1. Data Repository

Heart Disease Dataset

Public Health Dataset

Src: Kaggel https://www.kaggle.com/datasets/johnsmith88/heart-disease-dataset/data

Description:

The Heart Disease Dataset contains information about patients and various medical attributes used to predict the presence of heart disease. It contains features such as age, gender, chest pain type, resting blood pressure, serum cholesterol, fasting blood sugar, resting electrocardiographic results, maximum heart rate achieved, exercise-induced angina, oldpeak, slope, number of major vessels, thallium stress test result, and target variable that indicates whether the patient has heart disease.

Attributes / Feature Description:

Column Name	*Description*
age	The age of the patient in years. (عمر المريض) Ex: 30 , 45 , 60
sex	Gender of the patient (1 = male; 0 = female).
Cp: chest pain type ***نوع ألم الصدر الذي يعاني منه المريض***	Type of chest pain experienced by the patient (1-4): - 1: Typical angina (ذبحة صدرية نموذجية) - 2: Atypical angina (ذبحة صدرية غير نموذجية) - 3: Non-anginal pain (ألم غير صدري) - 4: Asymptomatic (بدون أعراض).
Trestbps: resting blood pressure ***ضغط الدم أثناء الراحة***	The resting blood pressure (in mm Hg) on admission to the hospital. Ex: 130 , 140 , 120
Chol: serum cholestoral ***مستوى الكوليسترول***	Serum cholesterol level in mg/dL. Ex: 180 , 200 , 250
Fbs: fasting blood sugar ***مستوى السكر في الدم اثناء الصيام***	Whether fasting blood sugar is >120 mg/dL (1 = true; 0 = false).

Restecg: resting electrocardiographic نتائج تخطيط القلب أثناء الراحة	Results of resting electrocardiographic test (values 0, 1, 2): • 0 : Normal • 1 : Having ST-T wave abnormality (e.g., T wave inversions, ST elevation/depression > 0.05 mV) حالة غير طبيعية ST-T وجود شذوذ في موجة • 2 : Showing probable or definite left ventricular hypertrophy by Estes' criteria إظهار تضخم محتمل أو مؤكد في البطين الأيسر
Thalach: maximum heart rate achieved أقصى معدل ضربات قلب تم تحقيقه	The maximum heart rate achieved during the test.
Exang: exercise induced angina الذبحة الصدرية الناجمة عن التمرين	Exercise-induced chest pain (1 = yes; 0 = no).
Oldpeak ***ST: Part of the heart's electrical cycle***	ST depression induced by exercise relative to rest. انخفاض ST الناجم عن التمرين نسبة إلى الراحة
Slope	The slope of the peak exercise ST segment (values 0-2): • 0 : Upsloping • 1 : Flat • 2 : Downsloping
Ca: number of major vessels عدد الأوعية الرئيسية	Number of major vessels (0-3) colored by fluoroscopy.
Thal نتيجة اختبار إجهاد الثاليوم *how well blood flows through your heart muscle while you're exercising or at rest*	Thallium stress test result (0 = normal; 1 = fixed defect; 2 = reversible defect).
Target وجود أمراض القلب	Presence of heart disease (1 = disease; 0 = no disease).

1. Import needed library + read csv dataset file /Data Collection & Understanding: table , size , dimension , column

[1]:
```
# Step 1 : Data Collection and Understanding
# Import libraries used in data preparation
import pandas as pd
import numpy as np
```

[2]:
```
# Load the heart dataset .. in same folder
dataset = pd.read_csv("heart.csv") #Load dataset into a pandas DataFrame.
dataset #to ensure read it successfully
```

[2]:

	age	sex	cp	trestbps	chol	fbs	restecg	thalach	exang	oldpeak	slope	ca	thal	target
0	52	1	0	125	212	0	1	168	0	1.0	2	2	3	0
1	53	1	0	140	203	1	0	155	1	3.1	0	0	3	0
2	70	1	0	145	174	0	1	125	1	2.6	0	0	3	0
3	61	1	0	148	203	0	1	161	0	0.0	2	1	3	0
4	62	0	0	138	294	1	1	106	0	1.9	1	3	2	0
...	...	...	...	...	...	...	...	...	...	...	...	...	...	...
1020	59	1	1	140	221	0	1	164	1	0.0	2	0	2	1
1021	60	1	0	125	258	0	0	141	1	2.8	1	1	3	0
1022	47	1	0	110	275	0	0	118	1	1.0	1	1	2	0
1023	50	0	0	110	254	0	0	159	0	0.0	2	0	2	1
1024	54	1	0	120	188	0	1	113	0	1.4	1	1	3	0

1025 rows × 14 columns

[3]:
```
# get the dataset Size
size = dataset.shape
size
```

[3]:
```
(1025, 14)
```

[4]:
```
# get the dataset dimension
dimension = dataset.ndim
dimension
```

[4]:
```
2
```

[5]:
```
# get columns' titles
titles = dataset.columns
titles
```

[5]:
```
Index(['age', 'sex', 'cp', 'trestbps', 'chol', 'fbs', 'restecg', 'thalach',
       'exang', 'oldpeak', 'slope', 'ca', 'thal', 'target'],
      dtype='object')
```

[6]:
```
 #describing a certain column with some basic statistics
desc = dataset['target'].describe()
desc
```

[6]:
```
count    1025.000000
mean        0.513171
std         0.500070
min         0.000000
25%         0.000000
50%         1.000000
75%         1.000000
max         1.000000
Name: target, dtype: float64
```

2. Data Exploration

Explore the dataset to understand its structure and content.

