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Course and Section: CPE 019 - CPE32S9
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Correlation Analaysis in Python

Objectives:
Part 1: The Dataset
Part 2: Scatterplot Graphs and Correlatable Variables
Part 3: Calculating Correlation with Python
Part 4: Visualizing

Scenario/Background: Correlation is an important statistical relationship that can indicate whether the variable values are linearly related.
In this lab, you will learn how to use Python to calculate correlation. In Part 1, you will setup the dataset. In Part 2, you will learn how to identify if the varibales in a given dataset are correlatable. Finally, in Part 3, you will use Python to clalculate the correlation between two sets of variable.

Required Resources

1 PC with Internet access
Raspberry Pi version 2 or higher
Python libraries: pandas, numpy, matplotlib, seaborn
Datafiles: brainsize.txt

Part 1: The Dataset

Step 1: Loading the Dataset From a File.

Before the dataset can be used, it must be loaded onto memory.

In the code below, The first line imports the pandas modules and defines pd as a descriptor that refers to the module.

The second line loads the dataset CSV file into a variable called brainFile.

The third line uses read_csv(), a pandas method, to convert the CSV dataset stored in brainFile into a dataframe. The dataframe is then stored in the brainFrame variable.

Run the cell below to execute the described functions.

```
# Code cell 1
import pandas as pd
brainFrame = pd.read_csv('/content/brainsize.txt', sep = '\t')
```

Step 2: Verifying the dataframe.

To make sure the dataframe has been correctly loaded and created, use the head() method. Another Pandas method, head() displays the first five entries of a dataframe.

```
# Code cell 2
brainFrame.head()
```

	Gender	FSIQ	VIQ	PIQ	Weight	Height	MRI_Count
0	Female	133	132	124	118.0	64.5	816932
1	Male	140	150	124	NaN	72.5	1001121
2	Male	139	123	150	143.0	73.3	1038437
3	Male	133	129	128	172.0	68.8	965353
4	Female	137	132	134	147.0	65.0	951545

```
brainFrame.tail()
```

	Gender	FSIQ	VIQ	PIQ	Weight	Height	MRI_Count
35	Female	133	129	128	153.0	66.5	948066
36	Male	140	150	124	144.0	70.5	949395
37	Female	88	86	94	139.0	64.5	893983
38	Male	81	90	74	148.0	74.0	930016
39	Male	89	91	89	179.0	75.5	935863

Part 2: Scatterplot Graphs and Correlatable Variables

Step 1: The pandas describe() method.

The pandas module includes the describe() method which performs same common calculations against a given dataset. In addition to provide common results including count, mean, standard deviation, minimum, and maximum, describe() is also a great way to quickly test the validity of the values in the dataframe.

Run the cell below to output the results computed by describe() against the brainFrame dataframe.

```
# Code cell 3
brainFrame.describe()
```

	FSIQ	VIQ	PIQ	Weight	Height	MRI_Count
count	40.000000	40.000000	40.00000	38.000000	39.000000	4.000000e+01
mean	113.450000	112.350000	111.02500	151.052632	68.525641	9.087550e+05
std	24.082071	23.616107	22.47105	23.478509	3.994649	7.228205e+04
min	77.000000	71.000000	72.00000	106.000000	62.000000	7.906190e+05
25%	89.750000	90.000000	88.25000	135.250000	66.000000	8.559185e+05
50%	116.500000	113.000000	115.00000	146.500000	68.000000	9.053990e+05
75%	135.500000	129.750000	128.00000	172.000000	70.500000	9.500780e+05
max	144.000000	150.000000	150.00000	192.000000	77.000000	1.079549e+06

Step 2: Scatterplot Graphs

Scatterplot graphs are important when working with correlations as they allow for a quick visual verification of the nature of the relationship between the variables. This lab uses the Pearson correlation coefficient, which is sensitive only to a linear relationship between two variables. Other more robust correlation methods exist but are out of the scope of this lab.

a. Load the required modules

Before graphs can be plotted, it is necessary to import a few modules, namely numpy and matplotlib. Run the cell below to load these modules.

```
# Code cell 4
import numpy as np
import matplotlib.pyplot as plt
```

b. Separate the data.

