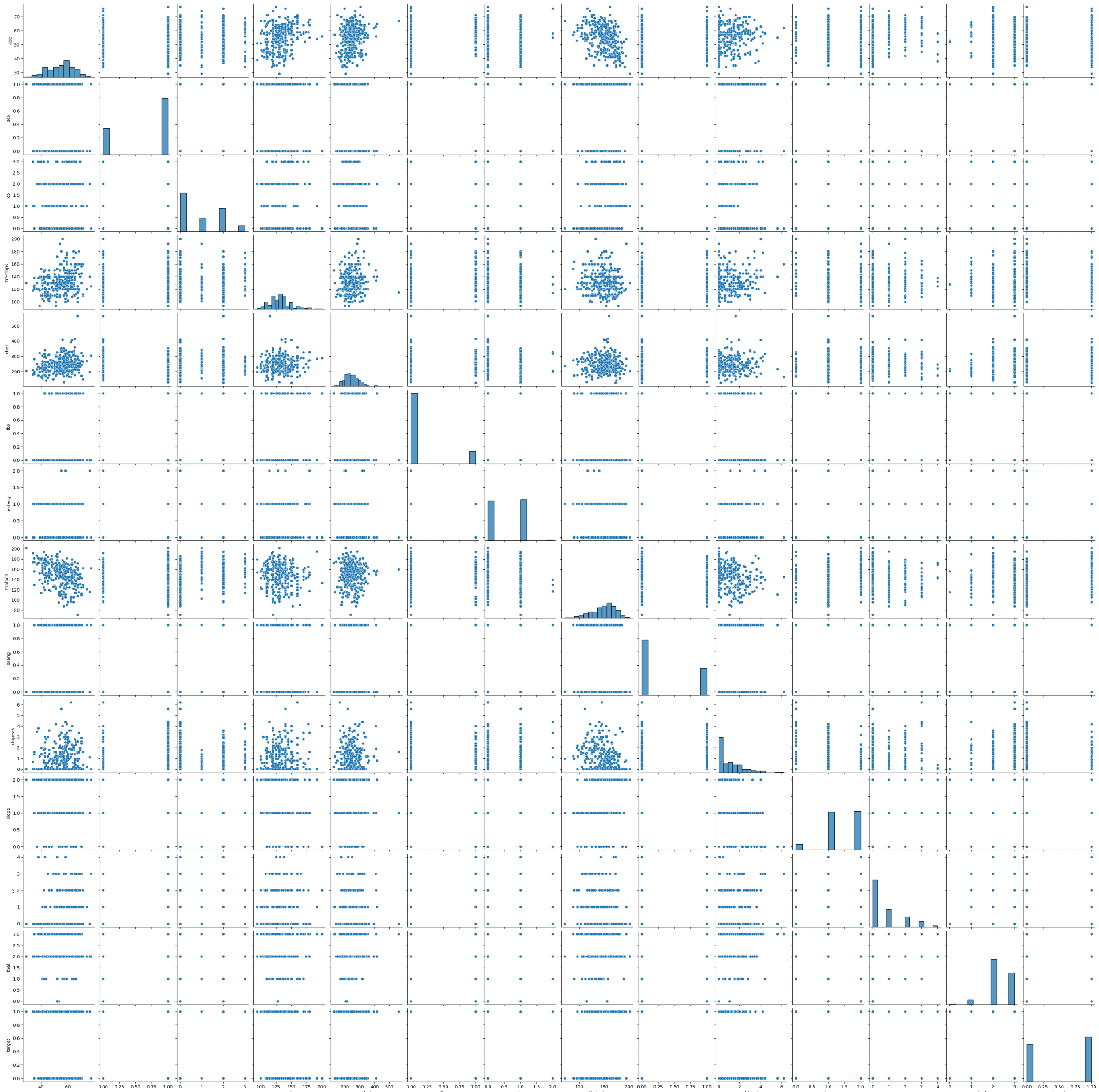
- Positive correlation with target: chest pain(cp),Maximum heart rate achieved during a stress test(thalach), slope and restecg
- Negative correlation with target: exang, oldpeak, thal, ca, sex, trestbps and age.

the state above colunms shows some corelation with our dependent colunm(target), hence, they are identified as the most relevant factors contributing to heart disease prediction.

CHECKING FOR PATTERNS USING SCATTERED PLOT

In [7]:
```
plt.figure(figsize=(13,17))
sns.pairplot(data)
plt.show()
```

```
<Figure size 1300x1700 with 0 Axes>
```



From the graphs above, using btarget as forcus we can see its linerity with oldpeak and thalach, which confirms what we have with our correlation map.

CONCLUSION

```
* from my analysis done above, i hereby conclude that the below table
contains the most relevant factors contributing to heart disease
prediction. Hence, every colunm included except 'target' =
independent variables while
target = Dependant variable
```

In [8]:
```
df = data.drop(['fbs', 'chol'], axis=1)
df
```

Out[8]:

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

303 rows × 12 columns

Significance of feature selection in improving the performance and interpretability of the heart disease prediction model

- Selecting the features above has helped us eliminate redundances included in the dataframe.
- With the exclusion of reduncances such as 'chol' and 'fbs', our model performance has been enhanced.
- The less the noise in the model, the easier the interpretability.

In [9]:
```
# Analysis by Oluwadamilare Tobiloba
```

USING EXHAUSIVE METHOD FOR FEATURE SELECTION

In [10]:
```
data
```

Out[10]:

	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
...	...	...	...	...	...	...	...	...	...	...	...	...	...	...
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

303 rows × 14 columns

In [15]:
```
x = data.drop(['target'], axis = 1)
y = data['target']
feature_names = tuple (x.columns)
```

In [16]:
```
feature_names
```

Out[16]:
```
('age',
 'sex',
 'cp',
 'trestbps',
 'chol',
 'fbs',
 'restecg',
 'thalach',
 'exang',
 'oldpeak',
 'slope',
 'ca',
 'thal')
```

In [13]:
```
from sklearn.neighbors import KNeighborsClassifier as knn
from sklearn.linear_model import LogisticRegression as LGR
from mlxtend.feature_selection import ExhaustiveFeatureSelector
from mlxtend.plotting import plot_sequential_feature_selection
from sklearn.ensemble import RandomForestClassifier
from sklearn.tree import DecisionTreeClassifier
from sklearn.tree import DecisionTreeRegressor
from sklearn.linear_model import LinearRegression
```

In [19]:
```
efs = ExhaustiveFeatureSelector(LGR (max_iter = 100),
                               min_features = 3,
                               max_features =10,
                               scoring ='accuracy',
```

```
                               n_jobs = 8,
                               cv = 2)
```

In [21]:
```
efs = efs.fit(x,y)
```

```
Features: 8008/8008
```

In [22]:
```
# Print selected features
print("Best features:", efs.best_feature_names_)
```

```
Best features: ('sex', 'cp', 'trestbps', 'restecg', 'thalach', 'exang', 'oldpeak', 's
lope', 'ca', 'thal')
```

In [ ]:
```
```