[7]:
```
# Step 2 : Data Exploration
# Display the first 5 rows of the dataset
head = dataset.head()
head
```

[7]:

	age	sex	cp	trestbps	chol	fbs	restecg	thalach	exang	oldpeak	slope	ca	thal	target
0	52	1	0	125	212	0	1	168	0	1.0	2	2	3	0
1	53	1	0	140	203	1	0	155	1	3.1	0	0	3	0
2	70	1	0	145	174	0	1	125	1	2.6	0	0	3	0
3	61	1	0	148	203	0	1	161	0	0.0	2	1	3	0
4	62	0	0	138	294	1	1	106	0	1.9	1	3	2	0

[8]:
```
# Display information about the dataset
info = dataset.info()
info
```

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

[9]:
```
# Display descriptive statistics of the edited dataset
desc = dataset.describe()
desc
```

[9]:

	age	sex	cp	trestbps	chol	fbs	restecg	thalach	exang	
count	1025.000000	1025.000000	1025.000000	1025.000000	1025.00000	1025.000000	1025.000000	1025.000000	1025.000000	102
mean	54.434146	0.695610	0.942439	131.611707	246.00000	0.149268	0.529756	149.114146	0.336585	
std	9.072290	0.460373	1.029641	17.516718	51.59251	0.356527	0.527878	23.005724	0.472772	
min	29.000000	0.000000	0.000000	94.000000	126.00000	0.000000	0.000000	71.000000	0.000000	
25%	48.000000	0.000000	0.000000	120.000000	211.00000	0.000000	0.000000	132.000000	0.000000	
50%	56.000000	1.000000	1.000000	130.000000	240.00000	0.000000	1.000000	152.000000	0.000000	
75%	61.000000	1.000000	2.000000	140.000000	275.00000	0.000000	1.000000	166.000000	1.000000	
max	77.000000	1.000000	3.000000	200.000000	564.00000	1.000000	2.000000	202.000000	1.000000	

Now I want make noisy , missing and inconsistent values in data set to make Data Preprocessing

In image below we notice that we have missing data “some attribute 1024 nested of 1025 value), noisy data 1400 value in mean 94

[10]:
```
# Step 3 : Data Cleaning and preperation
data = pd.read_csv("heart_after_edit.csv") #Load edit dataset into a pandas DataFrame.
data #to ensure read it successfully
```

[10]:

	age	sex	cp	trestbps	chol	fbs	restecg	thalach	exang	oldpeak	slope	ca	thal	target
0	52.0	1	0	125	212	0.0	1	168	0.0	1	2	2	3	0
1	53.0	5	0	120	203	1.0	0	155	1.0	3.1	0	0	3	0
2	NaN	1	0	145	174	0.0	1	125	1.0	2.6	0	0	3	0
3	61.0	1	0	148	203	0.0	1	161	0.0	0	2	1	3	NAN
4	62.0	0	0	138	294	1.0	1	106	0.0	1.9	1	3	2	0
...	...	...	...	...	...	...	...	...	...	...	...	...	...	...
1020	59.0	1	1	140	221	0.0	1	164	1.0	0	2	0	2	1
1021	60.0	1	0	125	258	0.0	0	141	1.0	2.8	1	1	3	0
1022	47.0	1	0	110	275	0.0	0	118	1.0	1	1	1	2	0
1023	50.0	0	0	110	254	0.0	0	159	0.0	0	2	0	2	1
1024	54.0	1	0	120	188	0.0	1	113	0.0	1.4	1	1	3	0

1025 rows × 14 columns

Rename Columns to be more clear

[11]:
```
data.rename(columns={'sex': 'gender'}, inplace=True) #rename coulmn
data.columns
```

[11]:
```
Index(['index', 'age', 'gender', 'cp', 'trestbps', 'chol', 'fbs', 'restecg',
       'thalach', 'exang', 'oldpeak', 'slope', 'ca', 'thal', 'target'],
      dtype='object')
```

[12]:
```
 #rename coulmn - more clear
data.columns = ['index', 'age', 'gender', 'chest_pain_type', 'resting_blood_pressure', 'cholesterol', 'fasting_blood_sugar', 'rest_electro', 'max_heart_
       'exercise_induced_angina', 'st_depression', 'st_slope', 'num_major_vessels', 'thal', 'target']

data.columns
```

[12]:
```
Index(['index', 'age', 'gender', 'chest_pain_type', 'resting_blood_pressure',
       'cholesterol', 'fasting_blood_sugar', 'rest_electro', 'max_heart_rate',
       'exercise_induced_angina', 'st_depression', 'st_slope',
       'num_major_vessels', 'thal', 'target'],
      dtype='object')
```

Exploration in new dataset

[13]:
```
desc = data.describe()
desc # Display descriptive statistics of the edited dataset
```

[13]:

	index	age	gender	chest_pain_type	resting_blood_pressure	cholesterol	fasting_blood_sugar	rest_electro	max_heart_rate	exercise_induced_a
count	1025.000000	1024.000000	1025.000000	1025.000000	1025.000000	1024.000000	1024.000000	1025.000000	1025.000000	1024.0
mean	512.649756	54.418945	0.699512	0.942439	184.712195	246.045898	0.149414	0.534634	149.114146	0.3
std	296.416605	9.063654	0.479512	1.029641	1699.772051	51.596779	0.356670	0.545776	23.005724	0.4
min	1.000000	29.000000	0.000000	0.000000	94.000000	126.000000	0.000000	0.000000	71.000000	0.0
25%	256.000000	48.000000	0.000000	0.000000	120.000000	211.000000	0.000000	0.000000	132.000000	0.0
50%	513.000000	56.000000	1.000000	1.000000	130.000000	240.000000	0.000000	1.000000	152.000000	0.0
75%	769.000000	61.000000	1.000000	2.000000	140.000000	275.000000	0.000000	1.000000	166.000000	1.0
max	1025.000000	77.000000	5.000000	3.000000	54548.000000	564.000000	1.000000	5.000000	202.000000	1.0

[14]:
```
#count missing values in each attribute
missing = pd.DataFrame({'missing': data.isnull().sum()})
missing
```

[14]:

	missing
index	0
age	1
gender	0
chest_pain_type	0
resting_blood_pressure	0
cholesterol	1
fasting_blood_sugar	1
rest_electro	0
max_heart_rate	0
exercise_induced_angina	1
st_depression	0
st_slope	0
num_major_vessels	0
thal	0

