In [1]:
```python
import numpy as np
import pandas as pd

import warnings
warnings.filterwarnings('ignore')
```

In [2]:
```python
hcare = pd.read_excel("1645792390_cep1_dataset.xlsx")
```

In [3]:
```python
hcare.head()
```

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

In [4]:
```python
hcare.shape
```

Out[4]:
```
(303, 14)
```

In [5]:
```python
hcare.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 [7]:
```python
# Checking for missing values
hcare.isnull().sum(axis = 0)
```

Out[7]:
```
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 [8]:
```python
hcare.describe()
```

Out[8]:

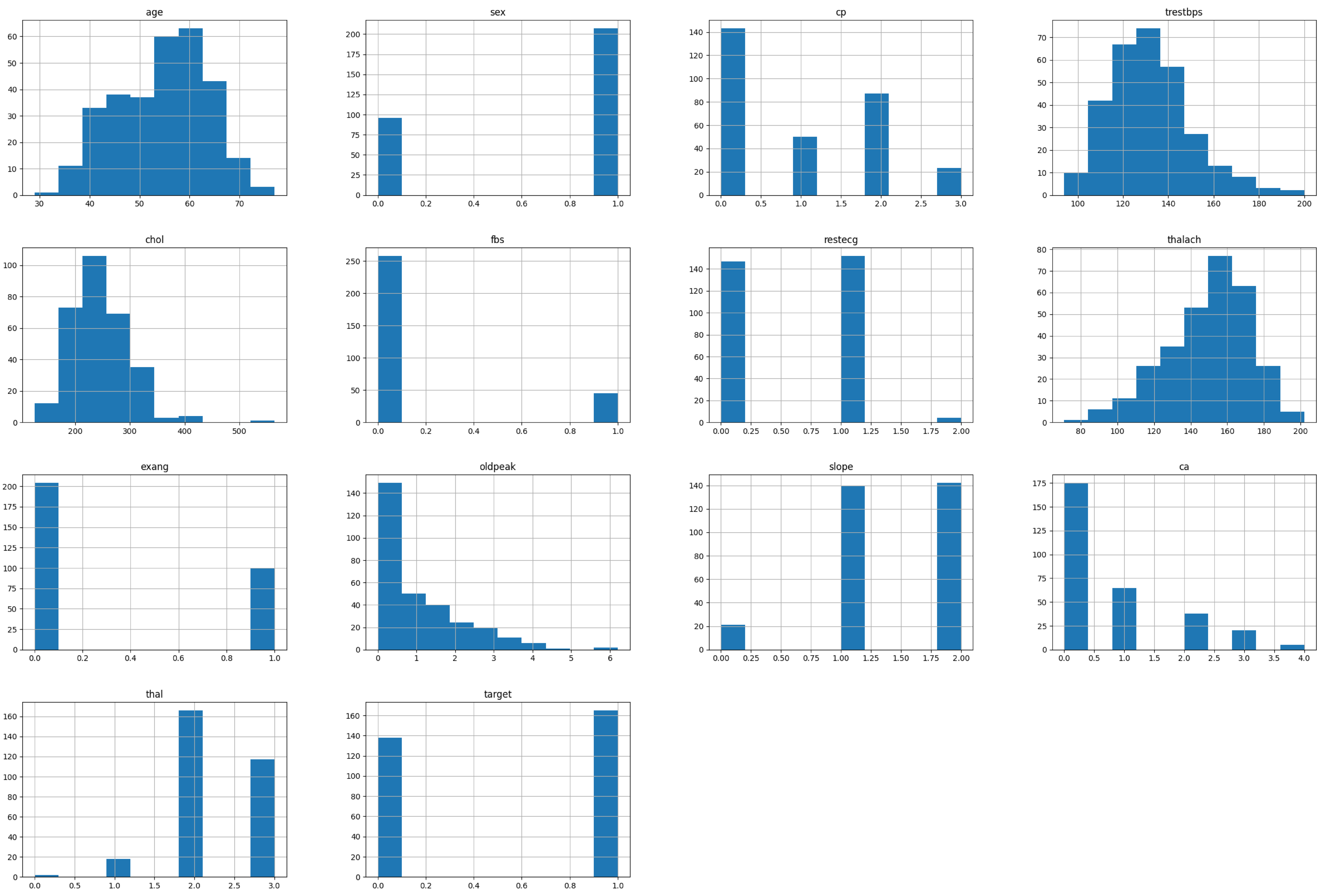
	age	sex	cp	trestbps	chol	fbs	restecg	thalach	exang	oldpeak	slope	ca	thal	target
count	303.000000	303.000000	303.000000	303.000000	303.000000	303.000000	303.000000	303.000000	303.000000	303.000000	303.000000	303.000000	303.000000	303.000000
mean	54.366337	0.683168	0.966997	131.623762	246.264026	0.148515	0.528053	149.646865	0.326733	1.039604	1.399340	0.729373	2.313531	0.544554
std	9.082101	0.466011	1.032052	17.538143	51.830751	0.356198	0.525860	22.905161	0.469794	1.161075	0.616226	1.022606	0.612277	0.498835
min	29.000000	0.000000	0.000000	94.000000	126.000000	0.000000	0.000000	71.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000
25%	47.500000	0.000000	0.000000	120.000000	211.000000	0.000000	0.000000	133.500000	0.000000	0.000000	1.000000	0.000000	2.000000	0.000000
50%	55.000000	1.000000	1.000000	130.000000	240.000000	0.000000	1.000000	153.000000	0.000000	0.800000	1.000000	0.000000	2.000000	1.000000
75%	61.000000	1.000000	2.000000	140.000000	274.500000	0.000000	1.000000	166.000000	1.000000	1.600000	2.000000	1.000000	3.000000	1.000000
max	77.000000	1.000000	3.000000	200.000000	564.000000	1.000000	2.000000	202.000000	1.000000	6.200000	2.000000	4.000000	3.000000	1.000000

