Pandas and Seaborn based homework

DSE5002 HD Sheets, revised Feb 2025

We will be working with the heart.csv data set

https://www.kaggle.com/fedesoriano/heart-failure-prediction?select=heart.csv

using tools in pandas and seaborn, and ideas from the two Jupyter notebooks we've seen this week

In [70]:
```
!pip install pandas numpy seaborn plotnine
```

```
Requirement already satisfied: pandas in c:\users\water\anaconda3\envs\dse5002\lib\s
ite-packages (2.2.3)
Requirement already satisfied: numpy in c:\users\water\anaconda3\envs\dse5002\lib\si
te-packages (2.2.4)
Requirement already satisfied: seaborn in c:\users\water\anaconda3\envs\dse5002\lib
\site-packages (0.13.2)
Requirement already satisfied: plotnine in c:\users\water\anaconda3\envs\dse5002\lib
\site-packages (0.14.5)
Requirement already satisfied: python-dateutil>=2.8.2 in c:\users\water\anaconda3\en
vs\dse5002\lib\site-packages (from pandas) (2.9.0.post0)
Requirement already satisfied: pytz>=2020.1 in c:\users\water\anaconda3\envs\dse5002
\lib\site-packages (from pandas) (2025.1)
Requirement already satisfied: tzdata>=2022.7 in c:\users\water\anaconda3\envs\dse50
02\lib\site-packages (from pandas) (2025.1)
Requirement already satisfied: matplotlib!=3.6.1,>=3.4 in c:\users\water\anaconda3\e
nvs\dse5002\lib\site-packages (from seaborn) (3.10.1)
Requirement already satisfied: mizani~=0.13.0 in c:\users\water\anaconda3\envs\dse50
02\lib\site-packages (from plotnine) (0.13.1)
Requirement already satisfied: scipy>=1.8.0 in c:\users\water\anaconda3\envs\dse5002
\lib\site-packages (from plotnine) (1.15.2)
Requirement already satisfied: statsmodels>=0.14.0 in c:\users\water\anaconda3\envs
\dse5002\lib\site-packages (from plotnine) (0.14.4)
Requirement already satisfied: contourpy>=1.0.1 in c:\users\water\anaconda3\envs\dse
5002\lib\site-packages (from matplotlib!=3.6.1,>=3.4->seaborn) (1.3.1)
Requirement already satisfied: cycler>=0.10 in c:\users\water\anaconda3\envs\dse5002
\lib\site-packages (from matplotlib!=3.6.1,>=3.4->seaborn) (0.12.1)
Requirement already satisfied: fonttools>=4.22.0 in c:\users\water\anaconda3\envs\ds
e5002\lib\site-packages (from matplotlib!=3.6.1,>=3.4->seaborn) (4.56.0)
Requirement already satisfied: kiwisolver>=1.3.1 in c:\users\water\anaconda3\envs\ds
e5002\lib\site-packages (from matplotlib!=3.6.1,>=3.4->seaborn) (1.4.8)
Requirement already satisfied: packaging>=20.0 in c:\users\water\anaconda3\envs\dse5
002\lib\site-packages (from matplotlib!=3.6.1,>=3.4->seaborn) (24.2)
Requirement already satisfied: pillow>=8 in c:\users\water\anaconda3\envs\dse5002\li
b\site-packages (from matplotlib!=3.6.1,>=3.4->seaborn) (11.1.0)
Requirement already satisfied: pyparsing>=2.3.1 in c:\users\water\anaconda3\envs\dse
5002\lib\site-packages (from matplotlib!=3.6.1,>=3.4->seaborn) (3.2.1)
Requirement already satisfied: six>=1.5 in c:\users\water\anaconda3\envs\dse5002\lib
\site-packages (from python-dateutil>=2.8.2->pandas) (1.16.0)
Requirement already satisfied: patsy>=0.5.6 in c:\users\water\anaconda3\envs\dse5002
\lib\site-packages (from statsmodels>=0.14.0->plotnine) (1.0.1)
```

In [71]:
```
import pandas as pd
import numpy as np
import seaborn as sns
import plotnine as p9
```

In [72]:
```
# make sure heart.csv is in your current working directory, or list the full path n

infile=r".\data\heart.csv"

bp_df=pd.read_csv(infile)
bp_df.head()
```

Out[72]:

	Age	Sex	ChestPainType	RestingBP	Cholesterol	FastingBS	RestingECG	MaxHR	Exer
0	40	M	ATA	140	289	0	Normal	172	
1	49	F	NAP	160	180	0	Normal	156	
2	37	M	ATA	130	283	0	ST	98	
3	48	F	ASY	138	214	0	Normal	108	
4	54	M	NAP	150	195	0	Normal	122	

Find or create the following

a.) -Find the dimensions, memory used, and other basic information

b.) -Run the data summary

c.) Change the appropriate variables to type Categorical

d.) -Create a pivot table (using the Pandas groupby operation) showing mean Resting BP by Sex, Resting ECG and HeartDisease-What does this tell you? What else can you figure out using a Pivot table, show me two other helpful pivot tables based on different variables, different groupings or different aggregation functions (count, mean, max etc)

e.) -Show a histogram and the ECDF (empirical cumulative distribution function) for several continuous variables in the data set, in broad terms, what do the distributions look like, normal? exponential, poison-like?, uniform? Does this match your expectations?

```
https://seaborn.pydata.org/generated/seaborn.ecdfplot.html
https://matplotlib.org/stable/api/_as_gen/matplotlib.pyplot.ecdf.html
```

f.) -Show An SNS Pairplot, the most informative version you can find, set the hue based on Heart Disease, try using at least one other variable as the Hue. Discuss what you think you are seeing in this plot

g.) Create several useful or informative boxplots of continuous variables by category, using Seaborn or PlotNine. Find an interesting result or contrast among the variables, discuss what you think it means or implies

h.) Create violin plots of these same results

i.) Find the mean, median and standard deviation of the Max heartrate variable in this data set

Turn this into a pivot table, grouping by one or more predictors.

Create all these results in this Notebook and turn it in

Source

Pandas Docs

Part A

a.) -Find the dimensions, memory used, and other basic information

In [73]:
```
bp_df.info()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 918 entries, 0 to 917
Data columns (total 12 columns):
 #   Column          Non-Null Count  Dtype  
---  ------          --------------  -----  
 0   Age             918 non-null    int64  
 1   Sex             918 non-null    object 
 2   ChestPainType   918 non-null    object 
 3   RestingBP       918 non-null    int64  
 4   Cholesterol     918 non-null    int64  
 5   FastingBS       918 non-null    int64  
 6   RestingECG      918 non-null    object 
 7   MaxHR           918 non-null    int64  
 8   ExerciseAngina  918 non-null    object 
 9   Oldpeak         918 non-null    float64
 10  ST_Slope        918 non-null    object 
 11  HeartDisease    918 non-null    int64  
dtypes: float64(1), int64(6), object(5)
memory usage: 86.2+ KB
```

Part B

b.) -Run the data summary

In [74]:
```
bp_df.describe()
```

Out[74]:

	Age	RestingBP	Cholesterol	FastingBS	MaxHR	Oldpeak	HeartDisea
count	918.000000	918.000000	918.000000	918.000000	918.000000	918.000000	918.0000
mean	53.510893	132.396514	198.799564	0.233115	136.809368	0.887364	0.5533
std	9.432617	18.514154	109.384145	0.423046	25.460334	1.066570	0.4974
min	28.000000	0.000000	0.000000	0.000000	60.000000	-2.600000	0.0000
25%	47.000000	120.000000	173.250000	0.000000	120.000000	0.000000	0.0000
50%	54.000000	130.000000	223.000000	0.000000	138.000000	0.600000	1.0000
75%	60.000000	140.000000	267.000000	0.000000	156.000000	1.500000	1.0000
max	77.000000	200.000000	603.000000	1.000000	202.000000	6.200000	1.0000

Part C

c.) Change the appropriate variables to type Categorical

Starting with the long approach here, I think this can be improved, though.

In [75]:
```
# Get unique values from the categorical columns
chest_pain_cats, sex_cats, resting_ecg_cats, exercise_angina_cats, st_slope_cats, h

#Set the chest pain type column to categorical with the categories defined by the u
bp_df["ChestPainType"] = pd.Categorical(bp_df["ChestPainType"], categories=chest_pa
bp_df["Sex"] = pd.Categorical(bp_df["Sex"], categories=sex_cats)
bp_df["RestingECG"] =  pd.Categorical(bp_df["RestingECG"], categories=resting_ecg_c
bp_df["ExerciseAngina"] = pd.Categorical(bp_df["ExerciseAngina"], categories=exerci
bp_df["ST_Slope"] = pd.Categorical(bp_df["ST_Slope"], categories=st_slope_cats)
bp_df["HeartDisease"] = pd.Categorical(bp_df["HeartDisease"], categories=heart_dise
bp_df["FastingBS"] = pd.Categorical(bp_df["FastingBS"], categories=fasting_bs_cats)

#Verify
bp_df.info()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 918 entries, 0 to 917
Data columns (total 12 columns):
 #   Column          Non-Null Count  Dtype
---  ------          --------------  -----
 0   Age             918 non-null    int64
 1   Sex             918 non-null    category
 2   ChestPainType   918 non-null    category
 3   RestingBP       918 non-null    int64
 4   Cholesterol     918 non-null    int64
 5   FastingBS       918 non-null    category
 6   RestingECG      918 non-null    category
 7   MaxHR           918 non-null    int64
 8   ExerciseAngina  918 non-null    category
 9   Oldpeak         918 non-null    float64
 10  ST_Slope        918 non-null    category
 11  HeartDisease    918 non-null    category
dtypes: category(7), float64(1), int64(4)
memory usage: 43.2 KB
```

Now, let's make this a bit more functional...

