

# HW1\_BasicStatistics

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## 1 Homework Assignment 1 - Basic Statistics - revision notebook

Beatriz Gamboa Pereira - 201705220

```
[41]: import pandas as pd
import matplotlib.pyplot as plt
import numpy as np
import statsmodels.api as sm
```

In this work, I will be exploring the dataset used in the first practical lesson, namely SAheart, from kaggle.

```
[2]: mydata = pd.read_csv('SAheart.csv')
mydata
```

```
[2]:
```

	sbp	tobacco	ldl	adiposity	famhist	typea	obesity	alcohol	age	chd
0	160	12.00	5.73	23.11	Present	49	25.30	97.20	52	Si
1	144	0.01	4.41	28.61	Absent	55	28.87	2.06	63	Si
2	118	0.08	3.48	32.28	Present	52	29.14	3.81	46	No
3	170	7.50	6.41	38.03	Present	51	31.99	24.26	58	Si
4	134	13.60	3.50	27.78	Present	60	25.99	57.34	49	Si
..	...	...	...	...	...	...	...	...	...	...
457	214	0.40	5.98	31.72	Absent	64	28.45	0.00	58	No
458	182	4.20	4.41	32.10	Absent	52	28.61	18.72	52	Si
459	108	3.00	1.59	15.23	Absent	40	20.09	26.64	55	No
460	118	5.40	11.61	30.79	Absent	64	27.35	23.97	40	No
461	132	0.00	4.82	33.41	Present	62	14.70	0.00	46	Si

[462 rows x 10 columns]

In this sample, we can see that we have 462 **data objects** (patients) each with 10 **attributes**. Of those 10 attributes, 8 constitute numeric variables, either integers or floats; 1 is nominal, namely 'famhist'; and then we have 'chd', which is the class indicator of whether the patient has Coronary Heart Disease or not. This last one is the variable we want to predict as we analyse our data. We can test this by checking the data types of our dataset.

```
[3]: #checking the number of data objects and attributes
mydata.shape
```

```
[3]: (462, 10)
```

```
[4]: #checking the types of the attributes
mydata.dtypes
```

```
[4]: sbp                int64
tobacco               float64
ldl                   float64
adiposity             float64
famhist               object
typea                 int64
obesity               float64
alcohol               float64
age                   int64
chd                   object
dtype: object
```

## 1.1 Central tendency measures

Central tendency measures tell us where the sample is located, and how skewed it is relative to a normal distribution. The most common measures of central tendency are the mean, the median and the mode. The **mean** is the sum of all measurements divided by the number of measurements.

$$\bar{x} = \frac{1}{N} \sum_{i=1}^N x_i$$

where  $N$  is the number of observations in the sample and  $\{x_1, x_2, \dots, x_N\}$  are the observed values of the sample items. We can also have a **weighted mean** where data points have different contributions to the final value of the mean. When all data point have the same contribution, we get the mean as described before.

$$\bar{x} = \frac{\sum_{i=1}^n w_i x_i}{\sum_{i=1}^n w_i}$$

where  $\{w_1, w_2, \dots, w_n\}$  are the weights. The **median** is the middle value of your sample, which splits it into halves with equal amounts of datapoints. The **mode** is simply the most frequent value in the dataset. Therefore, we can have a mode for nominal variables, as well as numerical ones.

### 1.1.1 Mean

```
[5]: print(mydata.mean(), '\n\n')

#we can check the mean is the sum of all measurements divided by the number of
↪measurements
numeric_columns = mydata.select_dtypes([np.number]).columns
for col in numeric_columns:
    sum = 0
    for i in mydata[col]:
        sum += i
    mean = sum / 462
```

```
print(col.ljust(10),round(mean,6))
```

*#as we can see, the results are the same*

```
sbp          138.326840
tobacco      3.635649
ldl          4.740325
adiposity    25.406732
typea       53.103896
obesity     26.044113
alcohol     17.044394
age         42.816017
dtype: float64
```

```
sbp          138.32684
tobacco      3.635649
ldl          4.740325
adiposity    25.406732
typea       53.103896
obesity     26.044113
alcohol     17.044394
age         42.816017
```

