

TP2_ANIS

February 10, 2020

1 Chargement et prétraitements des données

```
In [1]: import numpy as np
import pandas as pd
import matplotlib.pyplot as plt

data= pd.read_csv("study.csv",delimiter=",")
data.head()

data.gender = data.gender.astype('category') # ou bien pd.Categorical(data.gender)
data.ethnicity = data.ethnicity.astype('category')

i = data[(data.age <= 15)].index # Je cherche l'index de ceux dont l'age est inferieur
data=data.drop(i)

In [2]: pd.Categorical(data.gender).describe()

Out [2]:
```

	counts	freqs
categories		
Female	507	0.620563
Male	310	0.379437

```
In [3]: pd.Categorical(data.ethnicity).describe()

Out [3]:
```

	counts	freqs
categories		
Asian	27	0.033048
Black	88	0.107711
Dominican	1	0.001224
Hispanic	75	0.091799
Indian	1	0.001224
Other	6	0.007344
Unknown	32	0.039168
White	587	0.718482

```
In [4]: data.describe()
```

```
Out [4]:
```

	age	weight	protein	protein2	protein3	n_visits
count	817.000000	817.000000	817.000000	817.000000	817.000000	817.000000
mean	41.994002	67.997307	244.293758	137.565483	100.981640	2.395349
std	21.623043	10.386467	46.767645	39.445960	29.033465	1.987492
min	15.100000	45.800000	140.000000	30.000000	50.000000	0.000000
25%	23.200000	60.600000	208.000000	111.000000	76.000000	1.000000
50%	37.100000	67.200000	245.000000	139.000000	102.000000	2.000000
75%	60.100000	74.400000	279.000000	164.000000	124.000000	3.000000
max	94.600000	95.700000	361.000000	227.000000	150.000000	8.000000

```
In [ ]:
```

2 Tableau des fréquences

```
In [5]: xi, ni = np.unique(data.n_visits, return_counts=True)
table=pd.DataFrame( data=ni, columns=["ni"],index=xi)
N=sum(table.ni)
table.insert(1, "fi", table.ni / N, True)
table.insert(2,"Fi",np.cumsum(table.fi), True)
table
```

```
Out [5]:
```

	ni	fi	Fi
0	154	0.188494	0.188494
1	160	0.195838	0.384333
2	145	0.177479	0.561812
3	156	0.190942	0.752754
4	111	0.135863	0.888617
5	18	0.022032	0.910649
6	27	0.033048	0.943696
7	25	0.030600	0.974296
8	21	0.025704	1.000000

```
In [6]: data.n_visits.describe()
```

```
Out [6]: count      817.000000
mean          2.395349
std           1.987492
min           0.000000
25%           1.000000
50%           2.000000
75%           3.000000
max           8.000000
Name: n_visits, dtype: float64
```