In [76]:
```python
# Read in the original df
bp_df_original=pd.read_csv(infile)

# Convert HeartDisease and FastingBS to objects, as these are the exceptions for th
bp_df_original["HeartDisease"] = bp_df_original["HeartDisease"].astype("object")
bp_df_original["FastingBS"] = bp_df_original["FastingBS"].astype("object")

# All columns with the dtype "object" will become our categorical columns. Loop thr
for col in bp_df_original.columns:
    if bp_df_original[f"{col}"].dtype == "object":
        categories = pd.unique(bp_df_original[f"{col}"])
        bp_df_original[f"{col}"] = pd.Categorical(bp_df_original[f"{col}"], categor

#Verify
bp_df_original.info()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 918 entries, 0 to 917
Data columns (total 12 columns):
 #   Column          Non-Null Count  Dtype
---  ------          --------------  -----
 0   Age             918 non-null    int64
 1   Sex             918 non-null    category
 2   ChestPainType   918 non-null    category
 3   RestingBP       918 non-null    int64
 4   Cholesterol     918 non-null    int64
 5   FastingBS       918 non-null    category
 6   RestingECG      918 non-null    category
 7   MaxHR           918 non-null    int64
 8   ExerciseAngina  918 non-null    category
 9   Oldpeak         918 non-null    float64
 10  ST_Slope        918 non-null    category
 11  HeartDisease    918 non-null    category
dtypes: category(7), float64(1), int64(4)
memory usage: 43.2 KB
```

Great, now this is flexible and can be applied to arbitrarily large data sets. Much better than manually doing each type change.

Part D

d.) -Create a pivot table (using the Pandas groupby operation) showing mean Resting BP by Sex, Resting ECG and HeartDisease-What does this tell you? What else can you figure out using a Pivot table, show me two other helpful pivot tables based on different variables, different groupings or different aggregation functions (count, mean, max etc)

In [77]:
```
bp_df[["RestingBP", "Sex"]].groupby(["Sex"]).mean()
```

```
C:\Users\water\AppData\Local\Temp\ipykernel_22168\233112352.py:1: FutureWarning: The
default of observed=False is deprecated and will be changed to True in a future vers
ion of pandas. Pass observed=False to retain current behavior or observed=True to ad
opt the future default and silence this warning.
```

Out[77]:

	RestingBP
Sex	
M	132.445517
F	132.212435

In [78]:
```
bp_df[["RestingBP", "RestingECG"]].groupby(["RestingECG"]).mean()
```

```
C:\Users\water\AppData\Local\Temp\ipykernel_22168\2621982121.py:1: FutureWarning: Th
e default of observed=False is deprecated and will be changed to True in a future ve
rsion of pandas. Pass observed=False to retain current behavior or observed=True to
adopt the future default and silence this warning.
```

Out[78]:

RestingECG	RestingBP
Normal	130.635870
ST	135.808989
LVH	134.335106

In [79]:
```
bp_df[["RestingBP", "HeartDisease"]].groupby(["HeartDisease"]).mean()
```

```
C:\Users\water\AppData\Local\Temp\ipykernel_22168\2443954490.py:1: FutureWarning: Th
e default of observed=False is deprecated and will be changed to True in a future ve
rsion of pandas. Pass observed=False to retain current behavior or observed=True to
adopt the future default and silence this warning.
```

Out[79]:

HeartDisease	RestingBP
0	130.180488
1	134.185039

These pivot tables help highlight the respective relationship between sex, resting ECG, heart disease, and mean resting blood pressure.

Now, lets take a look at how MaxHR is related to heart disease

In [80]:
```
bp_df[["MaxHR", "HeartDisease"]].groupby(["HeartDisease"]).mean()
```

```
C:\Users\water\AppData\Local\Temp\ipykernel_22168\1575525349.py:1: FutureWarning: Th
e default of observed=False is deprecated and will be changed to True in a future ve
rsion of pandas. Pass observed=False to retain current behavior or observed=True to
adopt the future default and silence this warning.
```

Out[80]:

HeartDisease	MaxHR
0	148.151220
1	127.655512

Okay, this is what I would expect. Heart disease has a significant impact on max heartrate, which is a good indicator of overall cardiovascular fitness. There is, however, a confounding variable here, which is age. Let's see the average ages of people with and without heart disease...

In [81]:
```
bp_df[["Age", "HeartDisease"]].groupby(["HeartDisease"]).mean()
```

```
C:\Users\water\AppData\Local\Temp\ipykernel_22168\1810670197.py:1: FutureWarning: The default of observed=False is deprecated and will be changed to True in a future version of pandas. Pass observed=False to retain current behavior or observed=True to adopt the future default and silence this warning.
```

Out[81]:

HeartDisease	Age
0	50.551220
1	55.899606

Ahhh, okay. Since max heart rate is a function of age, as is the propensity for heart disease, I hypothesized that the heart disease group might be older on average. This hypothesis ended up being correct, as the heart disease group is about 5 years older on average than the non-heart disease group. Without any further analysis, it is implied that both age and heart disease affect max heart rate.

Part E

e.) -Show a histogram and the ECDF (empirical cumulative distribution function) for several continuous variables in the data set, in broad terms, what do the distributions look like, normal? exponential, poison-like?, uniform? Does this match your expectations?

ECDF Source - Seaborn

ECDF Source - Matplotlib

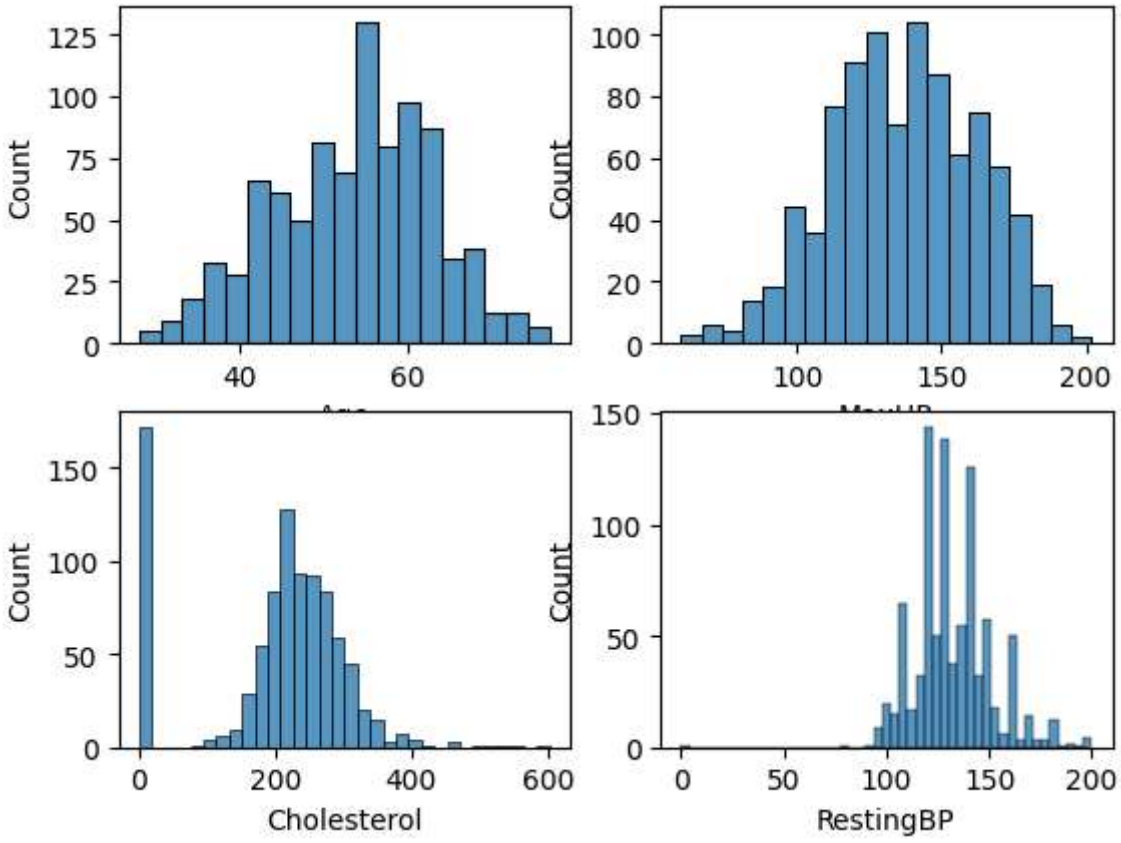
Let's do this with both seaborn and matplotlib to see how they differ. First, seaborn... Plot the hist and

ecdf for age, maxhr, cholestrol, and restingbp. I am going to cheat a bit and use the matplotlib subplot feature to pack everything into one plot and make this more compact.