### 1.1.2 Median

```
[6]: print(mydata.median(),'\n\n')
```

*#we can check it's the middle value of each column*  
*#since we have 462 datapoints, the median will be the average of the two middle*  
*→ values, 230 and 231*

```
for col in numeric_columns:
    sorteda = np.sort(np.array(mydata[col]))
    median = (sorteda[230] + sorteda[231]) / 2
    print(col.ljust(10),round(median,3))
```

*#as we can see, the results are the same*

```
sbp          134.000
tobacco      2.000
ldl          4.340
adiposity    26.115
typea       53.000
obesity     25.805
alcohol     7.510
age         45.000
dtype: float64
```

```

sbp      134.0
tobacco  2.0
ldl      4.34
adiposity 26.115
typea    53.0
obesity  25.805
alcohol  7.51
age      45.0

```

### 1.1.3 Mode

```

[7]: mydata.mode()
#where we have more than one value with se same frequency, we have more than
↪ one mode, hence the 4 rows

```

```

[7]:      sbp  tobacco   ldl  adiposity famhist  typea  obesity  alcohol   age  chd
0  134.0     0.0  3.57    21.10  Absent   52.0    24.86     0.0  16.0  No
1  136.0     NaN  3.95    27.55    NaN    NaN    26.09     NaN  NaN  NaN
2   NaN     NaN  4.37    29.30    NaN    NaN     NaN     NaN  NaN  NaN
3   NaN     NaN  NaN    30.79    NaN    NaN     NaN     NaN  NaN  NaN

```

## 1.2 Dispersion measures

Dispersion measures tell us how far apart the measures are, indicating if the distribution is more squeezed or stretched. We have the **range** of our measurements, which is the difference between the minimum and maximum values we have  $\text{range} = \text{Max} - \text{Min}$ ; the **quartiles**, which divide the data into four equal sized sets - the **median** which divides the data into two equal sized sets is the second quartile, so we have  $Q_1, Q_2$  or median and  $Q_3$ ; and the **IQR** - interquartile range  $IQR = Q_3 - Q_1$ . We can have a **five number summary** in which we get the  $\text{min}, Q_1, \text{median}, Q_3, \text{max}$ . Other measures of statistical dispersion include the **variance**,  $\sigma^2$ , and the **standard deviation**,  $\sigma$ . The variance is the mean of the squared differences of the observations to their mean

$$\sigma^2 = \frac{1}{N-1} \sum_{i=1}^N (x_i - \bar{x})^2$$

where  $N$  is the number of observations in the sample,  $\bar{x}$  is the mean value of the observations and  $\{x_1, x_2, \dots, x_N\}$  are the observed values of the sample items. And the standard deviation is the squared root of the variance

$$\sigma = \sqrt{\sigma^2}$$

```

[8]: mydata.describe(include='all')

```

```

[8]:      sbp      tobacco      ldl  adiposity famhist      typea  \
count  462.000000  462.000000  462.000000  462.000000    462  462.000000
unique      NaN      NaN      NaN      NaN      2      NaN
top      NaN      NaN      NaN      NaN  Absent      NaN
freq      NaN      NaN      NaN      NaN      270      NaN