We can see that the scale of each feature column is different and varied.

In [9]:
```python
# For visualizations
import matplotlib.pyplot as plt
from matplotlib import rcParams
from matplotlib.cm import rainbow
%matplotlib inline
import seaborn as sns
```

In [11]:
```python
# Histogram of the Heart Dataset

fig = plt.figure(figsize = (30,20))
hcare.hist(ax = fig.gca());
```

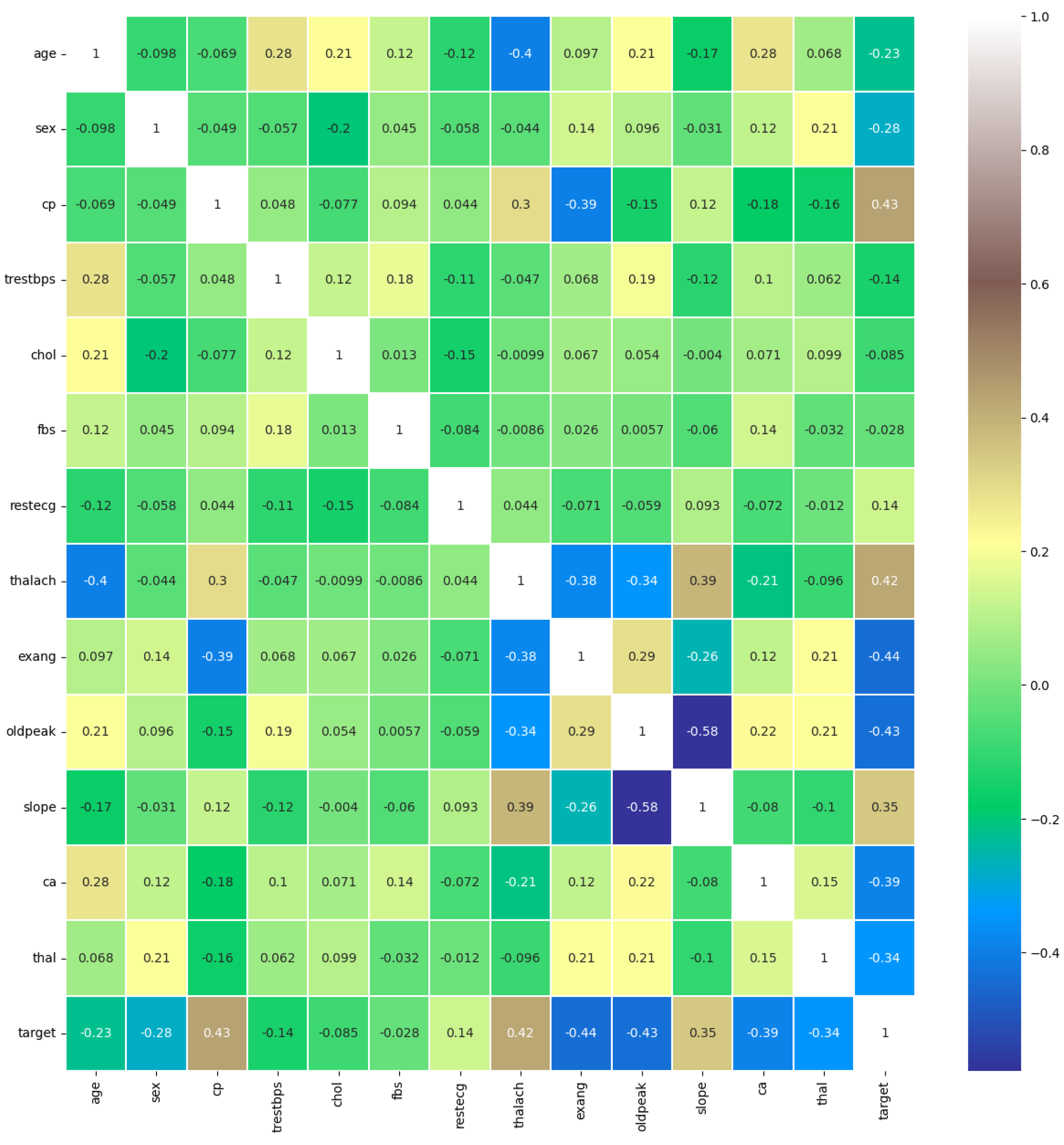


From the above histogram plots, we can see that the features are skewed and not normally distributed. Also, the scales are different between one and another.

Understanding the Data

Let us observe the creelation between different features with help of a heat mat.

In [24]:
```python
# Creating a correlation heatmap
sns.heatmap(hcare.corr(),annot=True, cmap='terrain', linewidths=0.1)
fig=plt.gcf()
fig.set_size_inches(15,15)
plt.show()
```