In [82]:
```
import matplotlib.pyplot as plt
```

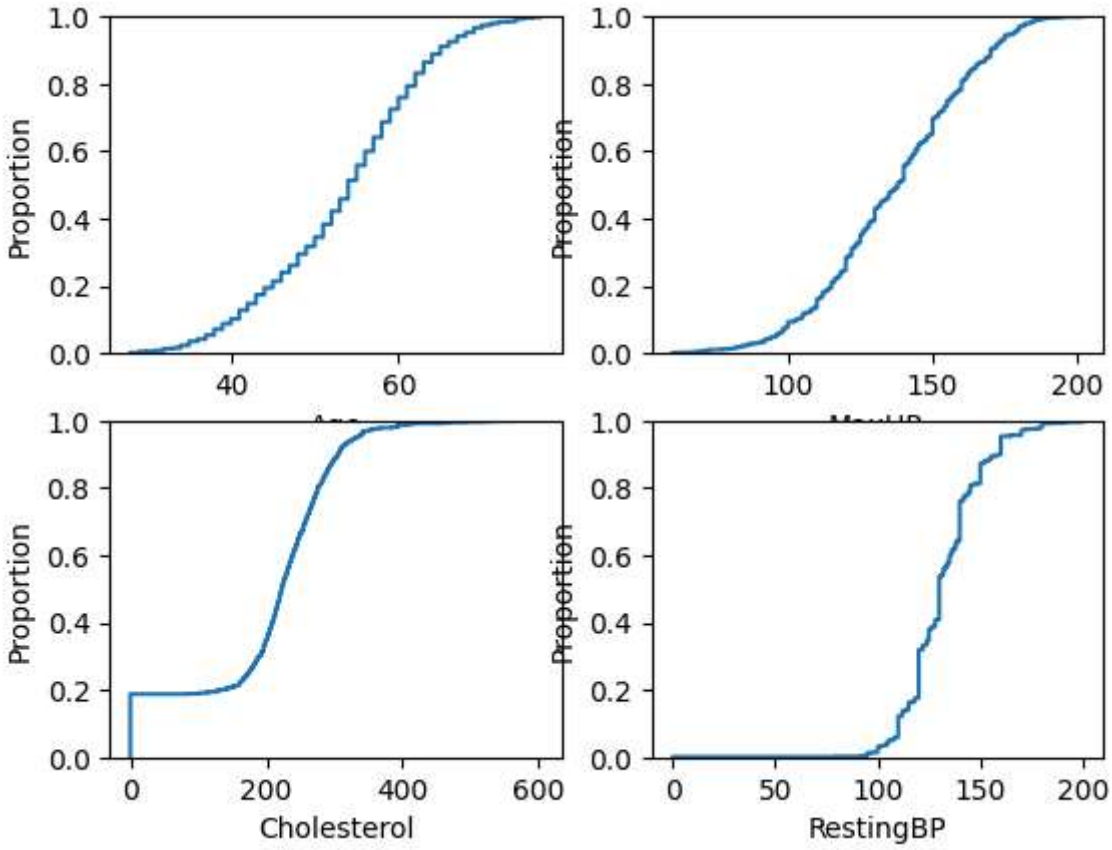
In [83]:
```
fig, axs = plt.subplots(nrows=2,ncols=2)
sns.histplot(bp_df["Age"], ax=axs[0,0])
sns.histplot(bp_df["MaxHR"], ax=axs[0,1])
sns.histplot(bp_df["Cholesterol"], ax=axs[1,0])
sns.histplot(bp_df["RestingBP"], ax=axs[1,1])
```

Out[83]: <Axes: xlabel='RestingBP', ylabel='Count'>



In [84]:
```
fig, axs = plt.subplots(nrows=2,ncols=2)
sns.ecdfplot(bp_df["Age"], ax=axs[0,0])
sns.ecdfplot(bp_df["MaxHR"], ax=axs[0,1])
sns.ecdfplot(bp_df["Cholesterol"], ax=axs[1,0])
sns.ecdfplot(bp_df["RestingBP"], ax=axs[1,1])
```

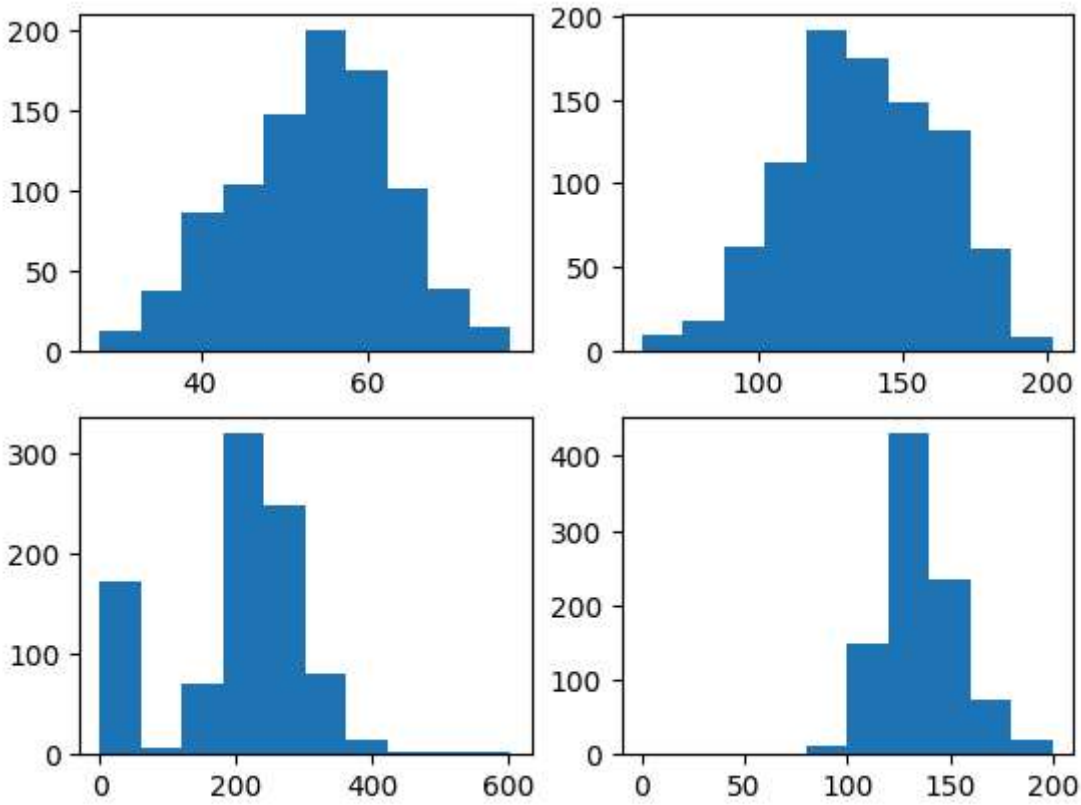
Out[84]: <Axes: xlabel='RestingBP', ylabel='Proportion'>



That was relatively painless. Now, let's try matplotlib.

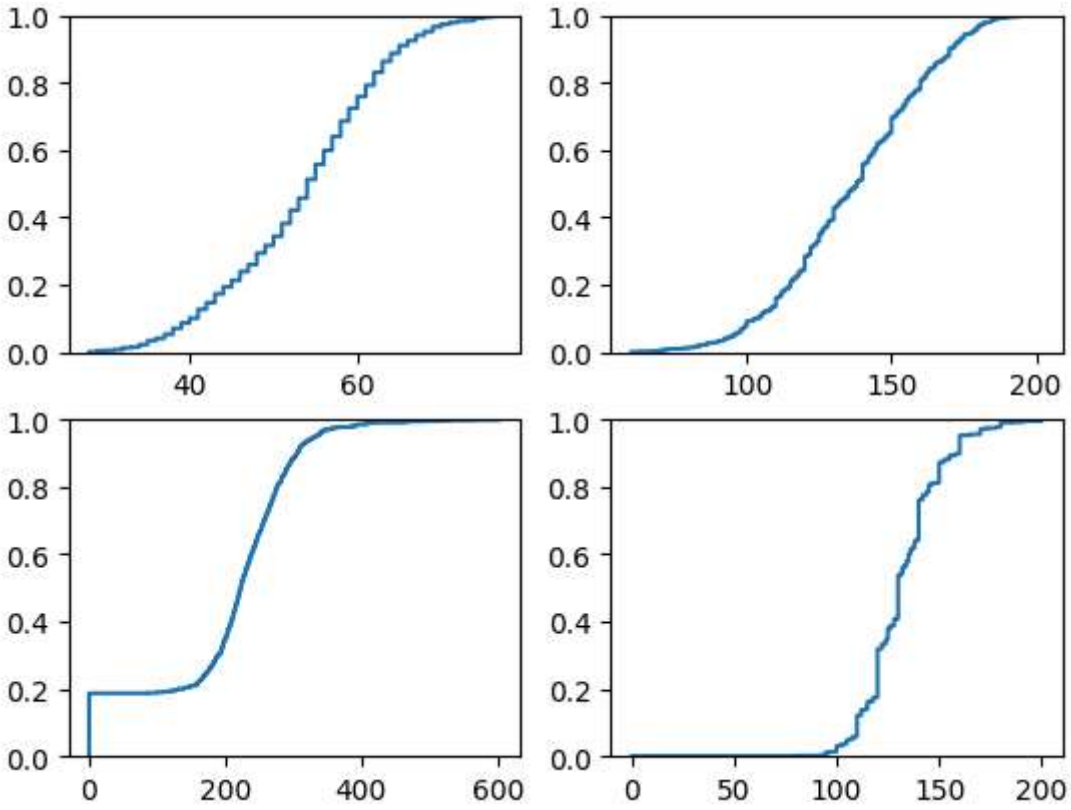
In [85]:
```
fig, axs = plt.subplots(nrows=2,ncols=2)
axs[0,0].hist(bp_df["Age"])
axs[0,1].hist(bp_df["MaxHR"])
axs[1,0].hist(bp_df["Cholesterol"])
axs[1,1].hist(bp_df["RestingBP"])
```