```

mean	138.326840	3.635649	4.740325	25.406732	NaN	53.103896
std	20.496317	4.593024	2.070909	7.780699	NaN	9.817534
min	101.000000	0.000000	0.980000	6.740000	NaN	13.000000
25%	124.000000	0.052500	3.282500	19.775000	NaN	47.000000
50%	134.000000	2.000000	4.340000	26.115000	NaN	53.000000
75%	148.000000	5.500000	5.790000	31.227500	NaN	60.000000
max	218.000000	31.200000	15.330000	42.490000	NaN	78.000000

	obesity	alcohol	age	chd
count	462.000000	462.000000	462.000000	462
unique	NaN	NaN	NaN	2
top	NaN	NaN	NaN	No
freq	NaN	NaN	NaN	302
mean	26.044113	17.044394	42.816017	NaN
std	4.213680	24.481059	14.608956	NaN
min	14.700000	0.000000	15.000000	NaN
25%	22.985000	0.510000	31.000000	NaN
50%	25.805000	7.510000	45.000000	NaN
75%	28.497500	23.892500	55.000000	NaN
max	46.580000	147.190000	64.000000	NaN

By using `describe()`, we can check most of the measures mentioned above. For the numerical variables, we can check the values of the mean and median (2nd Quartile) calculated above. We can check the standard deviation (and therefore the variance) with the formula mentioned, and calculate the range and IQR of each variable. For the nominal variables, we can see what's the most common output and how many times it occurs.

```
[14]: #checking the standard deviation
print(mydata.std(),'\n\n')

for i,col in enumerate(numeric_columns):
    sum = 0
    mean = mydata.mean()[i]
    for j in mydata[col]:
        sum += (j - mean) ** 2
    std = np.sqrt(1 / 461 * sum)
    print(col.ljust(10),round(std,6))
```

```
sbp          20.496317
tobacco      4.593024
ldl          2.070909
adiposity    7.780699
typea       9.817534
obesity      4.213680
alcohol     24.481059
age         14.608956
dtype: float64
```

sbp	20.496317
tobacco	4.593024
ldl	2.070909
adiposity	7.780699
typea	9.817534
obesity	4.21368
alcohol	24.481059
age	14.608956

```
[26]: #calculating range and interquartile range
print(''.ljust(10), 'range'.ljust(10), 'IQR')
for i,col in enumerate(numeric_columns):
    Range = mydata[col].max() - mydata[col].min()
    IQR = mydata[col].quantile(q=0.75) - mydata[col].quantile(q=0.25)
    print(col.ljust(10), str(round(Range,6)).ljust(10), round(IQR,6))
```

	range	IQR
sbp	117	24.0
tobacco	31.2	5.4475
ldl	14.35	2.5075
adiposity	35.75	11.4525
typea	65	13.0
obesity	31.88	5.5125
alcohol	147.19	23.3825
age	49	24.0

### 1.3 Outliers

**Outliers** are datapoint which differ significantly from other observations. They are sometimes excluded from data analysis. There are various ways to define outliers, but commonly, we have that outliers are values displaced from the outliers quartiles from 1.5 times the interquartile range, that is

$$x \leq Q_1 - 1.5 \times IQR \vee x \geq Q_3 + 1.5 \times IQR$$

One of the simplest ways to visualise outliers is with the box plot.

### 1.4 Multivariate Statistics

As the name indicates, multivariate statistics is when we work with more than one variable at a time. Some of the most important measurements of multivariate statistics are the **covariance** which is how much two variables jointly change

$$\text{cov}(X, Y) = \langle (X - \langle X \rangle) (Y - \langle Y \rangle) \rangle$$

and the **correlation** is a measure of how much two variable agree with each other

$$\text{corr}(X, Y) = \frac{\text{cov}(X, Y)}{\sigma_X \sigma_Y}$$

where  $\sigma_X$  and  $\sigma_Y$  are the standard deviations of the two variables  $X$  and  $Y$  (Wikipedia). The correlation matrix is symmetric and its diagonal values are all 1, that is, all variables have maximum correlation with themselves.

```
[28]: #we can check the properties above by getting the correlation matrix of the
      ↪variables in this dataset
mydata.corr()
```

```
[28]:
```