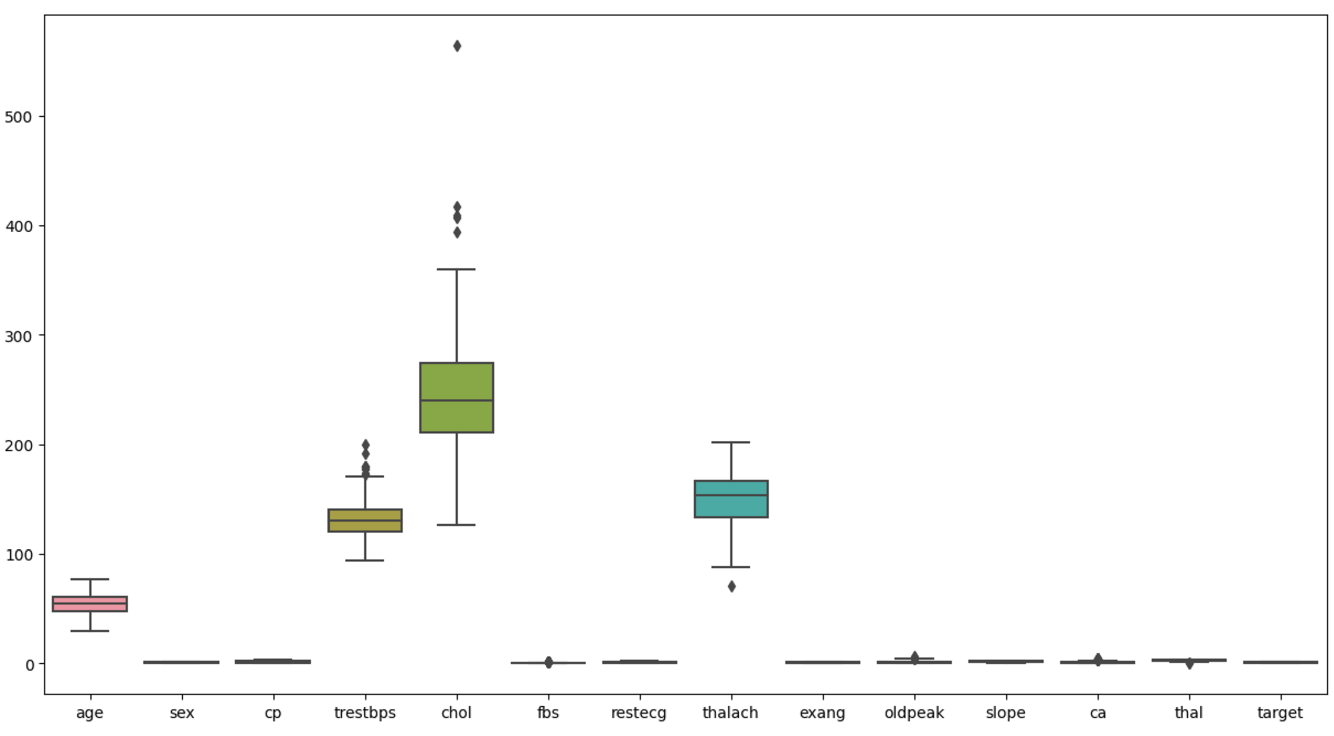


From the above HeatMap, we can see that cp and thalach are the features with highest positive correlation whereas exang, oldpeak and ca are negatively correlated.While other features do not hold much correlation with the response variable "target".

Outlier Detection

Since the dataset is not large, we cannot discard the outliers. We will treat the outliers as potential observations.

In [13]:
```python
# Boxplots
fig_dims = (15,8)
fig, ax = plt.subplots(figsize=fig_dims)
sns.boxplot(data=hcare, ax=ax);
```



Handling Imbalance

Imbalance in a dataset leads to inaccuracy and high precision, recall scores. There are certain resampling techniques such as undersampling and oversampling to handle these issues.

Considering our dataset, the response variable target has two outcomes "Patients with Heart Disease" and "Patients without Heart Disease". Let us now observe their distribution in the dataset.

In [14]:
```python
hcare["target"].value_counts()
```

Out[14]:
```
target
1    165
0    138
Name: count, dtype: int64
```

From the above chart, we can conclude even when the distribution is not exactly 50:50, but still the data is good enough to use on machine learning algorithms and to predict standard metrics like Accuracy and AUC scores. So, we do not need to resample this dataset.

Train-Test Split

Let us distribute the data into **training** and **test** datasets using the **train_test_split()** function.