Out[85]:
```
(array([  1.,   0.,   0.,   0.,  12., 148., 430., 234.,  73.,  20.]),
 array([  0.,  20.,  40.,  60.,  80., 100., 120., 140., 160., 180., 200.]),
 <BarContainer object of 10 artists>)
```



In [86]:
```
fig, axs = plt.subplots(nrows=2,ncols=2)
axs[0,0].ecdf(bp_df["Age"])
axs[0,1].ecdf(bp_df["MaxHR"])
axs[1,0].ecdf(bp_df["Cholesterol"])
axs[1,1].ecdf(bp_df["RestingBP"])
```

Out[86]:
```
<matplotlib.lines.Line2D at 0x1cf954560c0>
```



Slightly different, but I would say comparable effort. In the future, it seems like matplotlib will be better for this kind of analysis because of the multiplotting feature. That was not something I could find in seaborn for unrelated plots.

Time to discuss the plots... they are strongly normally distributed, aside from outliers in the cholesterol and resting blood pressure charts. Cholesterol has a large count of 0, which I assume are people who did not have their cholesterol measured, otherwise they would be dead. I assume the same is true for the set of blood pressure measurements that were 0, but that seems to only be one person.

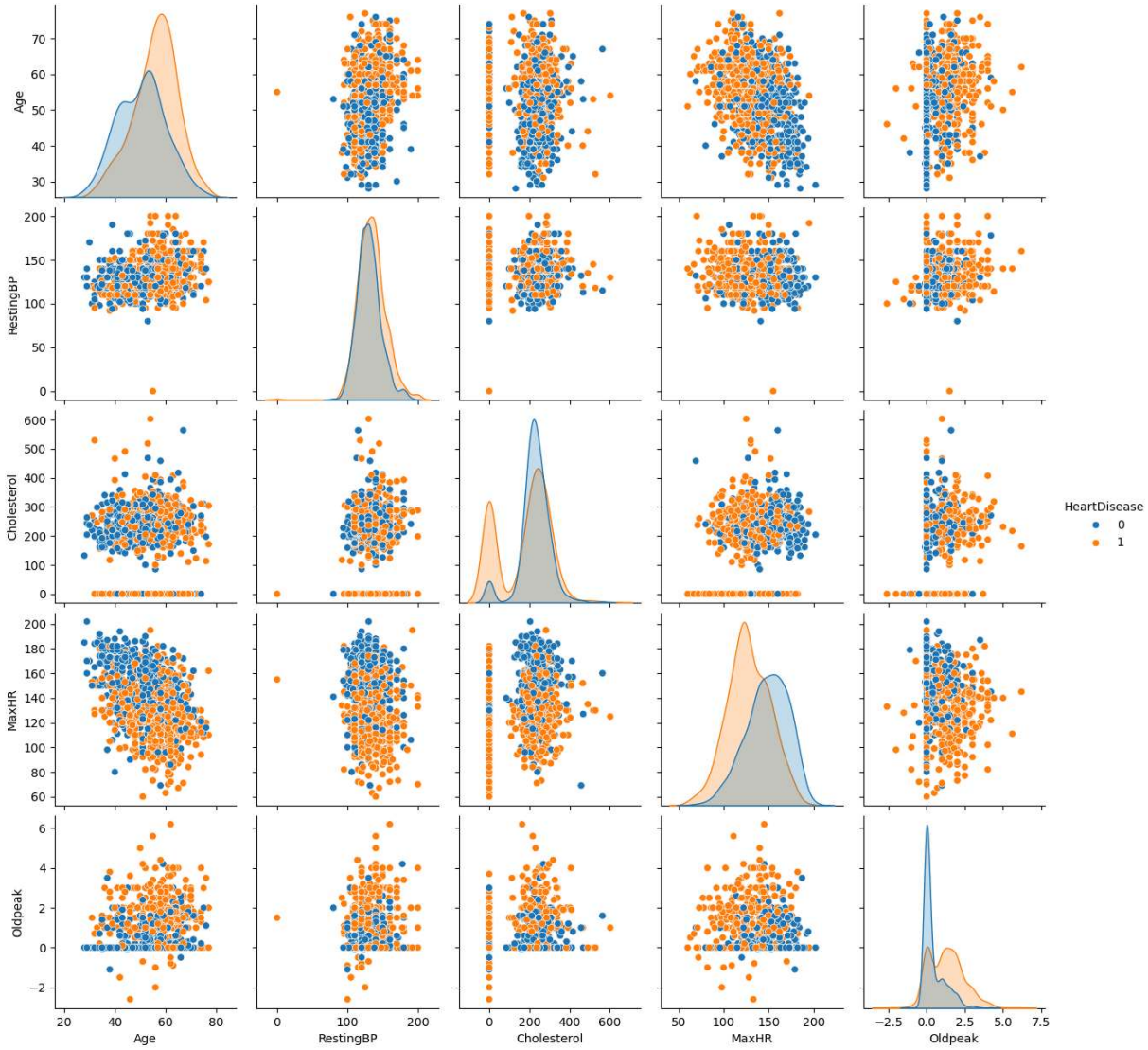
Part F

f.) -Show An SNS Pairplot, the most informative version you can find, set the hue based on Heart Disease, try using at least one other variable as the Hue. Discuss what you think you

are seeing in this plot

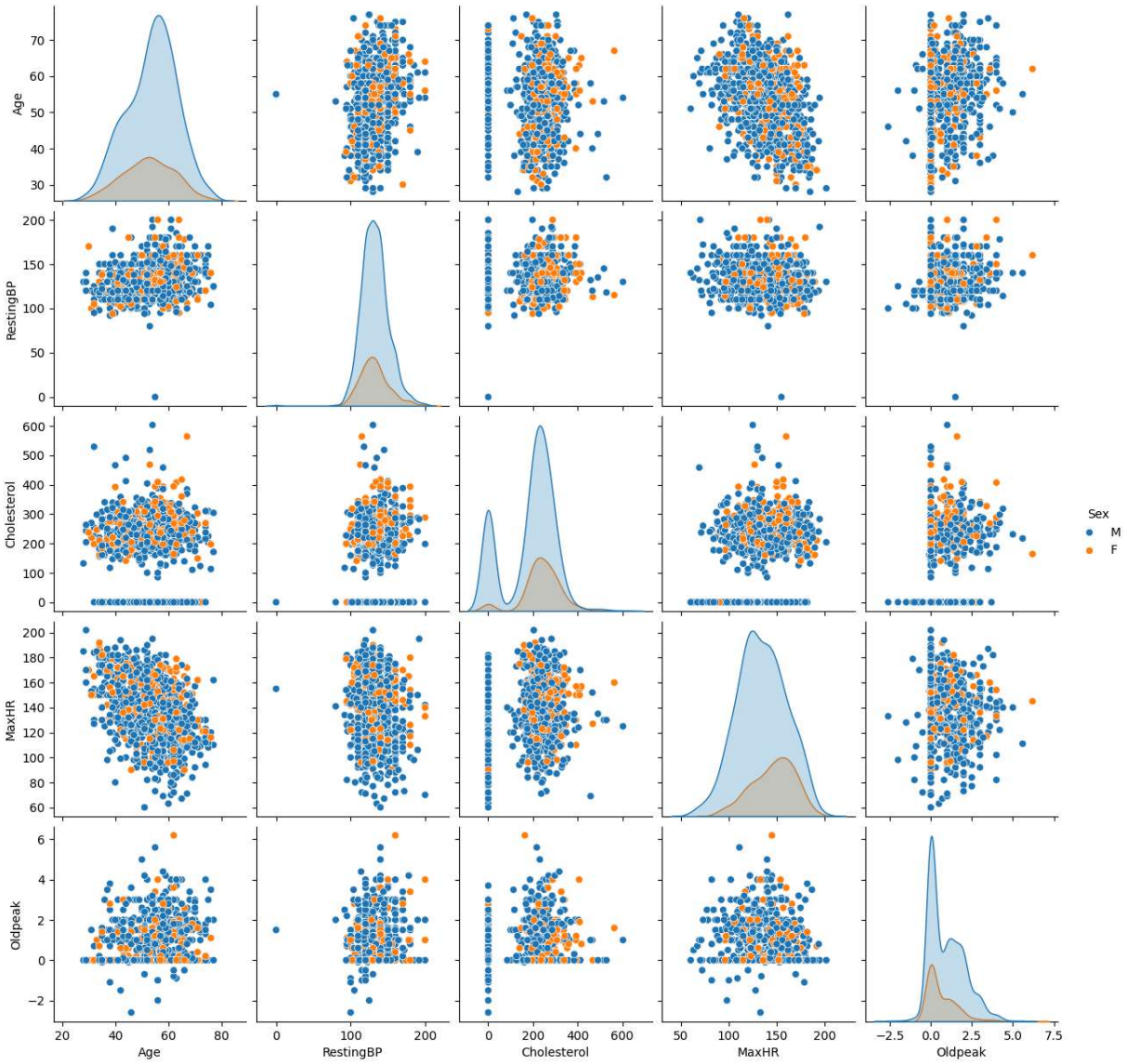
In [87]:
```
sns.pairplot(bp_df, hue="HeartDisease")
```

Out[87]: <seaborn.axisgrid.PairGrid at 0x1cf928559d0>



In [88]:
```
sns.pairplot(bp_df, hue="Sex")
```

Out[88]: <seaborn.axisgrid.PairGrid at 0x1d0029fe450>



The pairplot chart seems to compare all continuous variables against each other, with the hue as the categorical measure. The grid spaces where the variables are compared to themselves feature a distribution plot. This is very similar to the pairplot in R, but unlike R, the correlation between the variables is not explicitly defined.