3 Représentation graphique unidimensionnelle

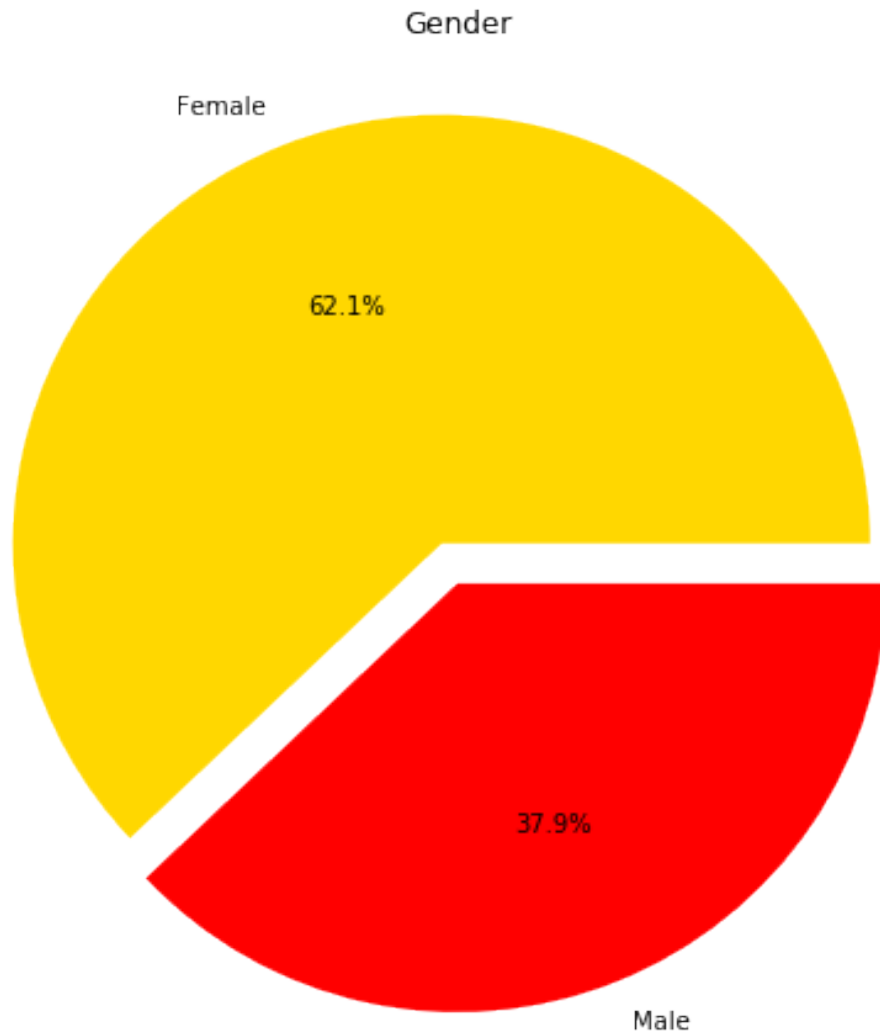
```
In [7]: plt.figure(figsize=(8,8))
vals, counts= np.unique(data.gender, return_counts=True)
```

```

labels = vals
sizes = counts
colors = ['gold', "red"]
explode = (0.1, 0) # explode 1st slice

# Plot
plt.title('Gender')
plt.pie(sizes,explode=explode, labels=labels, colors=colors,autopct='%1.1f%%');