To ensure the results do not get skewed because of the differences in male and female bodies, the dateframe is split into two dataframes: one containing all male entries and another with only female instances.

Running the cell below creates the two new dataframes, menDf and womenDf, each one containing the respective entries.

```
# Code cell 5
menDf = brainFrame[(brainFrame.Gender == 'Male')]
womenDf = brainFrame[(brainFrame.Gender == 'Female')]
```

c. Plot the graphs.

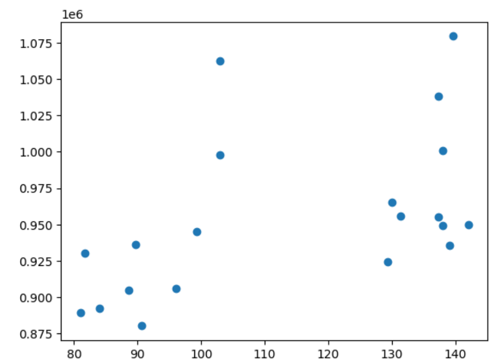
Because the dataset includes three different measures of intelligence (PIQ, FSIQ, and VIQ), the first line below uses Pandas mean() method to calculate the mean value between the three and store the result in the menMeanSmarts variable. Notice that the first line also refers to the menDf, the filtered dataframe containing only male entries.

The second line uses the matplotlib method scatter() to create a scatterplot graph between the menMeanSmarts variable and the MRI_Countattribute. The MRI_Count in this dataset can be thought as of a measure of the physical size of the subjects' brains.

The third line simply displays the graph.

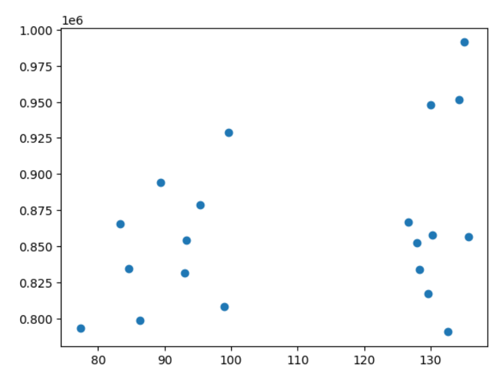
The fourth line is used to ensure the graph will be displayed in this notebook.

```
# Code cell 6
menMeanSmarts = menDf[["PIQ", "FSIQ", "VIQ"]].mean(axis=1)
plt.scatter(menMeanSmarts, menDf["MRI_Count"])
plt.show()
%matplotlib inline
```



Similarly, the code below creates a scatterplot graph for the women-only filtered dataframe.

```
# Code cell 7
# Graph the women-only filtered dataframe
#womenMeanSmarts = ?
#plt.scatter(?, ?)
womenMeanSmarts = womenDf[["PIQ", "FSIQ", "VIQ"]].mean(axis=1)
plt.scatter(womenMeanSmarts, womenDf["MRI_Count"])
plt.show()
%matplotlib inline
```



Part 3: Calculating Correlation with Python

Step 1: Calculate correlation against brainFrame.

The pandas corr() method provides an easy way to calculate correlation against a dataframe. By simply calling the method against a dataframe, one can get the correlation between all variables at the same time.

```
 # Code cell 8
brainFrame.corr(method='pearson')
```

```
<ipython-input-15-cab48f3abe05>:2: FutureWarning: The default value of numeric_only in DataFrame.corr is deprecated. In a future version, it will default to False. Select only valid columns or specify the value of n
  brainFrame.corr(method='pearson')
```

	FSIQ	VIQ	PIQ	Weight	Height	MRI_Count
FSIQ	1.000000	0.946639	0.934125	-0.051483	-0.086002	0.357641
VIQ	0.946639	1.000000	0.778135	-0.076088	-0.071068	0.337478
PIQ	0.934125	0.778135	1.000000	0.002512	-0.076723	0.386817
Weight	-0.051483	-0.076088	0.002512	1.000000	0.699614	0.513378
Height	-0.086002	-0.071068	-0.076723	0.699614	1.000000	0.601712
MRI_Count	0.357641	0.337478	0.386817	0.513378	0.601712	1.000000

Notice at the left-to-right diagonal in the correlation table generated above. Why is the diagonal filled with 1s? Is that a coincidence? Explain.