3. Data Cleaning - Preprocessing Data

A. Missing Data Label : Delete rows

[13]:
```
# print target coulmn to say data
data['target']
```

[13]:
```
0         0
1         0
2         0
3       NAN
4         0
       ...
1020      1
1021      0
1022      0
1023      1
1024      0
Name: target, Length: 1025, dtype: object
```

Incomplet

Noisy

[16]:
```
# target column is numeric
data['target'] = pd.to_numeric(data['target'], errors='coerce')

# Drop rows with missing target values empty or null
# data = data.dropna(subset=['target']) or
data = data[pd.notnull(data['target'])]

# convert to int type
data['target'] = data['target'].astype(int)

# drop rows where target values are not 0 or 1
data = data[data['target'].isin([0, 1])].reset_index(drop=True)

data.info()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 1023 entries, 0 to 1022
Data columns (total 15 columns):
 #   Column                   Non-Null Count  Dtype
---  ------                   --------------  -----
 0   index                    1023 non-null   int64
 1   age                      1022 non-null   float64
 2   gender                   1023 non-null   int64
 3   chest_pain_type          1023 non-null   int64
 4   resting_blood_pressure   1023 non-null   int64
 5   cholesterol              1022 non-null   float64
 6   fasting_blood_sugar      1022 non-null   float64
 7   rest_electro             1023 non-null   int64
 8   max_heart_rate           1023 non-null   int64
 9   exercise_induced_angina  1022 non-null   float64
 10  st_depression            1023 non-null   object
 11  st_slope                 1023 non-null   int64
 12  num_major_vessels        1023 non-null   int64
 13  thal                     1023 non-null   int64
 14  target                   1023 non-null   int32
dtypes: float64(4), int32(1), int64(9), object(1)
memory usage: 116.0+ KB
```

After:

```
[17]: data['target']
```

```
[17]: 0       0
      1       0
      2       0
      3       0
      4       1
             ..
      1018    1
      1019    0
      1020    0
      1021    1
      1022    0
      Name: target, Length: 1023, dtype: int32
```

B. Missing data: NAN value in cholesterol column "drop it"

```
[18]: data = data[pd.notnull(data['cholesterol'])]
```

```
[19]: #count missing values in each attribute
      missing = pd.DataFrame({'missing': data.isnull().sum()})
      missing
```

[19]:

	missing
index	0
age	1
gender	0
chest_pain_type	0
resting_blood_pressure	0
cholesterol	0
fasting_blood_sugar	1
rest_electro	0
max_heart_rate	0
exercise_induced_angina	1
st_depression	0
st_slope	0
num_major_vessels	0
thal	0
target	0

C. Missing/Incomplete data: NAN value in age column

```
[20]: # show age befor processing
      data['age']
```

```
[20]: 0       52.0
      1       53.0
      2        NaN
      3       62.0
      4       58.0
              ...
      1018    59.0
      1019    60.0
      1020    47.0
      1021    50.0
      1022    54.0
      Name: age, Length: 1022, dtype: float64
```

```
[21]: # Ensure age column is numeric
      data['age'] = pd.to_numeric(data['age'], errors='coerce')

      # Drop rows with missing age values and reset index
      data = data.dropna(subset=['age']).reset_index(drop=True)
      # or do this data = data['age'].fillna(data['age'].mean())
      data['age']
```

```
[21]: 0       52.0
      1       53.0
      2       62.0
      3       58.0
      4       58.0
              ...
      1016    59.0
      1017    60.0
      1018    47.0
      1019    50.0
      1020    54.0
      Name: age, Length: 1021, dtype: float64
```

```
[22]: data.describe()
```

[22]:

	index	age	gender	chest_pain_type	resting_blood_pressure	cholesterol	fasting_blood_sugar	rest_electro	max_heart_rate	exercise_induced_
count	1021.000000	1021.000000	1021.000000	1021.000000	1021.000000	1021.000000	1020.000000	1021.000000	1021.000000	1020
mean	514.476983	54.421156	0.698335	0.941234	184.874633	246.218413	0.150000	0.533790	149.092067	0
std	295.524507	9.061711	0.480081	1.028264	1703.099676	51.570039	0.357247	0.546005	23.016902	0
min	1.000000	29.000000	0.000000	0.000000	94.000000	126.000000	0.000000	0.000000	71.000000	0
25%	259.000000	48.000000	0.000000	0.000000	120.000000	211.000000	0.000000	0.000000	132.000000	0
50%	515.000000	56.000000	1.000000	1.000000	130.000000	240.000000	0.000000	1.000000	152.000000	0
75%	770.000000	61.000000	1.000000	2.000000	140.000000	275.000000	0.000000	1.000000	166.000000	1
max	1025.000000	77.000000	5.000000	3.000000	54548.000000	564.000000	1.000000	5.000000	202.000000	1

D. Noisy data: Empty value in gender Column/ outliers

[23]:
```
# removing rows where gender is either 0 or 1 and reset index
data = data[data['gender'].isin([0, 1])]

data.reset_index(drop=True, inplace=True)

data.describe()
```

[23]:

	index	age	gender	chest_pain_type	resting_blood_pressure	cholesterol	fasting_blood_sugar	rest_electro	max_heart_rate	exercis
count	1020.000000	1020.000000	1020.000000	1020.000000	1020.000000	1020.000000	1019.000000	1020.000000	1020.000000	
mean	514.979412	54.422549	0.694118	0.942157	184.938235	246.260784	0.149166	0.534314	149.086275	
std	295.232878	9.066047	0.461006	1.028346	1703.933930	51.577553	0.356427	0.546017	23.027449	
min	1.000000	29.000000	0.000000	0.000000	94.000000	126.000000	0.000000	0.000000	71.000000	
25%	259.750000	48.000000	0.000000	0.000000	120.000000	211.000000	0.000000	0.000000	132.000000	
50%	515.500000	56.000000	1.000000	1.000000	130.000000	240.000000	0.000000	1.000000	152.000000	
75%	770.250000	61.000000	1.000000	2.000000	140.000000	275.250000	0.000000	1.000000	166.000000	
max	1025.000000	77.000000	1.000000	3.000000	54548.000000	564.000000	1.000000	5.000000	202.000000	