	sbp	tobacco	ldl	adiposity	typea	obesity	\
sbp	1.000000	0.212247	0.158296	0.356500	-0.057454	0.238067	
tobacco	0.212247	1.000000	0.158905	0.286640	-0.014608	0.124529	
ldl	0.158296	0.158905	1.000000	0.440432	0.044048	0.330506	
adiposity	0.356500	0.286640	0.440432	1.000000	-0.043144	0.716556	
typea	-0.057454	-0.014608	0.044048	-0.043144	1.000000	0.074006	
obesity	0.238067	0.124529	0.330506	0.716556	0.074006	1.000000	
alcohol	0.140096	0.200813	-0.033403	0.100330	0.039498	0.051620	
age	0.388771	0.450330	0.311799	0.625954	-0.102606	0.291777	

	alcohol	age
sbp	0.140096	0.388771
tobacco	0.200813	0.450330
ldl	-0.033403	0.311799
adiposity	0.100330	0.625954
typea	0.039498	-0.102606
obesity	0.051620	0.291777
alcohol	1.000000	0.101125
age	0.101125	1.000000

## 1.5 Graphical Displays

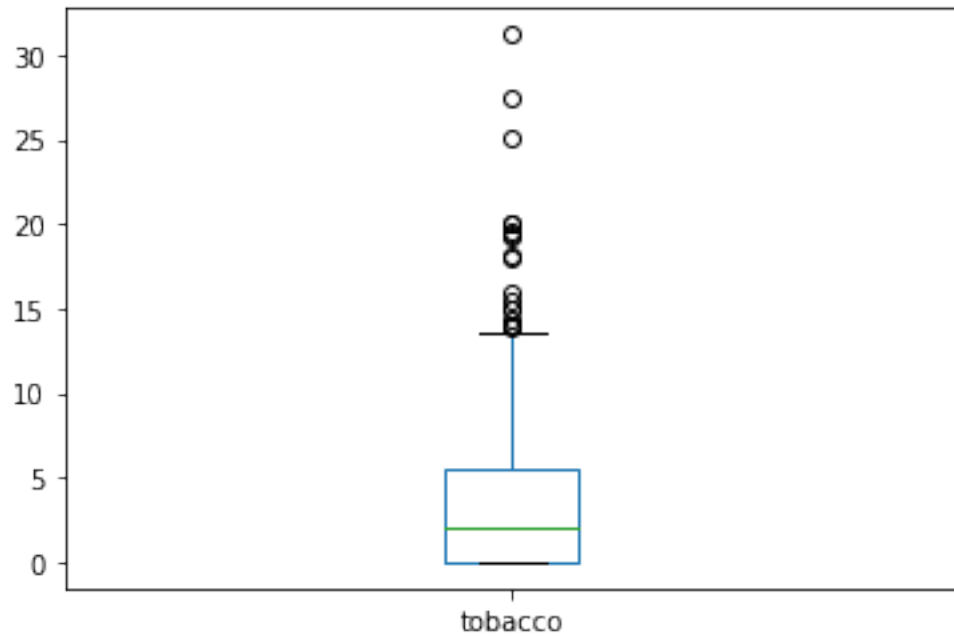
Pandas has several ways to display graphics of our data that are useful in statistical analysis. Here we explore the box plot, the bar plot, the pie plot, the histogram, the density plot, the quantile plot, and for multivariate statistics, the scatter plot.

### 1.5.1 Box plot

Displays the dataset based on the five-number summary described above, that is, the minimum, maximum, and the 3 quartiles. The minimum and maximum displayed do not include outliers, so it's a clear way to see them.

```
[32]: #lets check for our data, say for the tobacco column
mydata['tobacco'].plot.box()
#we can see several outliers above the maximum value
```

```
[32]: <AxesSubplot:>
```