Still looking at the correlation table above, notice that the values are mirrored; values below the 1 diagonal have a mirrored counterpart above the 1 diagonal. Is that a coincidence? Explain.

Using the same corr() method, it is easy to calculate the correlation of the variables contained in the female-only dataframe:

```
# Code cell 9
womenDf.corr(method='pearson')
```

```
<ipython-input-16-a6271751808a>:2: FutureWarning: The default value of numeric_only in DataFrame.corr is deprecated. In a future version, it will default to False. Select only valid columns or specify the value of n
  womenDf.corr(method='pearson')
```

	FSIQ	VIQ	PIQ	Weight	Height	MRI_Count
FSIQ	1.000000	0.955717	0.939382	0.038192	-0.059011	0.325697
VIQ	0.955717	1.000000	0.802652	-0.021889	-0.146453	0.254933
PIQ	0.939382	0.802652	1.000000	0.113901	-0.001242	0.396157
Weight	0.038192	-0.021889	0.113901	1.000000	0.552357	0.446271
Height	-0.059011	-0.146453	-0.001242	0.552357	1.000000	0.174541
MRI_Count	0.325697	0.254933	0.396157	0.446271	0.174541	1.000000

And the same can be done for the male-only dataframe:

```
 # Code cell 10
# Use corr() for the male-only dataframe with the pearson method
#?.corr(?)
menDf.corr(method='pearson')
```

```
<ipython-input-17-71c6c33fd81a>:4: FutureWarning: The default value of numeric_only in DataFrame.corr is deprecated. In a future version, it will default to False. Select only valid columns or specify the value of n
  menDf.corr(method='pearson')
```

	FSIQ	VIQ	PIQ	Weight	Height	MRI_Count
FSIQ	1.000000	0.944400	0.930694	-0.278140	-0.356110	0.498369
VIQ	0.944400	1.000000	0.766021	-0.350453	-0.355588	0.413105
PIQ	0.930694	0.766021	1.000000	-0.156863	-0.287676	0.568237
Weight	-0.278140	-0.350453	-0.156863	1.000000	0.406542	-0.076875
Height	-0.356110	-0.355588	-0.287676	0.406542	1.000000	0.301543
MRI_Count	0.498369	0.413105	0.568237	-0.076875	0.301543	1.000000

Part 4: Visualizing

Step 1: Install Seaborn.

To make it easier to visualize the data correlations, heatmap graphs can be used. Based on colored squares, heatmap graphs can help identify correlations in a glance.

The Python module named seaborn makes it very easy to plot heatmap graphs.