E. Missing Data : Fill empty value in fasting_blood_suger column replace with min "print result before and after"

[24]:
```
# rows where the fasting_blood_sugar column has empty values
before = data[data['fasting_blood_sugar'].isna()]
before
```

[24]:

	index	age	gender	chest_pain_type	resting_blood_pressure	cholesterol	fasting_blood_sugar	rest_electro	max_heart_rate	exercise_induced_angina	s
978	984	64.0	1	0	128	263.0	NaN	1	105	1.0	

[25]:
```
# Replace NaN values in fasting_blood_sugar column with the mean
data['fasting_blood_sugar'].fillna(data['fasting_blood_sugar'].min(), inplace=True)

#row after replacement
after_row = data.loc[978]
print("Row with index 978 after replacement:")
print(after_row)
```

```
Row with index 978 after replacement:
index                      984
age                       64.0
gender                       1
chest_pain_type              0
resting_blood_pressure     128
cholesterol              263.0
fasting_blood_sugar        0.0
rest_electro                 1
max_heart_rate             105
exercise_induced_angina    1.0
st_depression              0.2
st_slope                     1
num_major_vessels            1
thal                         3
target                       1
```

Same for exercise_induced_angina column

```
[27]: # rows where the exercise_induced_angina column has empty values
before = data[data['exercise_induced_angina'].isna()]
before
```

[27]:

	index	age	gender	chest_pain_type	resting_blood_pressure	cholesterol	fasting_blood_sugar	rest_electro	max_heart_rate	exercise_induced_angina	st_
4	8	55.0	1	0	160	289.0	0.0	0	145	NaN	

```
[28]: # Replace NaN values in exercise_induced_angina column with the median
data['exercise_induced_angina'].fillna(data['exercise_induced_angina'].median(), inplace=True)

#row after replacement
after_row = data.loc[4]
print("Row with index 4 after replacement:")
print(after_row)
```

```
Row with index 4 after replacement:
index                       8
age                      55.0
gender                      1
chest_pain_type             0
resting_blood_pressure    160
cholesterol             289.0
fasting_blood_sugar       0.0
rest_electro                0
max_heart_rate            145
exercise_induced_angina   0.0
st_depression             0.8
st_slope                    1
num_major_vessels           1
thal                        3
target                      0
Name: 4, dtype: object
```

F. Noisy Data : Manually edit

```
[29]: data.describe()
```

[29]:

	index	age	gender	chest_pain_type	resting_blood_pressure	cholesterol	fasting_blood_sugar	rest_electro	max_heart_rate	exercise_
count	1020.000000	1020.000000	1020.000000	1020.000000	1020.000000	1020.000000	1020.000000	1020.000000	1020.000000	
mean	514.979412	54.422549	0.694118	0.942157	184.938235	246.260784	0.149020	0.534314	149.086275	
std	295.232878	9.066047	0.461006	1.028346	1703.933930	51.577553	0.356282	0.546017	23.027449	
min	1.000000	29.000000	0.000000	0.000000	94.000000	126.000000	0.000000	0.000000	71.000000	
25%	259.750000	48.000000	0.000000	0.000000	120.000000	211.000000	0.000000	0.000000	132.000000	
50%	515.500000	56.000000	1.000000	1.000000	130.000000	240.000000	0.000000	1.000000	152.000000	
75%	770.250000	61.000000	1.000000	2.000000	140.000000	275.250000	0.000000	1.000000	166.000000	
max	1025.000000	77.000000	1.000000	3.000000	54548.000000	564.000000	1.000000	5.000000	202.000000	

[30]:
```
# Find max value in the resting_blood_pressure column
index = data['resting_blood_pressure'].idxmax()
#or data[data.resting_blood_pressure == 54548]

print(f"index : {index}, \nrow data : \n{data.loc[index]} ")
```

```
index : 2,
row data :
index                       6
age                      58.0
gender                      0
chest_pain_type             0
resting_blood_pressure    54548
cholesterol              248.0
fasting_blood_sugar        0.0
rest_electro                0
max_heart_rate            122
exercise_induced_angina   0.0
st_depression               1
st_slope                    1
num_major_vessels           0
thal                        2
target                      1
Name: 2, dtype: object
```

[31]:
```
# Manually update the value of resting_blood_pressure
data.at[index, 'resting_blood_pressure'] = 120
# or data [120 , 4] = 120

data.loc[index]
```

[31]:
```
index                       6
age                      58.0
gender                      0
chest_pain_type             0
resting_blood_pressure    120
cholesterol              248.0
fasting_blood_sugar        0.0
rest_electro                0
max_heart_rate            122
```

G. Remove duplication “find duplication “in columns” then drop”

[33]:
```
# Define the list of columns to check for duplicates
subset_list = ['index','age', 'gender', 'chest_pain_type', 'resting_blood_pressure', 'cholesterol',
               'fasting_blood_sugar', 'rest_electro', 'max_heart_rate', 'exercise_induced_angina',
               'st_depression', 'st_slope', 'num_major_vessels', 'thal', 'target']

#duplicate rows
duplicates = data[data.duplicated(subset=subset_list, keep='first')]

duplicates
```

[33]:

	index	age	gender	chest_pain_type	resting_blood_pressure	cholesterol	fasting_blood_sugar	rest_electro	max_heart_rate	exercise_induced_angina	st_d
365	12	43.0	0	0	132	341.0	1.0	0	136	1.0	

[34]:
```
# Remove duplicate rows, keeping the first occurrence
data.drop_duplicates(subset=subset_list, keep='first', inplace=True)
data.head()
```