Part G

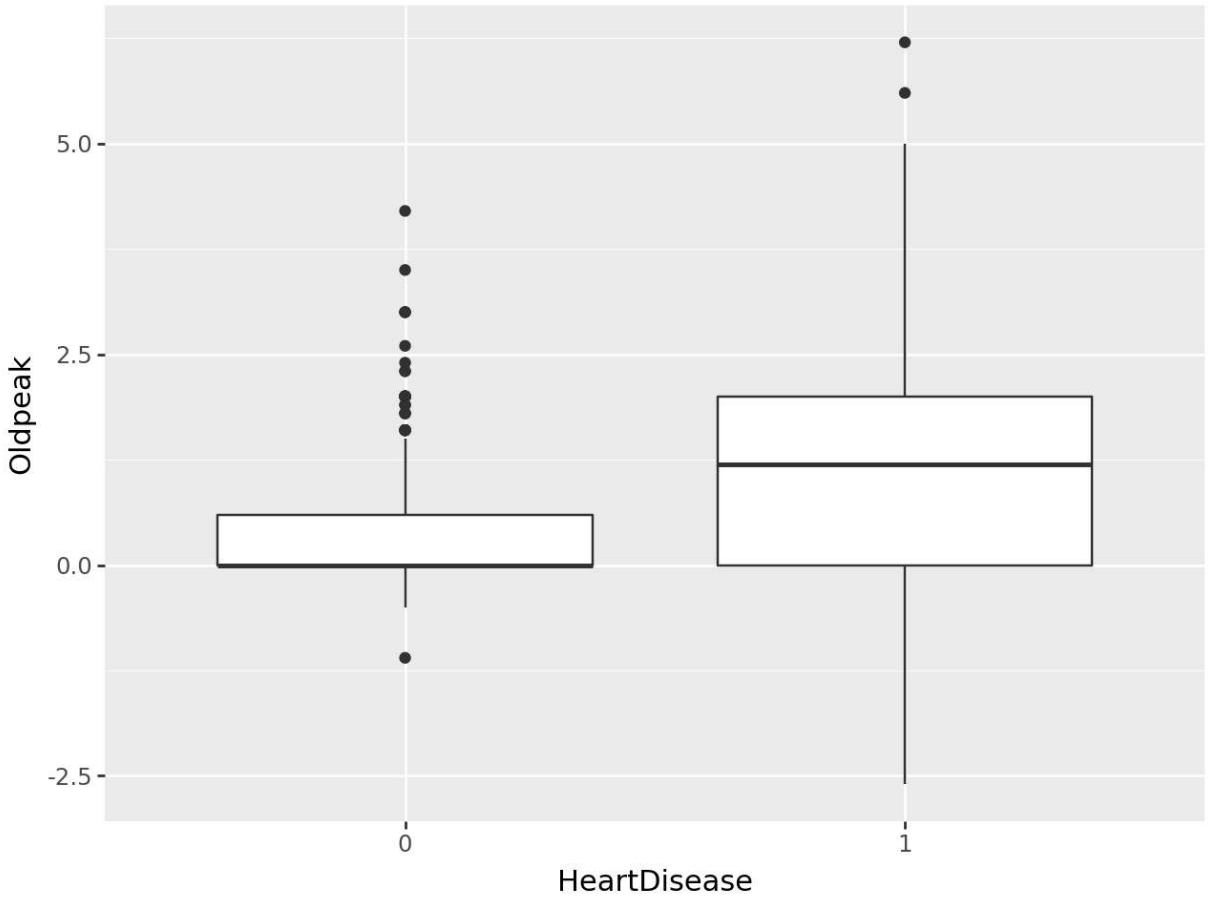
g.) Create several useful or informative boxplots of continuous variables by category, using Seaborn or PlotNine. Find an interesting result or contrast among the variables, discuss what you think it means or implies

Using plotnine here to see how it works...

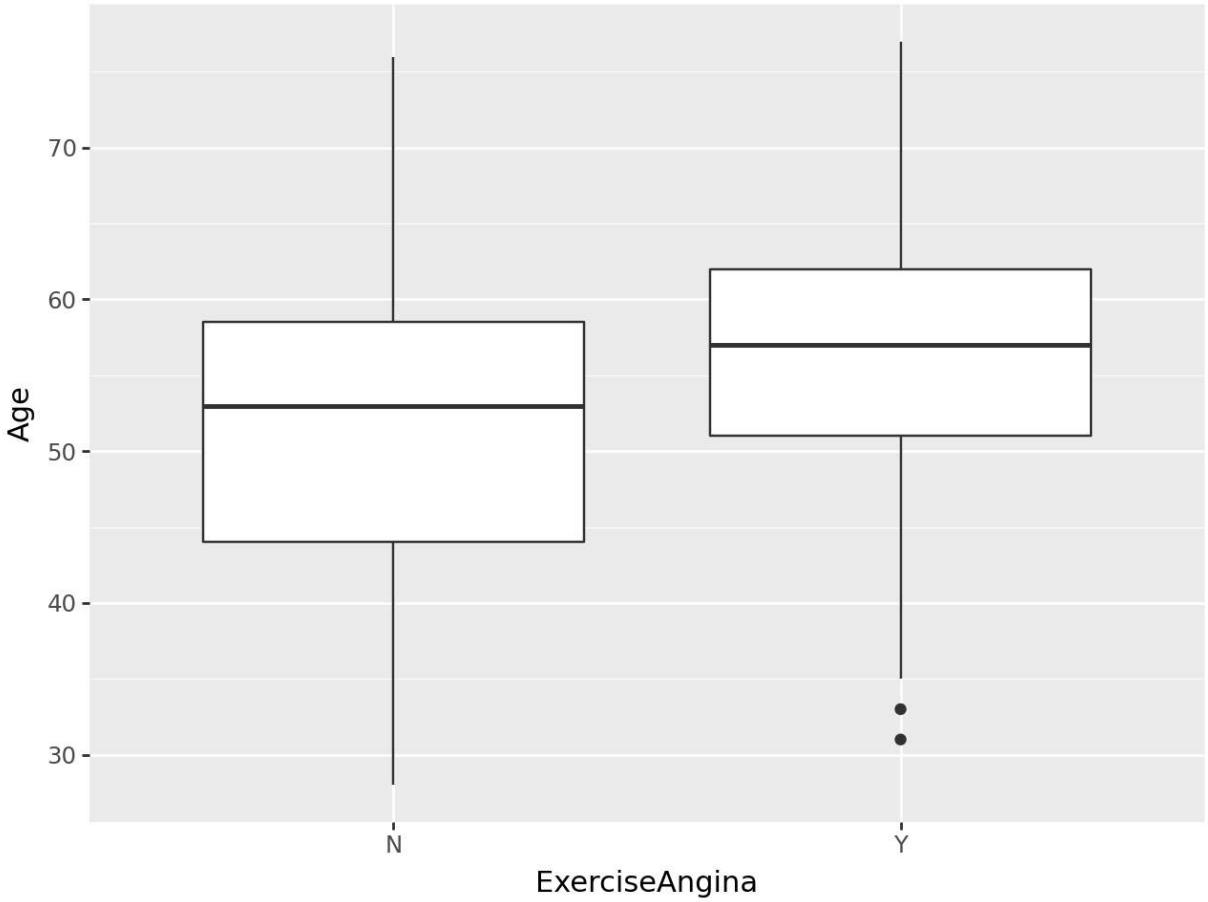
PlotNine Reference

Immediately, I get the sense that this is a python implementation of the ggplot R library. The syntax is identical.