First, run the cell below to download and install the seaborn module.

```
 # Code cell 11
!pip install seaborn
```

```
Requirement already satisfied: seaborn in /usr/local/lib/python3.10/dist-packages (0.13.1)
Requirement already satisfied: numpy!=1.24.0,>=1.20 in /usr/local/lib/python3.10/dist-packages (from seaborn) (1.23.5)
Requirement already satisfied: pandas>=1.2 in /usr/local/lib/python3.10/dist-packages (from seaborn) (1.5.3)
Requirement already satisfied: matplotlib!=3.6.1,>=3.4 in /usr/local/lib/python3.10/dist-packages (from seaborn) (3.7.1)
Requirement already satisfied: contourpy>=1.0.1 in /usr/local/lib/python3.10/dist-packages (from matplotlib!=3.6.1,>=3.4->seaborn) (1.2.0)
Requirement already satisfied: cycler>=0.10 in /usr/local/lib/python3.10/dist-packages (from matplotlib!=3.6.1,>=3.4->seaborn) (0.12.1)
Requirement already satisfied: fonttools>=4.22.0 in /usr/local/lib/python3.10/dist-packages (from matplotlib!=3.6.1,>=3.4->seaborn) (4.47.2)
Requirement already satisfied: kiwisolver>=1.0.1 in /usr/local/lib/python3.10/dist-packages (from matplotlib!=3.6.1,>=3.4->seaborn) (1.4.5)
Requirement already satisfied: packaging>=20.0 in /usr/local/lib/python3.10/dist-packages (from matplotlib!=3.6.1,>=3.4->seaborn) (23.2)
Requirement already satisfied: pillow>=6.2.0 in /usr/local/lib/python3.10/dist-packages (from matplotlib!=3.6.1,>=3.4->seaborn) (9.4.0)
Requirement already satisfied: pyparsing>=2.3.1 in /usr/local/lib/python3.10/dist-packages (from matplotlib!=3.6.1,>=3.4->seaborn) (3.1.1)
Requirement already satisfied: python-dateutil>=2.7 in /usr/local/lib/python3.10/dist-packages (from matplotlib!=3.6.1,>=3.4->seaborn) (2.8.2)
Requirement already satisfied: pytz>=2020.1 in /usr/local/lib/python3.10/dist-packages (from pandas>=1.2->seaborn) (2023.4)
Requirement already satisfied: six>=1.5 in /usr/local/lib/python3.10/dist-packages (from python-dateutil>=2.7->matplotlib!=3.6.1,>=3.4->seaborn) (1.16.0)
```

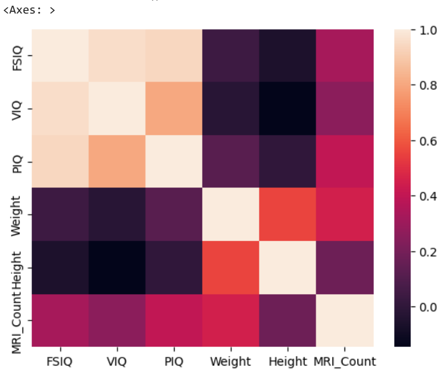
Step 2: Plot the correlation heatmap.

Now that the dataframes are ready, the heatmaps can be plotted. Below is a breakdown of the code in the cell below:

Line 1: Generates a correlation table based on the womenNoGenderDf dataframe and stores it on wcorr.
Line 2: Uses the seaborn heatmap() method to generate and plot the heatmap. Notice that heatmap() takes wcorr as a parameter.
Line 3: Use to export and save the generated heatmap as a PNG image. While the line 3 is not active (it has the comment # character preceding it, forcing the interpreter to ignore it), it was kept for informational purposes.

```
 # Code cell 12
import seaborn as sns
wcorr = womenDf.corr()
sns.heatmap(wcorr)
#plt.savefig('attribute_correlations.png', tight_layout=True)
```

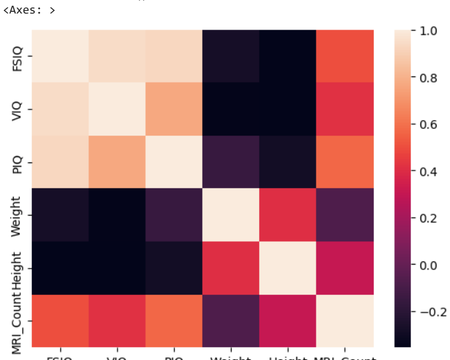
```
<ipython-input-19-2465c40f5efb>:3: FutureWarning: The default value of numeric_only in DataFrame.corr is deprecated. In a future version, it will default to False. Select only valid columns or specify the value of n
  wcorr = womenDf.corr()
<Axes: >
```



Similarly, the code below creates and plots a heatmap for the male-only dataframe.

```
# Code cell 14
mcorr = menDf.corr()
sns.heatmap(mcorr)
#plt.savefig('attribute_correlations.png', tight_layout=True)
```

```
<ipython-input-20-ff3e250059fc>:2: FutureWarning: The default value of numeric_only in DataFrame.corr is deprecated. In a future version, it will default to False. Select only valid columns or specify the value of n
  mcorr = menDf.corr()
<Axes: >
```



Many variable pairs present correlation close to zero. What does that mean?