[34]:

	index	age	gender	chest_pain_type	resting_blood_pressure	cholesterol	fasting_blood_sugar	rest_electro	max_heart_rate	exercise_induced_angina	st_dep
0	1	52.0	1	0	125	212.0	0.0	1	168	0.0	
1	5	62.0	0	0	138	294.0	1.0	1	106	0.0	
2	6	58.0	0	0	120	248.0	0.0	0	122	0.0	
3	7	58.0	1	0	114	318.0	0.0	2	140	0.0	
4	8	55.0	1	0	160	289.0	0.0	0	145	0.0	

H. Remove uneless column like index

```
[35]: data.drop(columns=['index'], inplace=True)

      # after delete column
      data.head()
```

[35]:

	age	gender	chest_pain_type	resting_blood_pressure	cholesterol	fasting_blood_sugar	rest_electro	max_heart_rate	exercise_induced_angina	st_depression	st_slope
0	52.0	1	0	125	212.0	0.0	1	168	0.0	1	2
1	62.0	0	0	138	294.0	1.0	1	106	0.0	1.9	1
2	58.0	0	0	120	248.0	0.0	0	122	0.0	1	1
3	58.0	1	0	114	318.0	0.0	2	140	0.0	4.4	0
4	55.0	1	0	160	289.0	0.0	0	145	0.0	0.8	1

Check missing:

```
[36]: #count missing values in each attribute
      missing = pd.DataFrame({'missing': data.isnull().sum()})
      missing
```

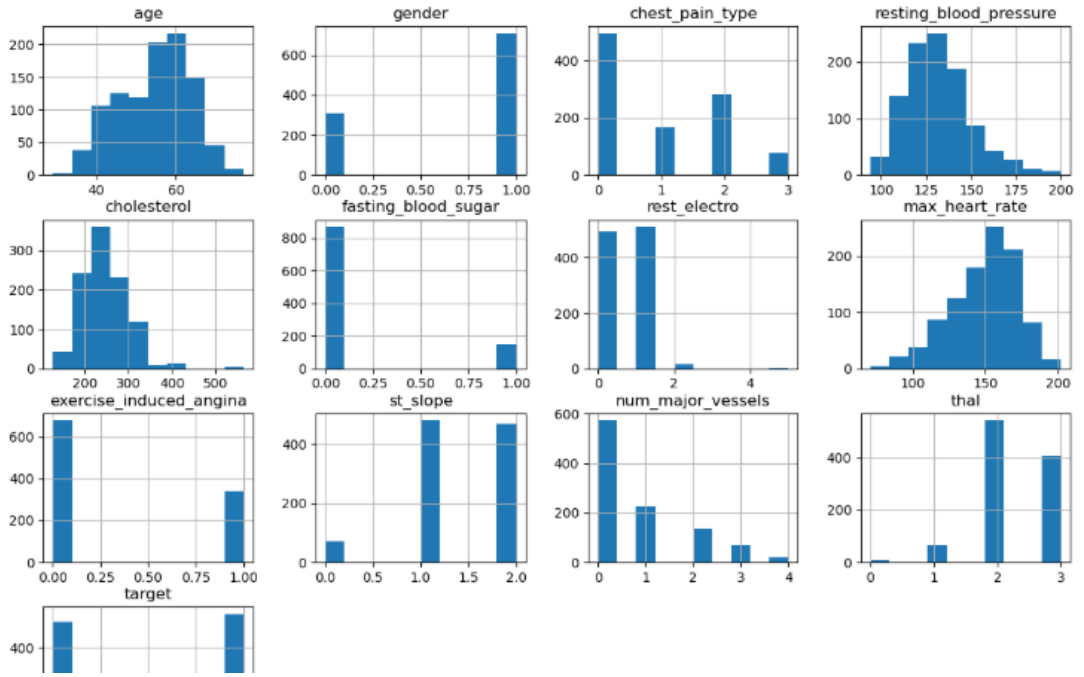
[36]:

	missing
age	0
gender	0
chest_pain_type	0
resting_blood_pressure	0
cholesterol	0
fasting_blood_sugar	0
rest_electro	0
max_heart_rate	0
exercise_induced_angina	0
st_depression	0
st_slope	0
num_major_vessels	0
thal	0
target	0

Now Data is ready for next Step

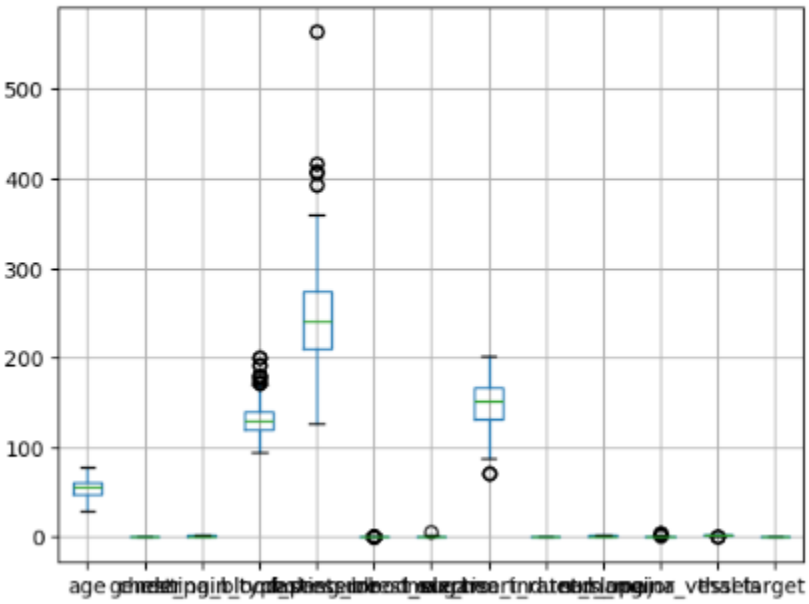
Data Exploration before transformation:

[37]:
```
import matplotlib.pyplot as plt

# Generate histograms for each column
data.hist(figsize=(14, 10))
plt.show()
```