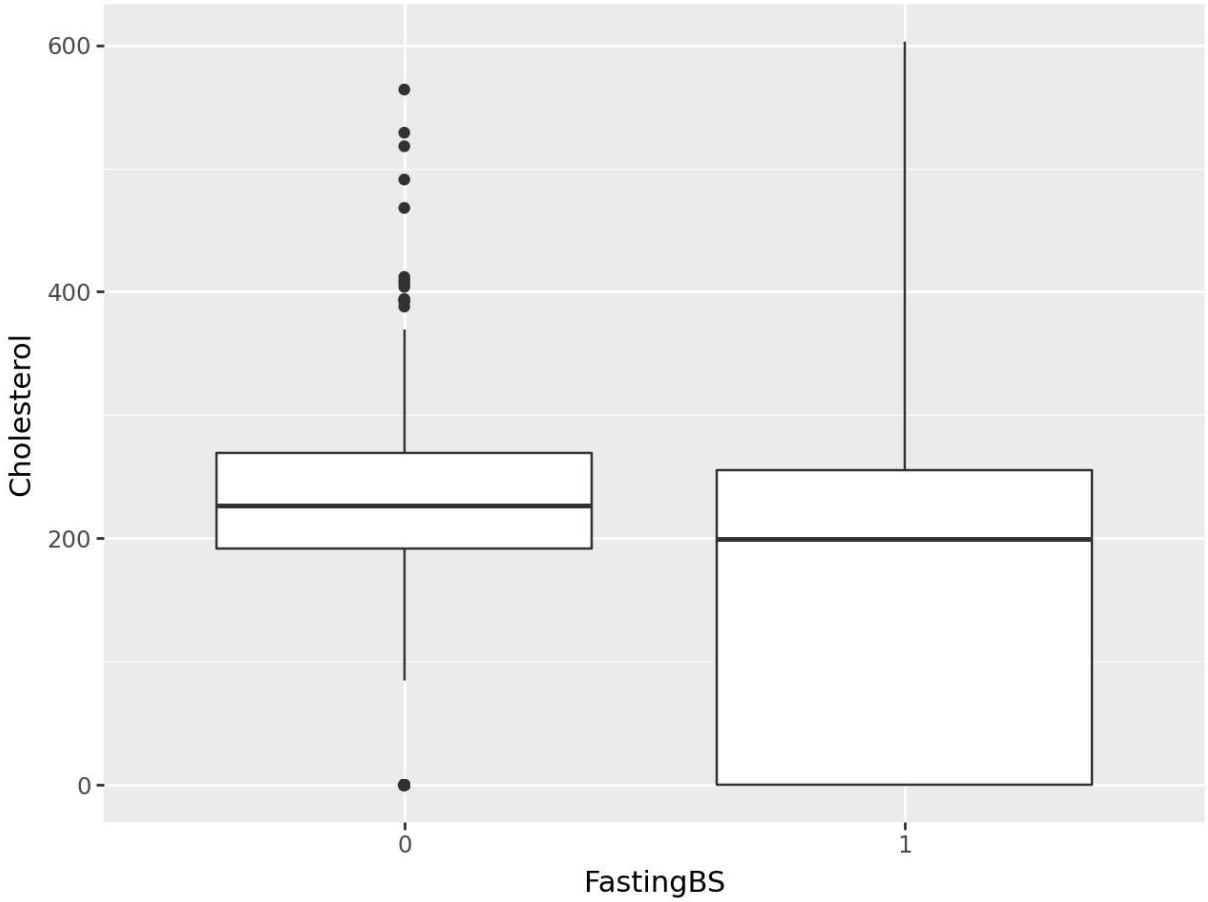
In [93]:
```
ggplot = p9.ggplot
geom_boxplot = p9.geom_boxplot
aes=p9.aes

(
    ggplot(bp_df)
    + geom_boxplot(aes(x="HeartDisease", y="Oldpeak"))
)
```



In [94]:
```
(
    ggplot(bp_df)
    + geom_boxplot(aes(x="ExerciseAngina", y="Age"))
)
```



In [95]:
```
(
    ggplot(bp_df)
    + geom_boxplot(aes(x="FastingBS", y="Cholesterol"))
)
```



Based on how these graphs look, it seems like plotnine literally ports R's rendering engine into python. Pretty neat. I already have R on my machine, but I would be interested in knowing if this package requires R to be installed, or if it installs the rendering engine as part of the package.

Part H

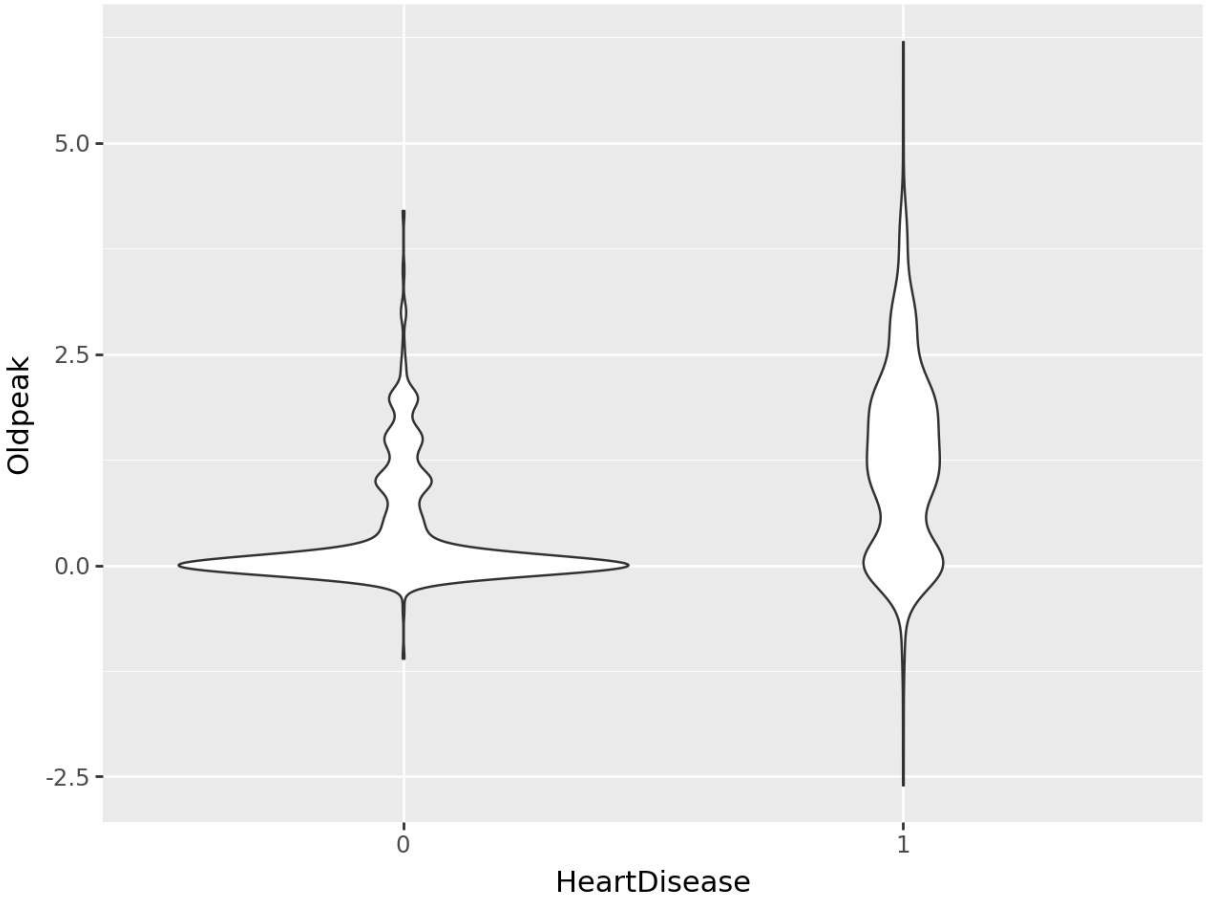
h.) Create violin plots of these same results

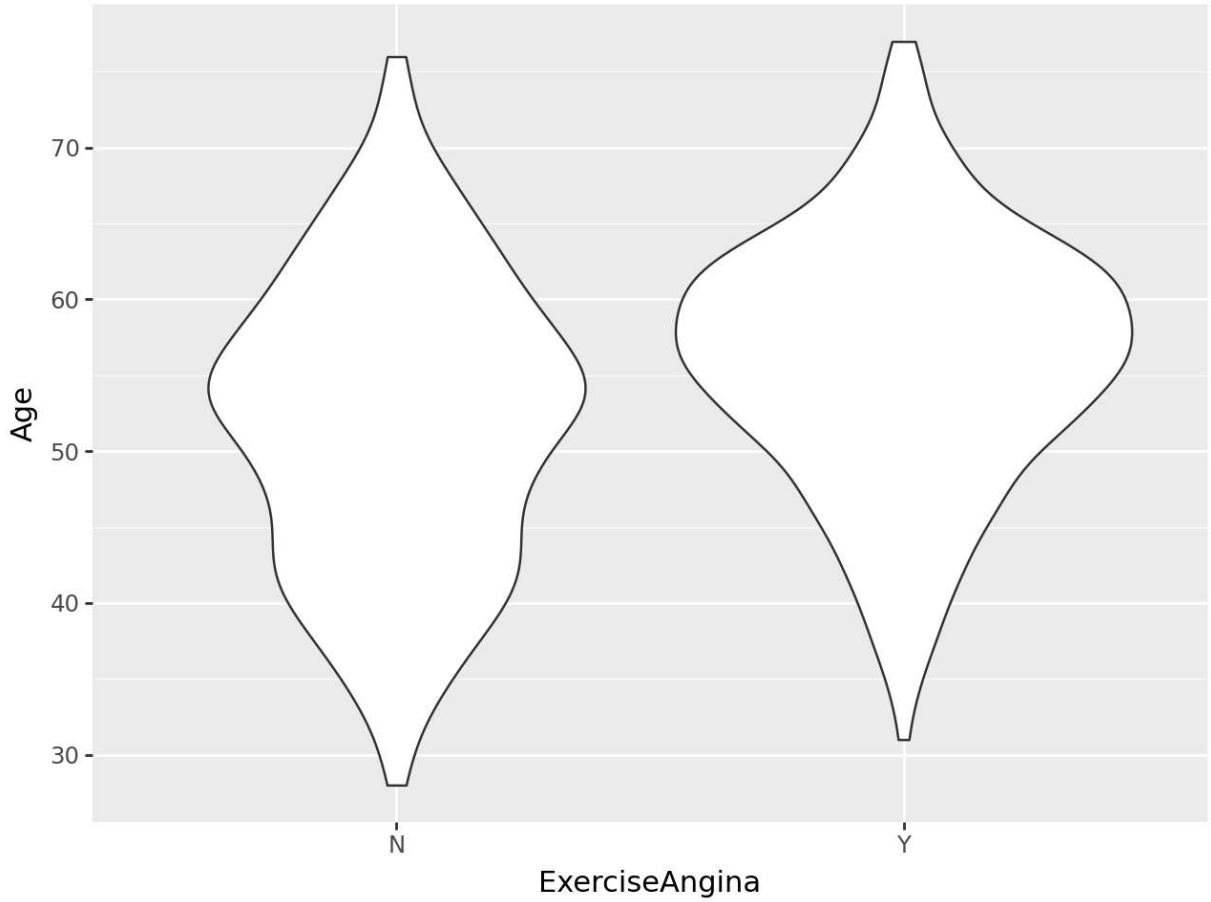
This is pretty easy to do in R with ggplot, but this would be a good time to compare and contrast libraries.