Having a correlation close to zero means that the relationship between these pairs of variables is very weak to none at all because in correlational analysis, correlation should be distant from zero to have a stronger relationship between the variables.

Why separate the genders?

We seperate the genders so that we could also compare the correlation between men and women.

What variables have stronger correlation with brain size (MRI_Count)? Is that expected? Explain.

From the women's data, the weight has the strongest correlation with the brain size. However, from the men's data, the PIQ along with the other measurements of IQ were the strongest in terms of their correlation to the brain size.

Supplementary Activity

Background/Scenario

This dataset include data for the estimation of obesity levels in individuals from the countries of Mexico, Peru and Colombia, based on their eating habits and physical condition. The data contains 17 attributes and 2111 records, the records are labeled with the class variable NObesity (Obesity Level), that allows classification of the data using the values of Insufficient Weight, Normal Weight, Overweight Level I, Overweight Level II, Obesity Type I, Obesity Type II and Obesity Type III. 77% of the data was generated synthetically using the Weka tool and the SMOTE filter, 23% of the data was collected directly from users through a web platform.

Importing the data

```
import pandas as pd
obesityLevels = pd.read_csv('/content/ObesityDataSet_raw_and_data_sinthetic.csv')
```

Verifying the data

```
obesityLevels.head()
```

	Gender	Age	Height	Weight	family_history_with_overweight	FAVC	FCVC	NCP	CAEC	SMOKE	CH2O	SCC	FAF	TUE	CALC	MTRANS	NObeyesdad
0	Female	21.0	1.62	64.0	yes	no	2.0	3.0	Sometimes	no	2.0	no	0.0	1.0	no	Public_Transportation	Normal_Weight
1	Female	21.0	1.52	56.0	yes	no	3.0	3.0	Sometimes	yes	3.0	yes	3.0	0.0	Sometimes	Public_Transportation	Normal_Weight
2	Male	23.0	1.80	77.0	yes	no	2.0	3.0	Sometimes	no	2.0	no	2.0	1.0	Frequently	Public_Transportation	Normal_Weight
3	Male	27.0	1.80	87.0	no	no	3.0	3.0	Sometimes	no	2.0	no	2.0	0.0	Frequently	Walking	Overweight_Level_I
4	Male	22.0	1.78	89.8	no	no	2.0	1.0	Sometimes	no	2.0	no	0.0	0.0	Sometimes	Public_Transportation	Overweight_Level_II

```
obesityLevels.tail()
```

	Gender	Age	Height	Weight	family_history_with_overweight	FAVC	FCVC	NCP	CAEC	SMOKE	CH2O	SCC	FAF	TUE	CALC	MTRANS	NObeyesdad
2106	Female	20.976842	1.710730	131.408528	yes	yes	3.0	3.0	Sometimes	no	1.728139	no	1.676269	0.906247	Sometimes	Public_Transportation	Obesity_Type_III
2107	Female	21.982942	1.748584	133.742943	yes	yes	3.0	3.0	Sometimes	no	2.005130	no	1.341390	0.599270	Sometimes	Public_Transportation	Obesity_Type_III
2108	Female	22.524036	1.752206	133.689352	yes	yes	3.0	3.0	Sometimes	no	2.054193	no	1.414209	0.646288	Sometimes	Public_Transportation	Obesity_Type_III
2109	Female	24.361936	1.739450	133.346641	yes	yes	3.0	3.0	Sometimes	no	2.852339	no	1.139107	0.586035	Sometimes	Public_Transportation	Obesity_Type_III
2110	Female	23.664709	1.738836	133.472641	yes	yes	3.0	3.0	Sometimes	no	2.863513	no	1.026452	0.714137	Sometimes	Public_Transportation	Obesity_Type_III

```
obesityLevels.describe()
```