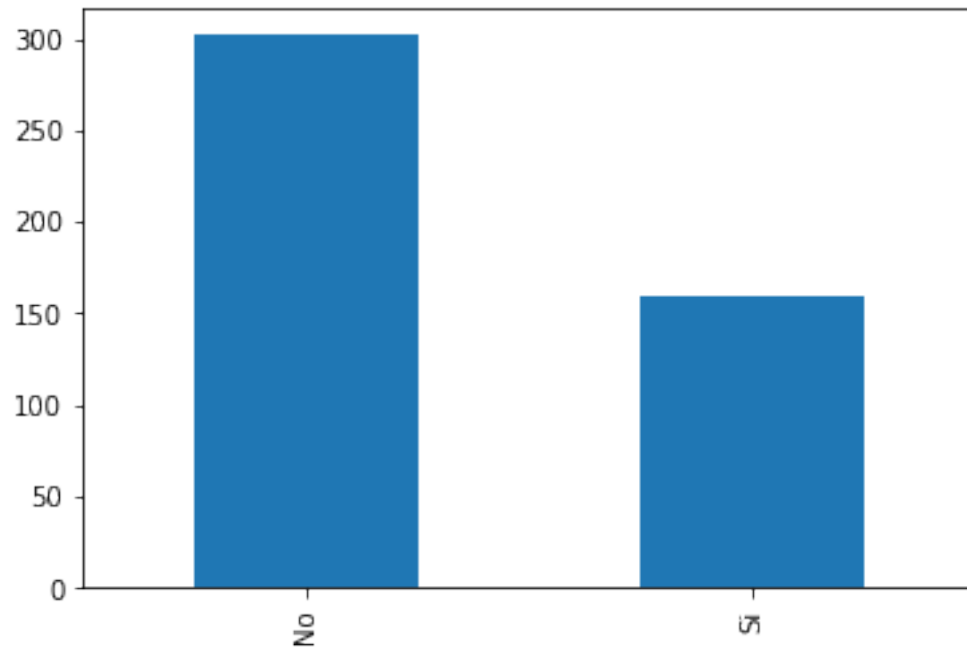
### 1.5.2 Bar plot

The bar plot presents categorical data with rectangular bars with heights proportional to the values they represent.

```
[34]: #example for 'chd'  
mydata['chd'].value_counts().plot.bar()
```

```
[34]: <AxesSubplot:>
```



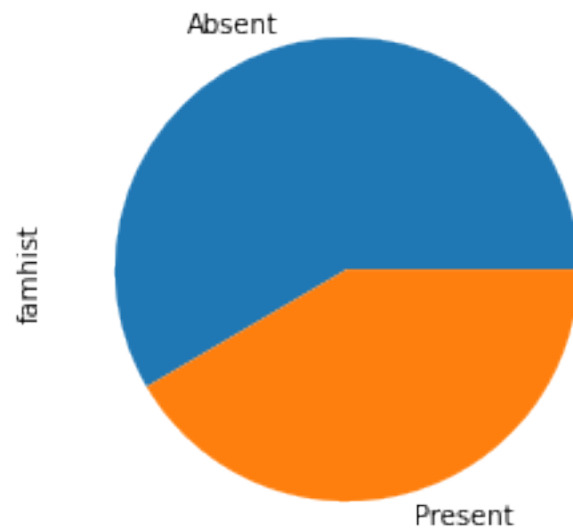


### 1.5.3 Pie plot

A pie plot is a circular display of data to illustrate numerical proportions. The arc length of each slice is proportional to the quantity it represents.

```
[36]: #lets check for 'famhist' this time  
mydata['famhist'].value_counts().plot.pie()
```

```
[36]: <AxesSubplot:ylabel='famhist'>
```