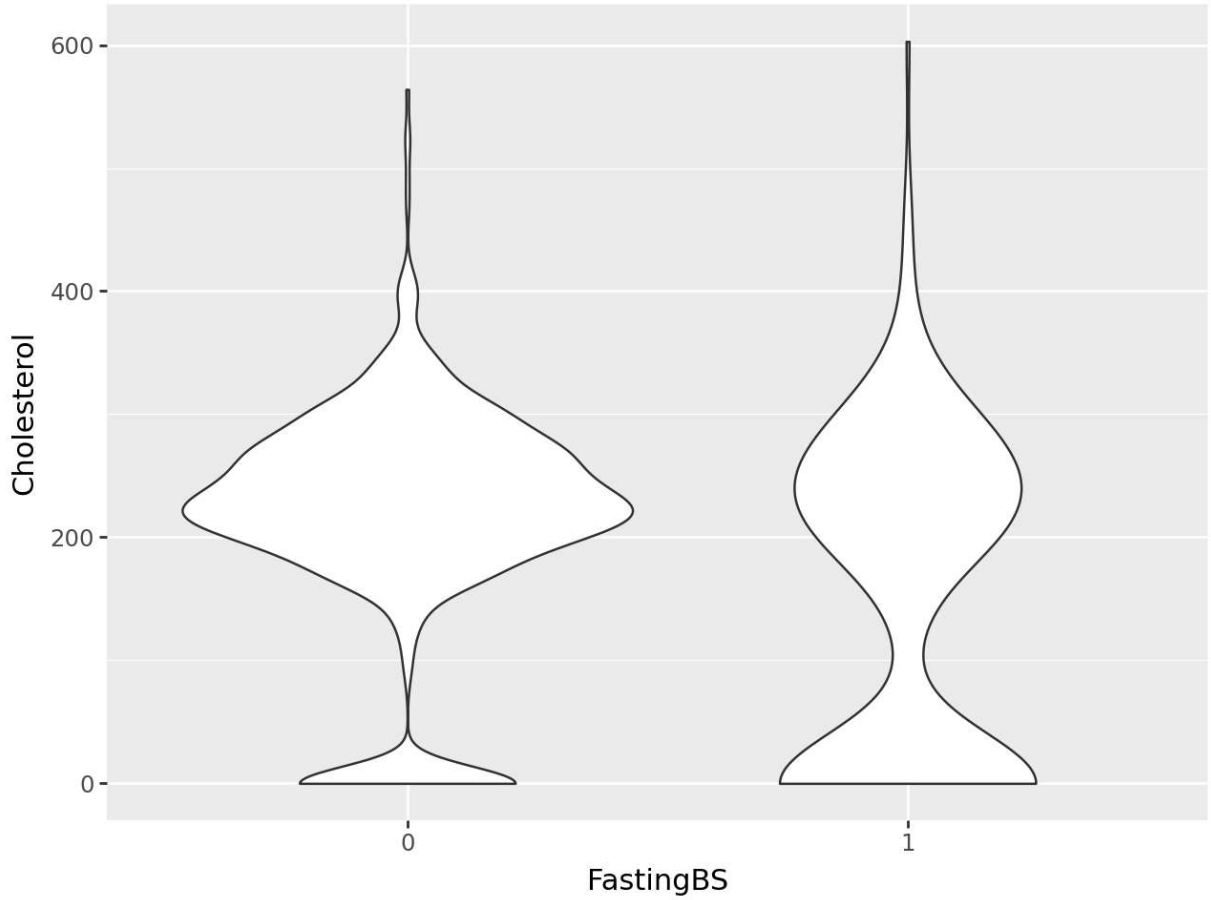
Plotnine implementation:

In [114…

```
geom_violin = p9.geom_violin

plt1 = (
    ggplot(bp_df)
    + geom_violin(aes(x="HeartDisease", y="Oldpeak"))
)

plt2 = (
    ggplot(bp_df)
    + geom_violin(aes(x="ExerciseAngina", y="Age"))
)

plt3 = (
    ggplot(bp_df)
    + geom_violin(aes(x="FastingBS", y="Cholesterol"))
)

for i, plot in enumerate([plt1,plt2,plt3]):
    plot.show()
```

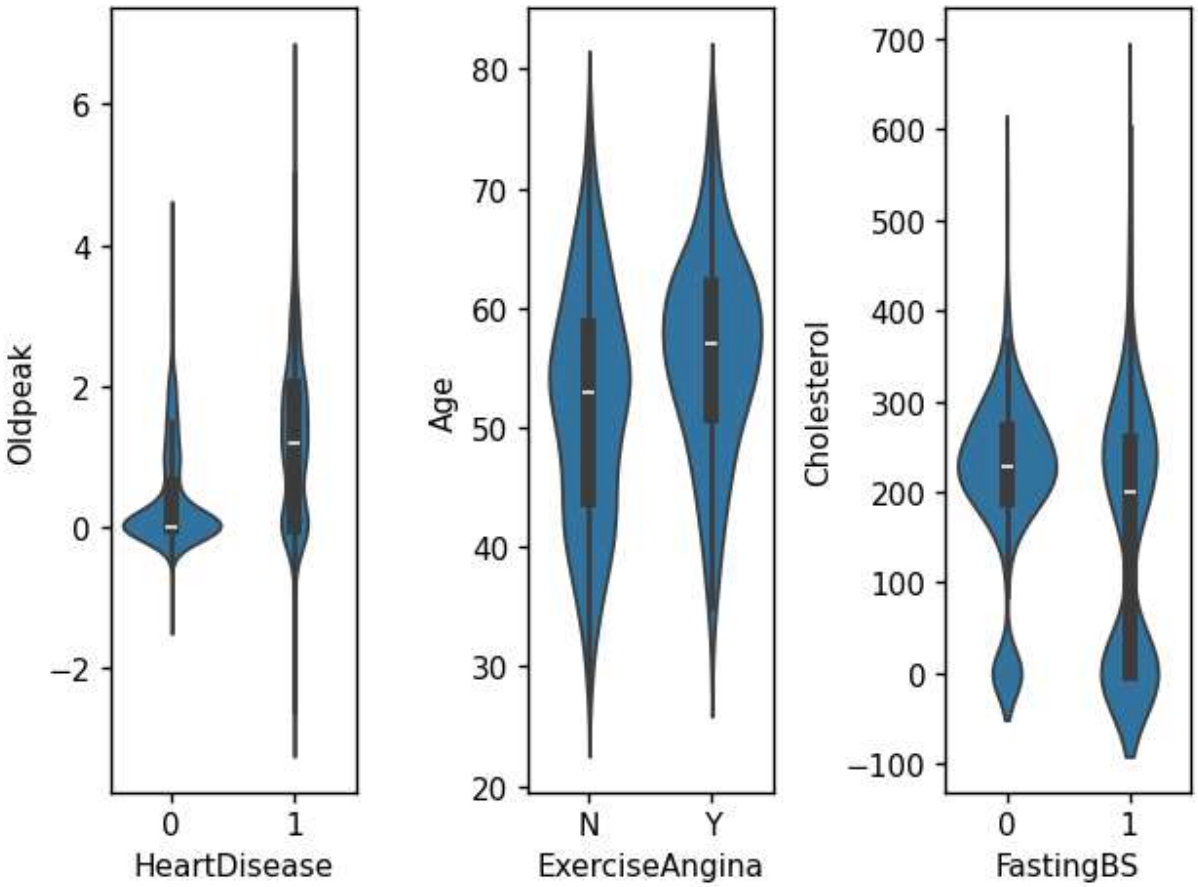



70
60
50
40
30
Age
N
Y
ExerciseAngina


600
400
200
0
Cholesterol
0
1
FastingBS

Seaborn Implementation:

In [ ]:
```
fig, axs = plt.subplots(ncols=3)

sns.violinplot(data=bp_df, x="HeartDisease", y="Oldpeak", ax=axs[0])
sns.violinplot(data=bp_df, x="ExerciseAngina", y="Age", ax=axs[1])
sns.violinplot(data=bp_df, x="FastingBS", y="Cholesterol", ax=axs[2])

plt.tight_layout()
```



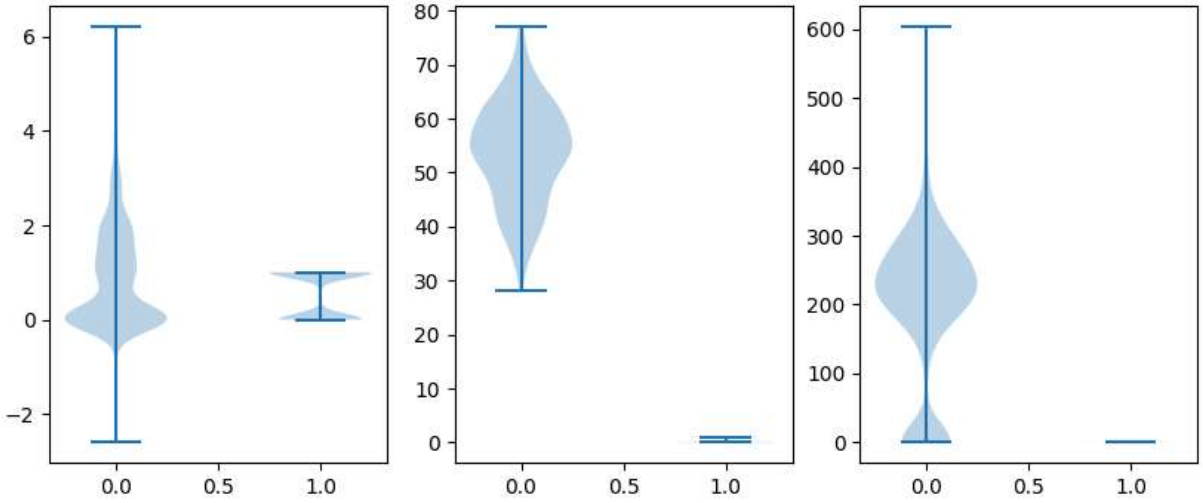
Matplotlib Implementation:

In [148…
```
fig, axs = plt.subplots(ncols=3, figsize=(10, 4))

# After messing around with this for a while, it became clear that matplotlibs viol
# categorical variable is not an integer. Let's convert ExerciseAngina to an int.
converted = bp_df["ExerciseAngina"].replace(["Y","N"], [1,0])

axs[0].violinplot(bp_df[["Oldpeak", "HeartDisease"]], positions=[0,1])
axs[1].violinplot([bp_df["Age"], converted], positions=[0,1])
axs[2].violinplot(bp_df[["Cholesterol","FastingBS"]], positions=[0,1])
```

```
C:\Users\water\AppData\Local\Temp\ipykernel_22168\3703374422.py:5: FutureWarning: Do
wncasting behavior in `replace` is deprecated and will be removed in a future versio
n. To retain the old behavior, explicitly call `result.infer_objects(copy=False)`. T
o opt-in to the future behavior, set `pd.set_option('future.no_silent_downcasting',
True)`
C:\Users\water\AppData\Local\Temp\ipykernel_22168\3703374422.py:5: FutureWarning: Th
e behavior of Series.replace (and DataFrame.replace) with CategoricalDtype is deprec
ated. In a future version, replace will only be used for cases that preserve the cat
egories. To change the categories, use ser.cat.rename_categories instead.
```

Out[148…

```
{'bodies': [<matplotlib.collections.FillBetweenPolyCollection at 0x1d01296b440>,
  <matplotlib.collections.FillBetweenPolyCollection at 0x1d014acbbc0>],
 'cmaxes': <matplotlib.collections.LineCollection at 0x1d012954bc0>,
 'cmins': <matplotlib.collections.LineCollection at 0x1d012f86e70>,
 'cbars': <matplotlib.collections.LineCollection at 0x1d0129031d0>}
```



I could be doing something wrong here, but it doesn't seem like matplotlib is equipped to properly handle categorical data in violin plots. Good thing there are two other libraries that do this just fine :).

Part I

i.) Find the mean, median and standard deviation of the Max heartrate variable in this data set. Turn this into a pivot table, grouping by one or more predictors.

In [149…

```
# First find these metrics on the MaxHR data alone.
mean = bp_df["MaxHR"].mean()
median = bp_df["MaxHR"].median()
std = bp_df["MaxHR"].std()

print(f"Mean: {mean}\t\tMedian: {median}\t\tStandard Deviation: {std}")
```

```
Mean: 136.80936819172112        Median: 138.0        Standard Deviation:
25.4603341382503
```

In [ ]:
```
# Now, pivot tables
bp_df[["MaxHR", "Age"]].groupby("Age").mean()
```

Out[ ]:

Age	MaxHR
28	185.0
29	170.0
30	170.0
31	151.5
32	155.0
33	167.5
34	174.0
35	156.0
36	175.0
37	158.0
38	150.0
39	150.0
40	152.0
41	159.0
42	151.0
43	144.0
44	153.0
45	144.0
46	136.5
47	145.0
48	138.0
49	145.0
50	140.0
51	139.0
52	143.5
53	130.0
54	140.0
55	136.0
56	124.5

Age	MaxHR
57	135.5
58	130.5
59	131.0
60	140.0
61	120.0
62	122.0
63	131.0
64	130.5
65	122.0
66	120.0
67	129.0
68	135.5
69	126.0
70	125.0
71	125.0
72	111.5
73	121.0
74	116.0
75	112.0
76	118.0
77	136.0

In [153…

```
bp_df[["MaxHR", "Age"]].groupby("Age").median()
```

Out[153…

Age	MaxHR
28	185.0
29	170.0
30	170.0
31	151.5
32	155.0
33	167.5
34	174.0
35	156.0
36	175.0
37	158.0
38	150.0
39	150.0
40	152.0
41	159.0
42	151.0
43	144.0
44	153.0
45	144.0
46	136.5
47	145.0
48	138.0
49	145.0
50	140.0
51	139.0
52	143.5
53	130.0
54	140.0
55	136.0
56	124.5

Age	MaxHR
57	135.5
58	130.5
59	131.0
60	140.0
61	120.0
62	122.0
63	131.0
64	130.5
65	122.0
66	120.0
67	129.0
68	135.5
69	126.0
70	125.0
71	125.0
72	111.5
73	121.0
74	116.0
75	112.0
76	118.0
77	136.0

In [154…

```
bp_df[["MaxHR", "Age"]].groupby("Age").std()
```

Out[154...

Age	MaxHR
28	NaN
29	21.939310
30	NaN
31	2.121320
32	24.035391
33	24.748737
34	16.399768
35	20.300022
36	21.979536
37	26.481898
38	22.860446
39	21.974661
40	30.222466
41	20.633271
42	23.724522
43	20.522125
44	24.378593
45	20.461745
46	21.433923
47	23.502395
48	27.712929
49	22.170873
50	18.450113
51	26.574361
52	28.934354
53	19.533673
54	21.962963
55	23.963387
56	24.259620

Age	MaxHR
57	26.561933
58	25.313596
59	22.205193
60	23.134948
61	24.477200
62	25.895134
63	26.509508
64	17.637585
65	26.519624
66	23.751653
67	25.542309
68	12.564942
69	18.589355
70	21.866478
71	20.844664
72	11.898879
73	NaN
74	11.328430
75	2.309401
76	2.828427
77	36.769553

Just for fun, let's group by multiple predictors. There are several ages, so this will have to be written to a csv to actually analyze.

In [160…

```
mean_data = bp_df[["MaxHR", "Age", "HeartDisease"]].groupby(["Age","HeartDisease"])
mean_data.to_csv(r"Data\Mean_data.csv")
```

```
C:\Users\water\AppData\Local\Temp\ipykernel_22168\736809882.py:1: FutureWarning: The
default of observed=False is deprecated and will be changed to True in a future vers
ion of pandas. Pass observed=False to retain current behavior or observed=True to ad
opt the future default and silence this warning.
```

In [161…
```
median_data = bp_df[["MaxHR", "Age", "HeartDisease"]].groupby(["Age","HeartDisease"
median_data.to_csv(r"Data\Median_data.csv")
```

```
C:\Users\water\AppData\Local\Temp\ipykernel_22168\4175941233.py:1: FutureWarning: Th
e default of observed=False is deprecated and will be changed to True in a future ve
rsion of pandas. Pass observed=False to retain current behavior or observed=True to
adopt the future default and silence this warning.
```

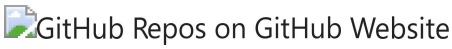
In [162…
```
std_data = bp_df[["MaxHR", "Age", "HeartDisease"]].groupby(["Age","HeartDisease"]).
std_data.to_csv(r"Data\std_data.csv")
```

```
C:\Users\water\AppData\Local\Temp\ipykernel_22168\2868568099.py:1: FutureWarning: Th
e default of observed=False is deprecated and will be changed to True in a future ve
rsion of pandas. Pass observed=False to retain current behavior or observed=True to
adopt the future default and silence this warning.
```

Here are the other deliverables for this week, just so this doesn't slip through the cracks:

Cloned GitHub Repo

GitHub Repos on GitHub Website



DSE5002 Repo on GitHub

Postgres Databases