	Age	Height	Weight	FCVC	NCP	CH2O	FAF	TUE
count	2111.000000	2111.000000	2111.000000	2111.000000	2111.000000	2111.000000	2111.000000	2111.000000
mean	24.312600	1.701677	86.586058	2.419043	2.685628	2.008011	1.010298	0.657866
std	6.345968	0.093305	26.191172	0.533927	0.778039	0.612953	0.850592	0.608927
min	14.000000	1.450000	39.000000	1.000000	1.000000	1.000000	0.000000	0.000000
25%	19.947192	1.630000	65.473343	2.000000	2.658738	1.584812	0.124505	0.000000
50%	22.777890	1.700499	83.000000	2.385502	3.000000	2.000000	1.000000	0.625350
75%	26.000000	1.768464	107.430682	3.000000	3.000000	2.477420	1.666678	1.000000
max	61.000000	1.980000	173.000000	3.000000	4.000000	3.000000	3.000000	2.000000

I didn't include a graph as I see it as unnecessary since we don't have multiple measurements for a single category like the IQs from the procedures.

```
import numpy as np
import matplotlib.pyplot as plt

menoL = obesityLevels[(obesityLevels.Gender == 'Male')]
womenoL = obesityLevels[(obesityLevels.Gender == 'Female')]
```

```
obesityLevels.corr(method='pearson')
```

```
<ipython-input-35-9494e6167544>:1: FutureWarning: The default value of numeric_only in DataFrame.corr is deprecated. In a future version, it will default to False. Select only valid columns or specify the value of n
  obesityLevels.corr(method='pearson')
```

	Age	Height	Weight	FCVC	NCP	CH2O	FAF	TUE
Age	1.000000	-0.025958	0.202560	0.016291	-0.043944	-0.045304	-0.144938	-0.296931
Height	-0.025958	1.000000	0.463136	-0.038121	0.243672	0.213376	0.294709	0.051912
Weight	0.202560	0.463136	1.000000	0.216125	0.107469	0.200575	-0.051436	-0.071561
FCVC	0.016291	-0.038121	0.216125	1.000000	0.042216	0.068461	0.019939	-0.101135
NCP	-0.043944	0.243672	0.107469	0.042216	1.000000	0.057088	0.129504	0.036326
CH2O	-0.045304	0.213376	0.200575	0.068461	0.057088	1.000000	0.167236	0.011965
FAF	-0.144938	0.294709	-0.051436	0.019939	0.129504	0.167236	1.000000	0.058562
TUE	-0.296931	0.051912	-0.071561	-0.101135	0.036326	0.011965	0.058562	1.000000

```
menoL.corr(method='pearson')
```

```
<ipython-input-36-0c92c50edcaa>:1: FutureWarning: The default value of numeric_only in DataFrame.corr is deprecated. In a future version, it will default to False. Select only valid columns or specify the value of n
  menoL.corr(method='pearson')
```

	Age	Height	Weight	FCVC	NCP	CH2O	FAF	TUE
Age	1.000000	0.040664	0.420845	0.058852	-0.075952	-0.108256	-0.062429	-0.236109
Height	0.040664	1.000000	0.376737	0.097251	0.235927	0.114341	0.156536	-0.041511
Weight	0.420845	0.376737	1.000000	0.051279	-0.079688	-0.009121	-0.137819	-0.126618
FCVC	0.058852	0.097251	0.051279	1.000000	-0.035841	-0.075996	0.180114	-0.047921
NCP	-0.075952	0.235927	-0.079688	-0.035841	1.000000	0.038170	0.135331	0.054318
CH2O	-0.108256	0.114341	-0.009121	-0.075996	0.038170	1.000000	0.180545	0.073380
FAF	-0.062429	0.156536	-0.137819	0.180114	0.135331	0.180545	1.000000	0.014895
TUE	-0.236109	-0.041511	-0.126618	-0.047921	0.054318	0.073380	0.014895	1.000000

```
womenoL.corr(method='pearson')
```