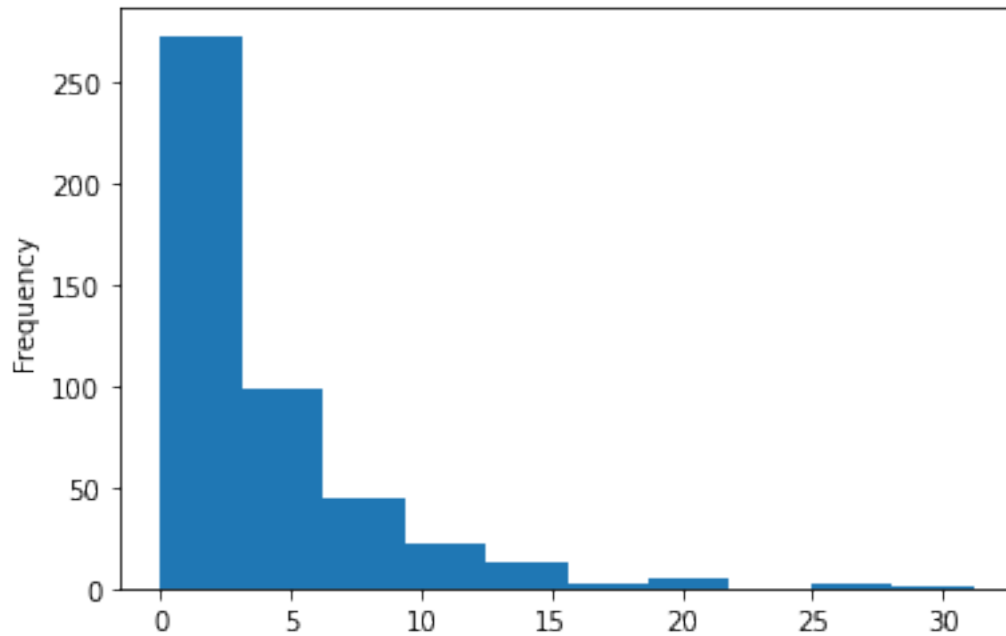


#### 1.5.4 Histogram

A histogram is an approximate representation of the distribution of numerical data, where we divide the range of values into a series of intervals - bins - and count how many values fall into each interval.

```
[37]: #lets see an histogram for the 'tobacco' variable  
mydata['tobacco'].plot.hist()
```

```
[37]: <AxesSubplot:ylabel='Frequency'>
```

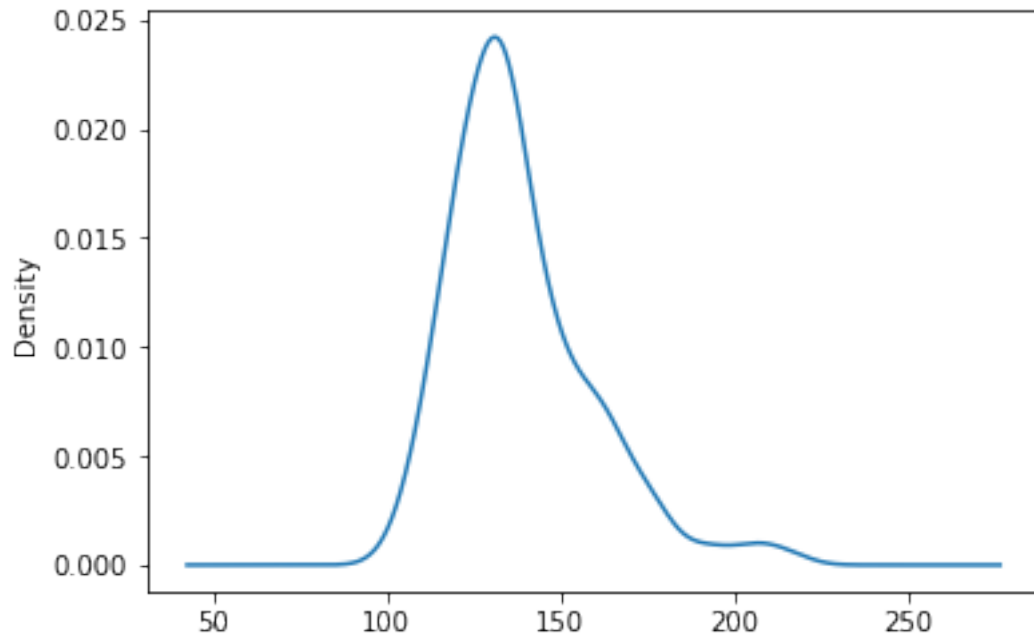


### 1.5.5 Density plot

A density plot is a plot used to observe the distribution of a variable in a dataset. It tries to estimate the probability density function of the variable, using kernel density estimates.

```
[39]: #example for the 'sbp' variable  
mydata['sbp'].plot.density()
```

```
[39]: <AxesSubplot:ylabel='Density'>
```