[38]:
```
data.boxplot()
```

[38]: <Axes: >



4. Feature Engineering

A. Age cluster/Bins:

Categorize age into different levels: child, Teenager, Young Adult, Middle Aged, Senior

[40]:
```
# Step 4: Feature Engineering
# Create a new feature based on age
bin_labels = ['Child', 'Teenager', 'Young Adult', 'Middle Aged', 'Senior']
data['age_group'] = pd.cut(data['age'], bins=[0, 12, 19, 35, 55, 100], labels=bin_labels)

# new feature
data[['age', 'age_group']]
```

[40]:

	age	age_group
0	52.0	Middle Aged
1	62.0	Senior
2	58.0	Senior
3	58.0	Senior
4	55.0	Middle Aged
...	...	...
1015	59.0	Senior
1016	60.0	Senior
1017	47.0	Middle Aged
1018	50.0	Middle Aged
1019	54.0	Middle Aged

1019 rows × 2 columns

B. Cholesterol level

Categorize **Cholesterol** into different levels: Good , Borderline and High

[41]:
```
# Create a new feature based on cholesterol 3 bins 0-200 , 200-240 , 240-1000
bin_labels = ['Good', 'Borderline', 'High']
data['chol_level'] = pd.cut(data['cholesterol'], bins=[0, 200, 240, 1000], labels=bin_labels)

data[['cholesterol', 'chol_level']]
```

[41]:

	cholesterol	chol_level
0	212.0	Borderline
1	294.0	High
2	248.0	High
3	318.0	High
4	289.0	High
...	...	...
1015	221.0	Borderline
1016	258.0	High
1017	275.0	High
1018	254.0	High
1019	188.0	Good

1019 rows × 2 columns

5. Data Transformation

- **Scaling/Normalization**: For numerical features like ['resting_blood_pressure', 'cholesterol', 'max_heart_rate'] to standardize the feature range.

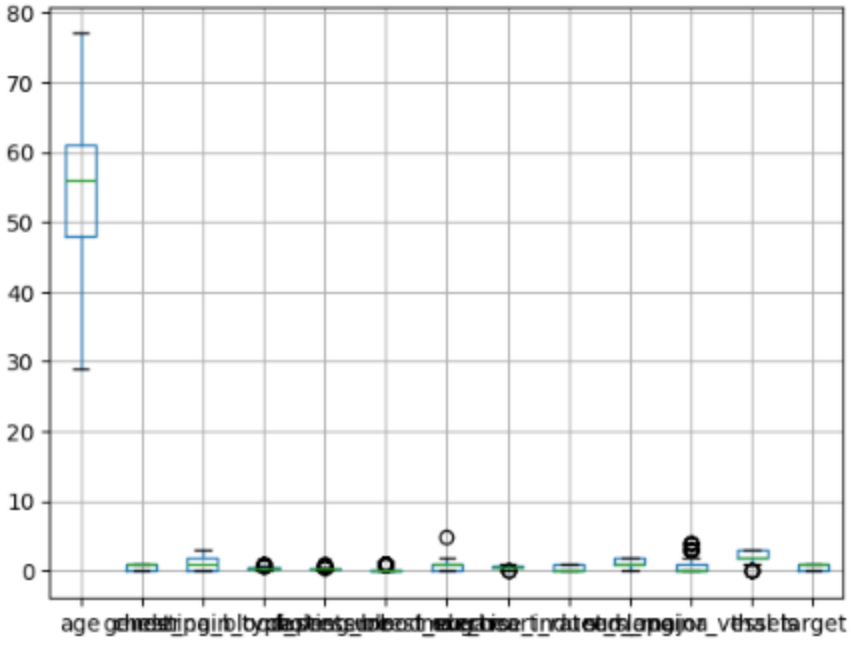
[42]:
```
# step 5 : Data Transformation
from sklearn.preprocessing import MinMaxScaler

# 1. scaling/normalization numerical Features
minMaxScaler = MinMaxScaler()

# numeric features to normaliz
numeric_features = ['resting_blood_pressure', 'cholesterol', 'max_heart_rate']

# fit scaler to numeric features
minMaxScaler.fit(data[numeric_features])

# transform the numeric features
data[numeric_features] = minMaxScaler.fit_transform(data[numeric_features])

data.head()
```

[42]:

	age	gender	chest_pain_type	resting_blood_pressure	cholesterol	fasting_blood_sugar	rest_electro	max_heart_rate	exercise_induced_angina	st_d
0	52.0	1	0	0.292453	0.196347	0.0	1	0.740458	0.0	
1	62.0	0	0	0.415094	0.383562	1.0	1	0.267176	0.0	
2	58.0	0	0	0.245283	0.278539	0.0	0	0.389313	0.0	
3	58.0	1	0	0.188679	0.438356	0.0	2	0.526718	0.0	
4	55.0	1	0	0.622642	0.372146	0.0	0	0.564885	0.0	