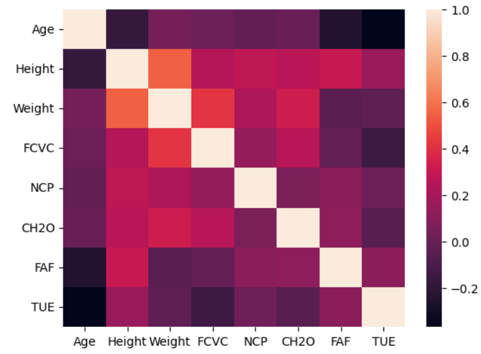
```
<ipython-input-37-90ab379f946c>:1: FutureWarning: The default value of numeric_only in DataFrame.corr is deprecated. In a future version, it will default to False. Select only valid columns or specify the value of n
  womenoL.corr(method='pearson')
```

	Age	Height	Weight	FCVC	NCP	CH2O	FAF	TUE
Age	1.000000	-0.179837	0.040272	0.006390	-0.021654	0.002100	-0.250961	-0.369597
Height	-0.179837	1.000000	0.542288	0.241191	0.277048	0.254874	0.301981	0.157585
Weight	0.040272	0.542288	1.000000	0.419869	0.217110	0.322086	-0.047820	-0.036257
FCVC	0.006390	0.241191	0.419869	1.000000	0.143056	0.249558	-0.015003	-0.154375
NCP	-0.021654	0.277048	0.217110	0.143056	1.000000	0.060436	0.104579	0.015906
CH2O	0.002100	0.254874	0.322086	0.249558	0.060436	1.000000	0.122381	-0.056829
FAF	-0.250961	0.301981	-0.047820	-0.015003	0.104579	0.122381	1.000000	0.103678
TUE	-0.369597	0.157585	-0.036257	-0.154375	0.015906	-0.056829	0.103678	1.000000

I used pearson to test the significance of the variables and their relationship to each of the other variables

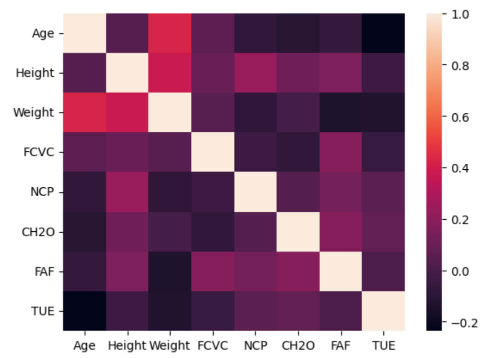
```
import seaborn as sns
wcorroL = womenoL.corr()
sns.heatmap(wcorroL)
```

```
<ipython-input-40-9aee32788a39>:2: FutureWarning: The default value of numeric_only in DataFrame.corr is deprecated. In a future version, it will default to False. Select only valid columns or specify the value of n
  wcorroL = womenoL.corr()
<Axes: >
```




```
import seaborn as sns
mcorroL = menoL.corr()
sns.heatmap(mcorroL)
```

```
<ipython-input-39-43bccd6cceb6>:2: FutureWarning: The default value of numeric_only in DataFrame.corr is deprecated. In a future version, it will default to False. Select only valid columns or specify the value of n
  mcorroL = menoL.corr()
<Axes: >
```



I have observed from the heatmap that from the women's data, the vegetables intake (FCVC) has the strongest relationship to the weight. On the men's data, FCVC also has the strongest relationship to the weight but is relatively weaker than the women's.

Conclusions/Lessons Learned

In this activity, we were introduced on how correlation analysis works in python. We were tasked to use the dataset with 40 samples correlating their traits and IQ to the size of their brain. We were given codes to load the dataset, verify the dataframe, scatterplot graphs, load required modules, separate data, plot the graphs, calculate correlation, and then plot the correlation heatmap. I have learned from this activity how to navigate the dataset and the basics of correlational analysis using python.

Dataset used

Estimation of obesity levels based on eating habits and physical condition . (2019). UCI Machine Learning Repository. https://doi.org/10.24432/C5H31Z.