```



```

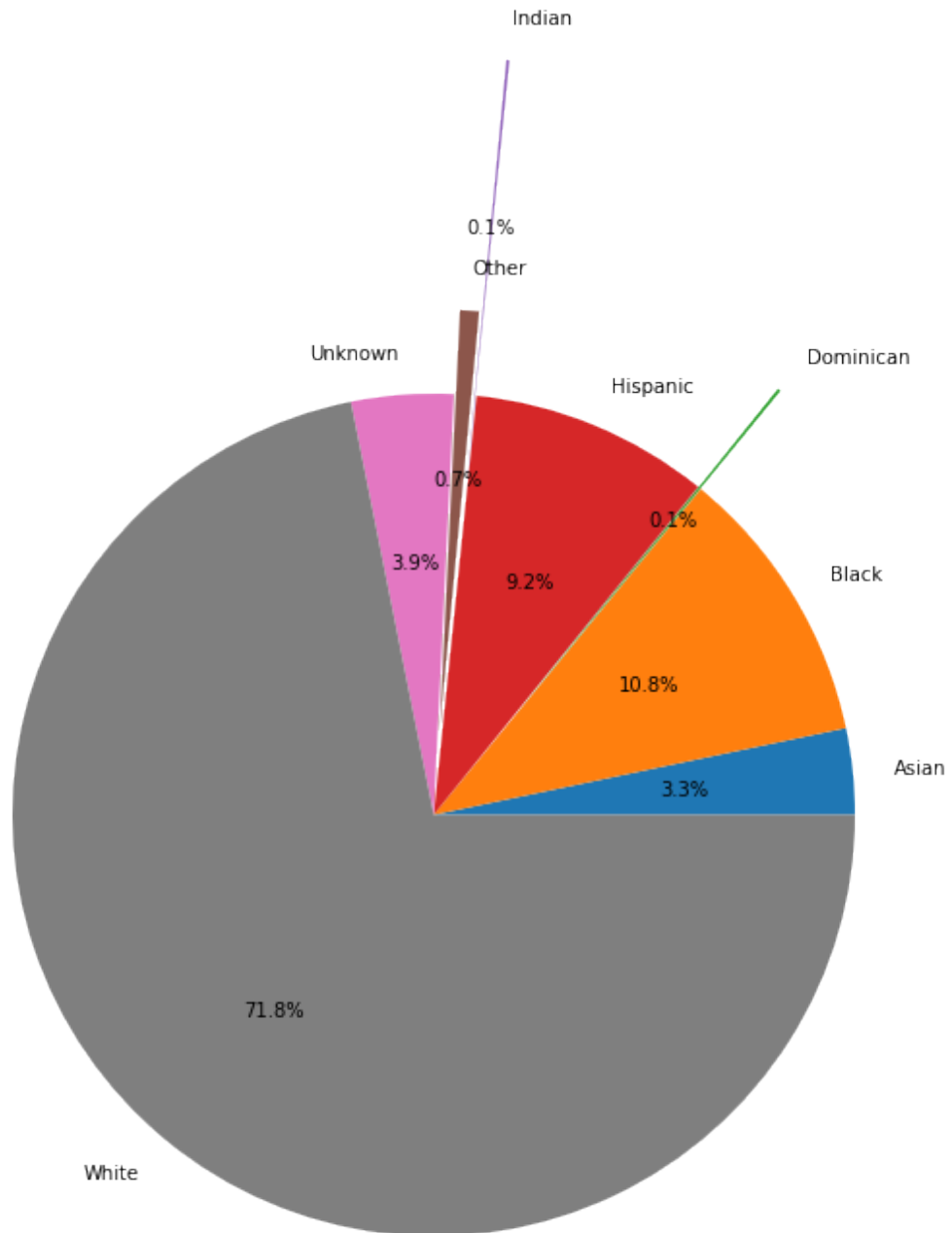
In [8]: plt.figure(figsize=(15,10))
        vals, counts= np.unique(data.ethnicity, return_counts=True)

```

```

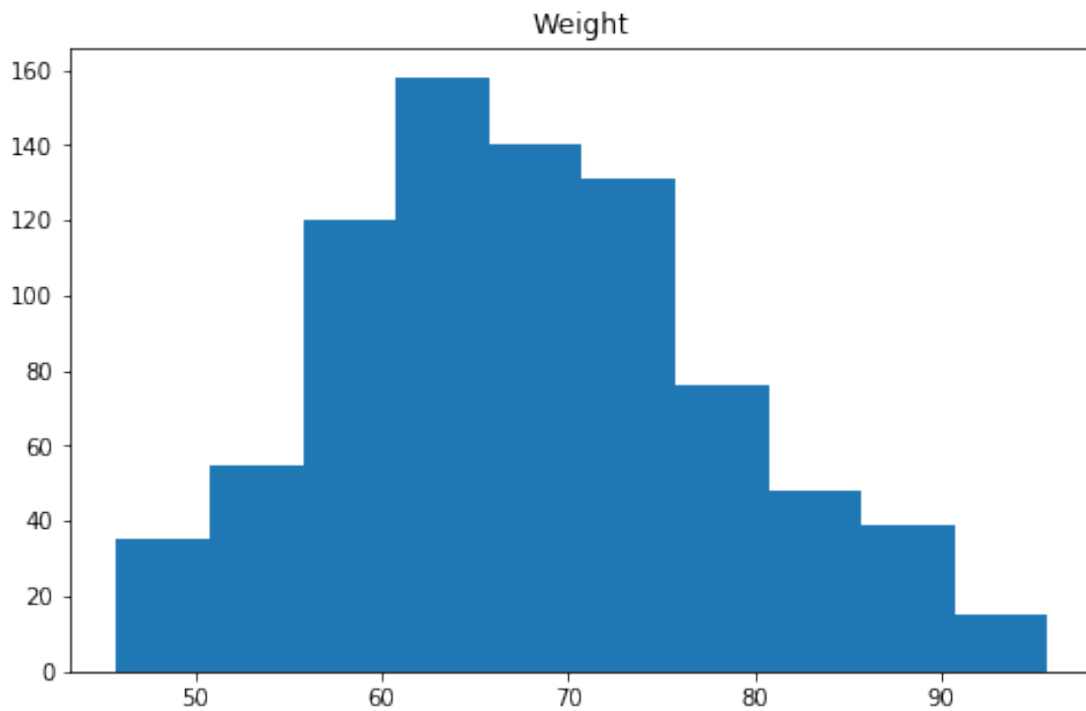
sizes=counts
labels= 'Asian', 'Black', 'Dominican', 'Hispanic', 'Indian', 'Other', 'Unknown', 'White'
explode=(0, 0,0.3,0,0.8,0.2,0,0)
plt.pie(sizes,explode=explode,labels=labels,autopct='%1.1f%%');