[43]:
```
data.boxplot()
```

[43]: <Axes: >



Here we find age can be normalized also

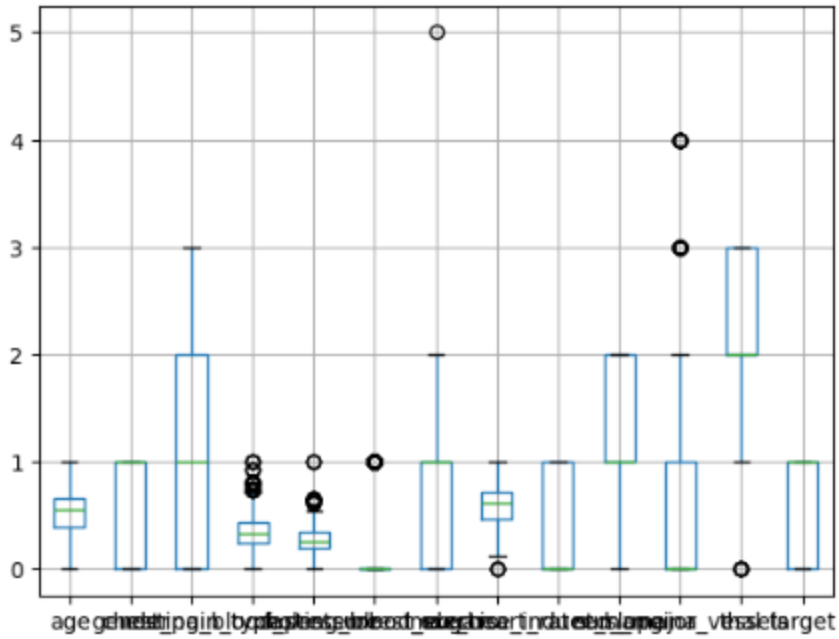
[44]:
```
# normalize age
data['age'] =minMaxScaler.fit_transform(data['age'].values.reshape(-1, 1))
data.head()
```

[44]:

	age	gender	chest_pain_type	resting_blood_pressure	cholesterol	fasting_blood_sugar	rest_electro	max_heart_rate	exercise_induced_angina	st_depression	s
0	0.479167	1	0	0.292453	0.196347	0.0	1	0.740458	0.0	1	
1	0.687500	0	0	0.415094	0.383562	1.0	1	0.267176	0.0	1.9	
2	0.604167	0	0	0.245283	0.278539	0.0	0	0.389313	0.0	1	
3	0.604167	1	0	0.188679	0.438356	0.0	2	0.526718	0.0	4.4	
4	0.541667	1	0	0.622642	0.372146	0.0	0	0.564885	0.0	0.8	

[45]:
```
data.boxplot()
```

[45]: <Axes: >



- **Ordinal Encoding**: For ordered categories like cp, restecg, and slope but not needed "already ordinal"

[52]:
```
#2 Categorical Encoding - Ordinal/Label Encoder
from sklearn.preprocessing import LabelEncoder

# Encode non-numeric columns
encoder = LabelEncoder()
data['st_depression'] = encoder.fit_transform(data['st_depression'])
data['age_group'] = encoder.fit_transform(data['age_group'])
data['chol_level'] = encoder.fit_transform(data['chol_level'])
```

Now we notice that rest_electro, num_major_vessels has outlier value:

1. rest_electro column

Detect outlier "outside range"

[46]:
```
# Calculate the IQR for restecg - interquartile range measure of  spread of the data
Q1 = data['rest_electro'].quantile(0.25) # Q1 represents the value below which 25% of the data points fall.
Q3 = data['rest_electro'].quantile(0.75) # Q3 represents the value below which 75% of the data points fall.

IQR = Q3 - Q1

# lower and upper bounds for outliers [-1 min , +1 max]
lower_bound = Q1 - 1 * IQR
upper_bound = Q3 + 1 * IQR

# outlier rows
outliers = data[(data['rest_electro'] < lower_bound) | (data['rest_electro'] > upper_bound)] #outside the range

outliers
```

[46]:

	age	gender	chest_pain_type	resting_blood_pressure	cholesterol	fasting_blood_sugar	rest_electro	max_heart_rate	exercise_induced_angina	st_depression	st_s
973	0.3125	1	0	0.150943	0.1621	0.0	5	0.80916	0.0	0	

Drop it "one row"

[47]:
```
# Drop the row with index 973
data.drop([973],inplace=True, axis=0)
data.reset_index(drop=True, inplace=True)

after_row = data.loc[973]
print("Row with index 973 after delete privious:")
print(after_row)
```

```
Row with index 973 after delete privious:
age                        0.583333
gender                            1
chest_pain_type                   0
resting_blood_pressure     0.433962
cholesterol                0.150685
fasting_blood_sugar             0.0
rest_electro                      1
max_heart_rate             0.587786
exercise_induced_angina         0.0
st_depression                   0.4
st_slope                          1
num_major_vessels                 0
thal                              1
target                            1
age_group                    Senior
chol_level                     Good
Name: 973, dtype: object
```

new row

2. num_major_vessels column

After research in num_major_vessels:

0-3: Indicates the typical range seen in patients, with 0 meaning no blockages and 3 meaning three major vessels are blocked. (left main coronary artery, left anterior descending artery, and right coronary artery).. 4 might indicate an exceptional case or data error, but it can also be used to flag special or severe cases that are outside the typical range. So I don't considered it outlier

```
[48]: # set of acceptable values
acceptable_values = {0, 1, 2, 3}

# outliers
outliers = data[~data['num_major_vessels'].isin(acceptable_values)]

outliers
```

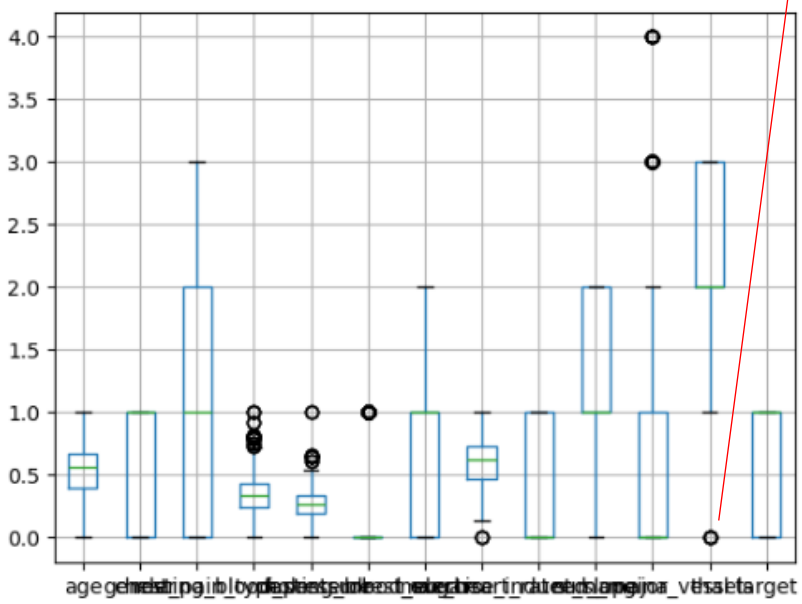
[48]:

cholesterol	fasting_blood_sugar	rest_electro	max_heart_rate	exercise_induced_angina	st_depression	st_slope	num_major_vessels	thal	target	age
0.111872	0.0	1	0.778626	0.0	0	2	4	2	1	
0.111872	0.0	1	0.778626	0.0	0	2	4	2	1	
0.221461	0.0	1	0.748092	0.0	0	2	4	2	1	
0.111872	0.0	1	0.778626	0.0	0	2	4	2	1	
0.111872	0.0	1	0.778626	0.0	0	2	4	2	1	
0.221461	0.0	1	0.748092	0.0	0	2	4	2	1	

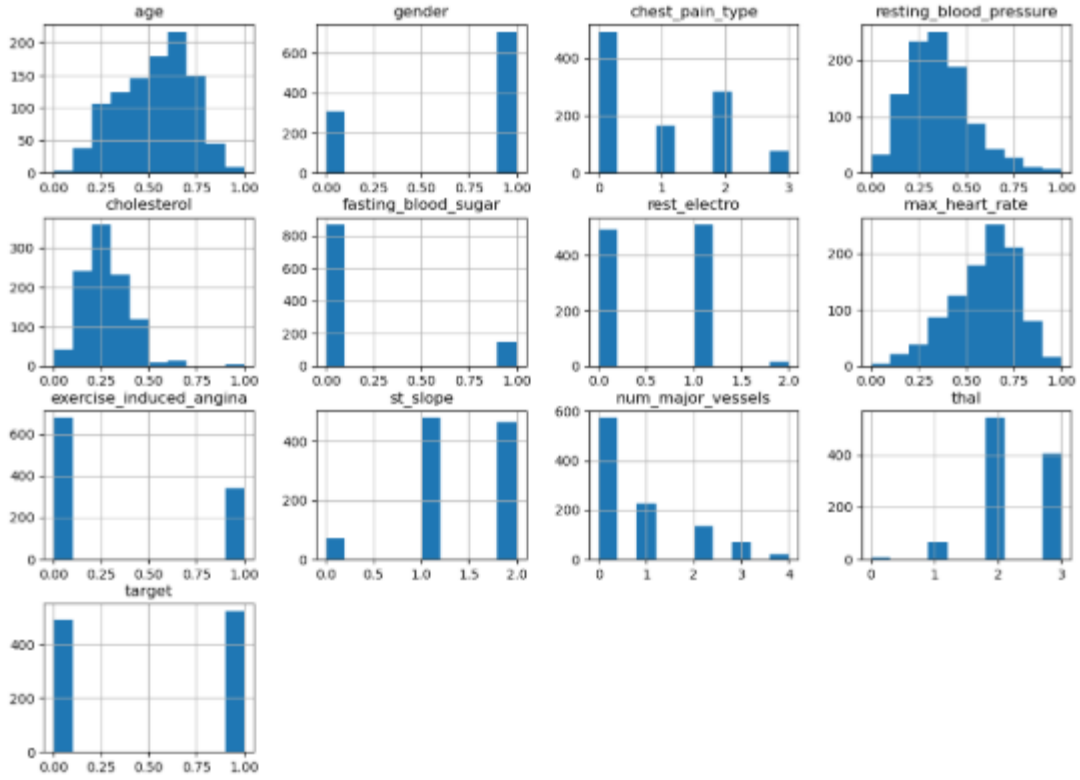
Thal ***نتيجة اختبار اجهاد الثاليوم*** *how well blood flows through your heart muscle while you're exercising or at rest*	Thallium stress test result (0 = normal; 1 = fixed defect; 2 = reversible defect).

```
[50]: data.boxplot()
```

[50]: <Axes: >



[51]:
```
# Generate histograms for each column
data.hist(figsize=(14, 10))
plt.show()
```



6. Finally split to make training and test set and calculate correctness

[53]:
```
from sklearn.model_selection import train_test_split as tts

# Split the data into training and testing sets
trainSet, testSet = tts(data, test_size=0.3)

trainSet
```

[53]:

	cholesterol	fasting_blood_sugar	rest_electro	max_heart_rate	exercise_induced_angina	st_depression	st_slope	num_major_vessels	thal	target	age_group	chol_level
2	0.244292	1.0	0	0.603053	0.0	22	0	0	1	1	1	0
4	0.394977	0.0	0	0.412214	1.0	9	1	2	2	0	1	2
3	0.164384	0.0	1	0.450382	1.0	16	1	0	3	0	2	1
1	0.230594	0.0	0	0.641221	0.0	6	1	0	3	1	1	0
3	0.315068	0.0	1	0.465649	0.0	12	1	0	3	0	0	2
.	...	...	...	...	...	...	...	...	...	...	...	...

[57]:

```
from sklearn.linear_model import LogisticRegression
from sklearn.metrics import accuracy_score, precision_score, recall_score

# we should encode non-numeric columns priviously LogisticRegression deal with numerics
# Separate features and target
train_features = trainSet.drop('target', axis=1)
train_target = trainSet['target']
test_features = testSet.drop('target', axis=1)
test_target = testSet['target']

# Train the model
model = LogisticRegression(max_iter=1000)
model.fit(train_features, train_target)

# Predict on the test set
predictions = model.predict(test_features)

# Calculate scores as percentages
accuracy = accuracy_score(test_target, predictions) * 100
precision = precision_score(test_target, predictions) * 100
recall = recall_score(test_target, predictions) * 100

# Print scores
print(f"Accuracy: {accuracy:.2f}%")
print(f"Precision: {precision:.2f}%")
print(f"Recall: {recall:.2f}%")
```

```
Accuracy: 83.33%
Precision: 79.77%
Recall: 89.61%
```