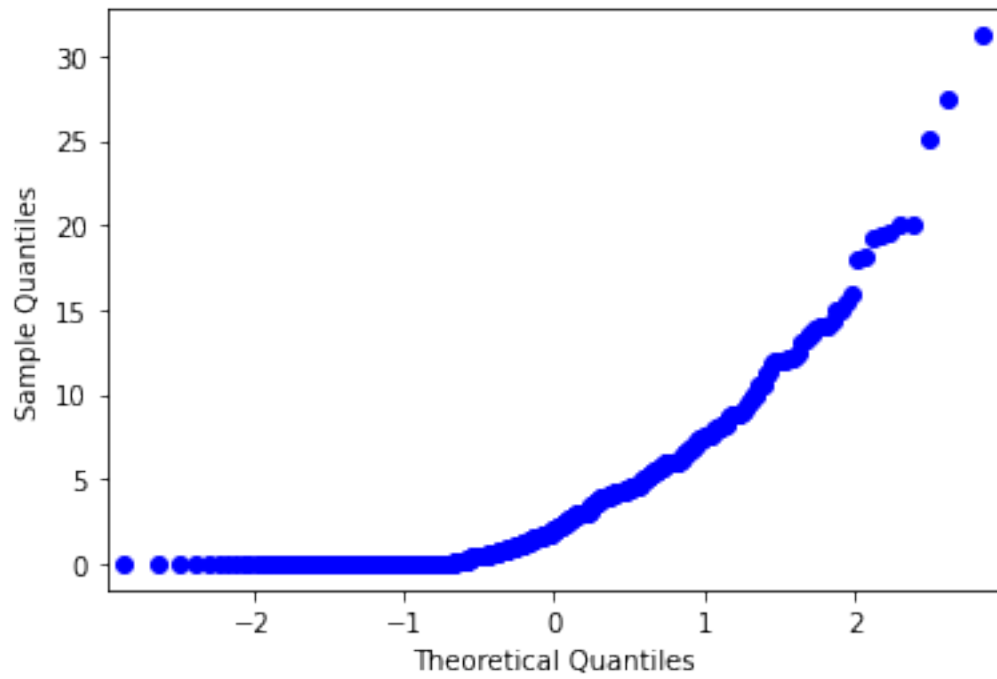
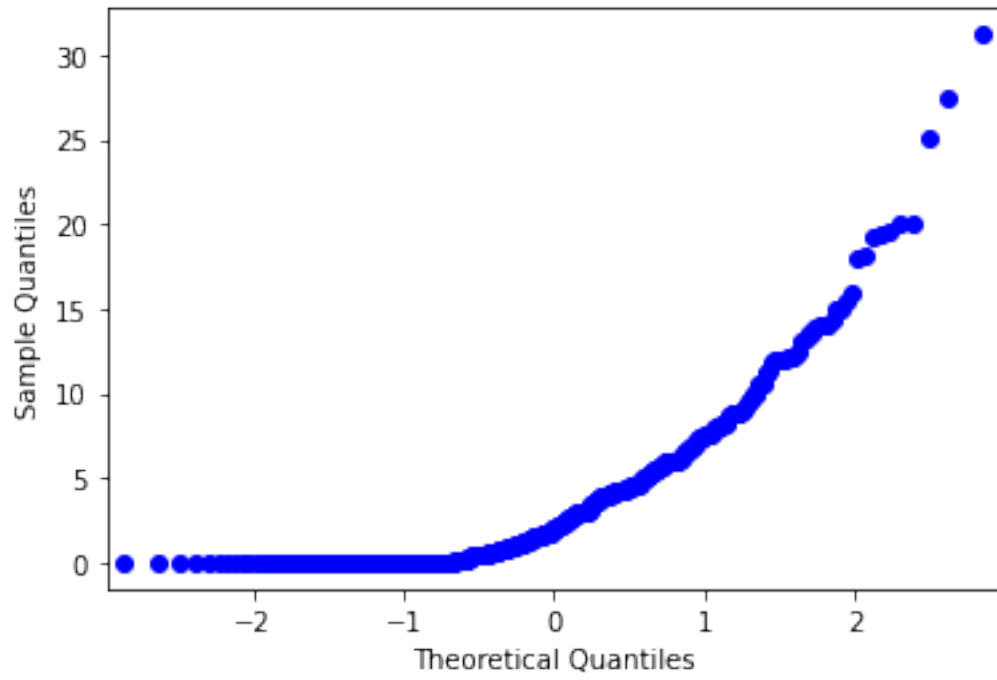