In [15]:
```python
X = hcare.drop("target",axis=1)
y = hcare["target"]
```

Logistic Regression

In [16]:
```python
from sklearn.model_selection import train_test_split
X_train,X_test,y_train,y_test = train_test_split(X,y,test_size=0.20,stratify=y,random_state=7)
```

In [17]:
```python
from sklearn.linear_model import LogisticRegression
```

In [18]:
```python
lr = LogisticRegression()
lr.fit(X_train, y_train)
```

Out[18]:
```
▾ LogisticRegression
LogisticRegression()
```

In [19]:
```python
pred = lr.predict(X_test)
```

In [20]:
```python
from sklearn.metrics import accuracy_score, confusion_matrix, classification_report
```

In [21]:
```python
# Accuracy on Test data
accuracy_score(y_test, pred)
```

Out[21]:
```
0.8032786885245902
```

In [22]:
```
# Accuracy on Train data
accuracy_score(y_train, lr.predict(X_train))
```

Out[22]: 0.8471074380165289

Building a predictive system

In [23]:
```
import warnings
in_data = (57,0,0,140,241,0,1,123,1,0.2,1,0,3)

# Changing the input data into a numpy array
in_data_as_numpy_array = np.array(in_data)

# Reshaping the numpy array as we predict it
in_data_reshape = in_data_as_numpy_array.reshape(1,-1)
pred = lr.predict(in_data_reshape)
print(pred)

if(pred[0] == 0):
    print('The person does not have heart disease.')
else:
    print('The person has heart disease.')
```

```
[0]
The person does not have heart disease.
```