```

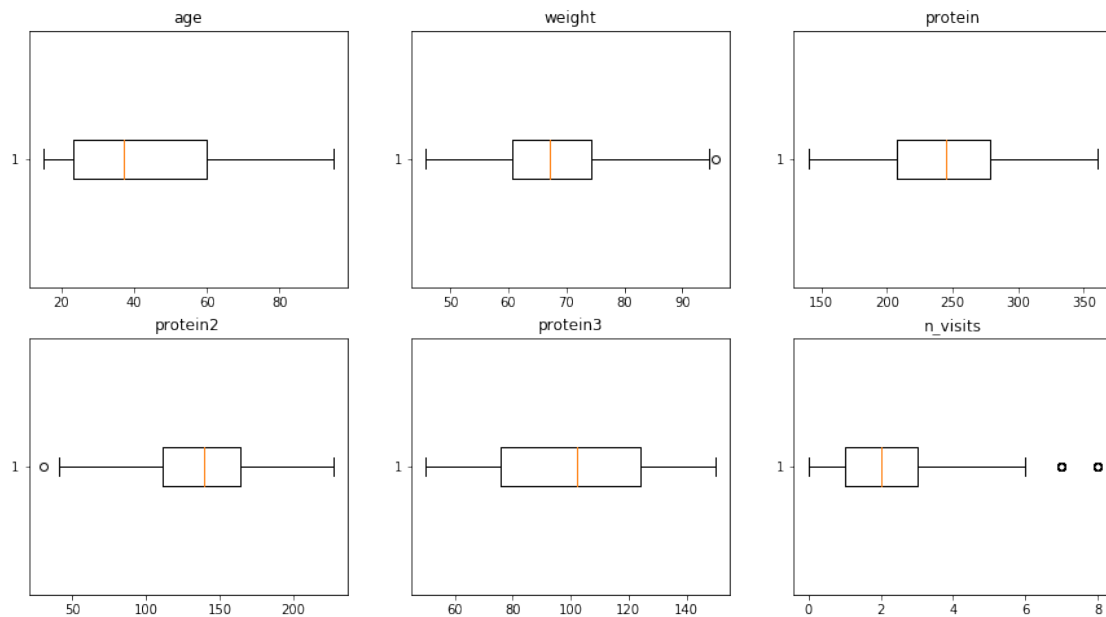


```
In [9]: plt.figure(figsize=(8,5))
```

```
plt.hist(data.weight);
plt.title("Weight");
```