### 1.5.6 Quantile plot

The quantile plot is a graphical method of comparing two probability distributions, by plotting their quantiles against each other.

```
[45]: #example with the 'tobacco' variable  
sm.qqplot(mydata['tobacco'])
```

[45]:

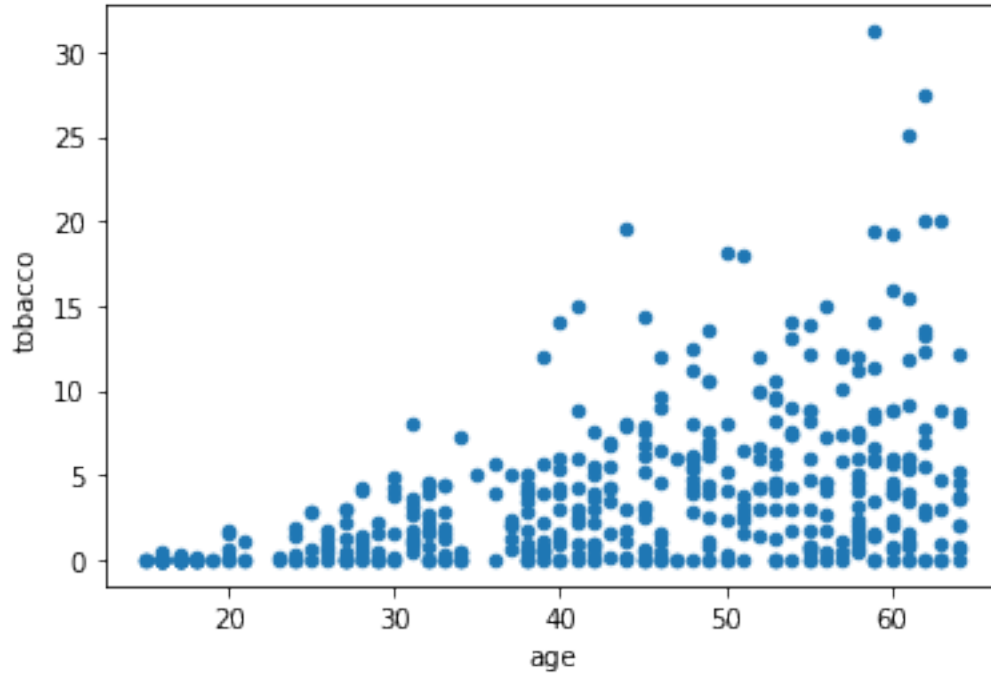


### 1.5.7 Scatter plots

Scatter plots use Cartesian coordinates to display values for typically two variables for a set of data. Particularly useful for multivariate statistics.

```
[46]: #example for 'age' and 'tobacco'  
mydata.plot.scatter('age', 'tobacco')
```

```
[46]: <AxesSubplot:xlabel='age', ylabel='tobacco'>
```



## 1.6 References

As references in this work, I used Wikipedia and material from the class lectures.