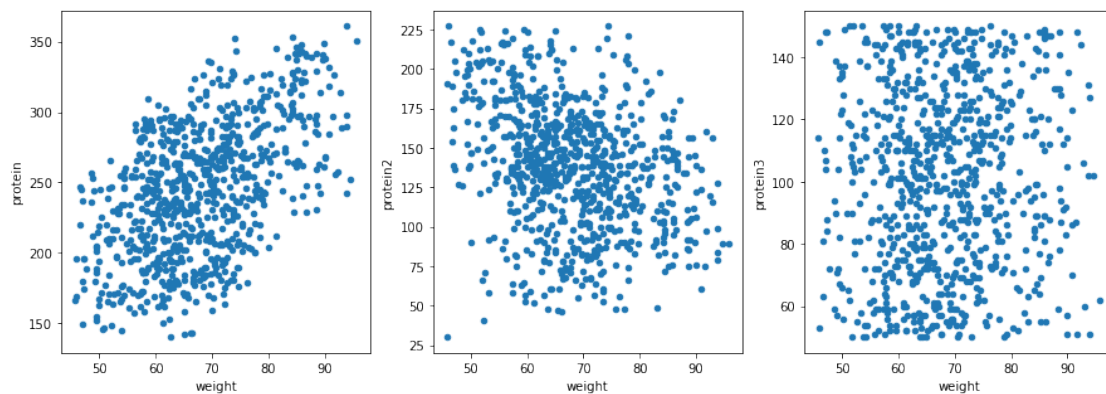


```
In [10]: plt.figure(figsize=(15,8))
plt.subplot(231)
plt.title('age')
plt.boxplot(data.age,vert=False);
plt.subplot(232)
plt.title('weight')
plt.boxplot(data.weight,vert=False);
plt.subplot(233)
plt.title('protein')
plt.boxplot(data.protein,vert=False);
plt.subplot(234)
plt.title('protein2')
plt.boxplot(data.protein2,vert=False);
plt.subplot(235)
plt.title('protein3')
plt.boxplot(data.protein3,vert=False);
plt.subplot(236)
plt.title('n_visits')
plt.boxplot(data.n_visits,vert=False);
```



4 Représentation graphique multidimensionnelle

```
In [11]: fig = plt.figure(figsize=(15,5));
ax1 = fig.add_subplot(131);
ax2 = fig.add_subplot(132);
ax3 = fig.add_subplot(133);
data.plot(kind='scatter',x='weight', y='protein', ax=ax1, legend=False);
data.plot(kind='scatter',x='weight', y='protein2', ax=ax2, legend=False);
data.plot(kind='scatter',x='weight', y='protein3', ax=ax3, legend=False);
```



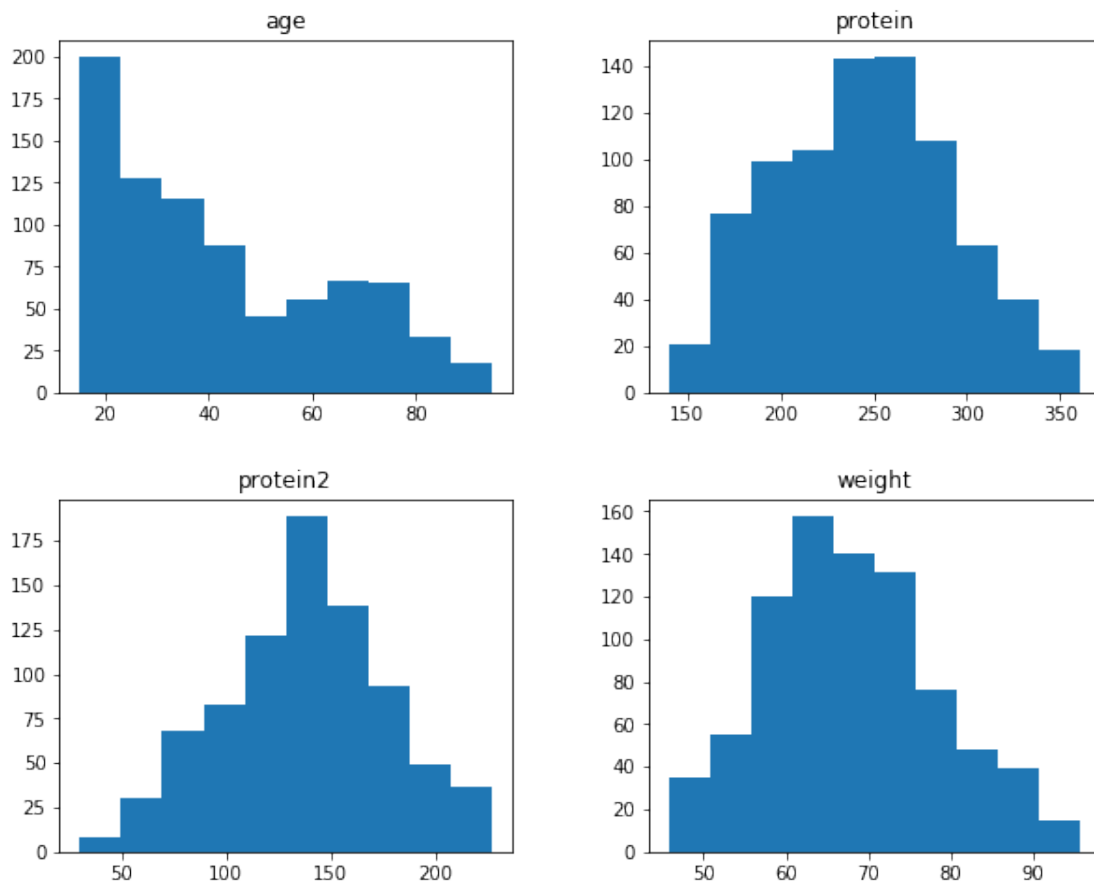
```
In [12]: data.drop(["n_visits", 'age', 'gender', 'ethnicity'], axis=1).corr()
```

```
Out[12]:
```

	weight	protein	protein2	protein3
weight	1.000000	0.527940	-0.304254	0.043547
protein	0.527940	1.000000	-0.221852	0.009820
protein2	-0.304254	-0.221852	1.000000	-0.019180
protein3	0.043547	0.009820	-0.019180	1.000000

```
In [13]: fig = plt.figure(figsize = (10,8));
ax = fig.gca();
data.drop(["n_visits", 'protein3'], axis=1).hist(grid=False,ax=ax);
```

```
/Users/macbookpro/anaconda/lib/python3.5/site-packages/IPython/core/interactiveshell.py:2961: UserWarning:
exec(code_obj, self.user_global_ns, self.user_ns)
```



```
In [14]: data.drop(["n_visits", 'gender', 'ethnicity'], axis=1).skew(axis = 0, skipna = True)
```

```
Out[14]: age          0.589952
weight      0.280581
protein     0.052732
protein2    -0.064582
protein3    -0.039009
dtype: float64
```

5 Recodage d'une variable

```
In [15]: data.age.describe()
```

```
Out[15]: count      817.000000  
         mean       41.994002  
         std        21.623043  
         min        15.100000  
         25%        23.200000  
         50%        37.100000  
         75%        60.100000  
         max        94.600000  
         Name: age, dtype: float64
```

```
In [16]: age5_cat=pd.qcut(data.age, 5)  
         data.insert(8,"age5_cat",age5_cat, True)
```

```
In [17]: data.head()
```

```
Out[17]:
```

	gender	ethnicity	age	weight	protein	protein2	protein3	n_visits	\
0	Female	White	72.0	76.0	246	88	136	8	
1	Female	Black	84.1	59.8	210	85	86	6	
2	Female	Black	79.7	56.0	205	91	110	7	
3	Female	White	75.7	66.7	286	68	54	2	
4	Female	White	74.6	72.1	171	81	99	8	

	age5_cat
0	(66.78, 94.6]
1	(66.78, 94.6]
2	(66.78, 94.6]
3	(66.78, 94.6]
4	(66.78, 94.6]

```
In [ ]:
```

```
In [ ]:
```

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In [ ]:
```