```python
from scipy import stats
import pandas as pd
import matplotlib.pyplot as plt
import seaborn as sns

# customise sns
sns.set_style("whitegrid")
```

About

In a previous notebook, we used `scipy.stats.probplot` to produce a normal probability plot. We expand on this further in this notebook by producing two further plots using the `tuple` of `arrays` returned by the function.

1. A "mirrored" plot that swaps the dependent and indendent variables.
2. A residual plot.

Let us first repeat the activity, as a reminder of what we did previously.

Computer activity B9

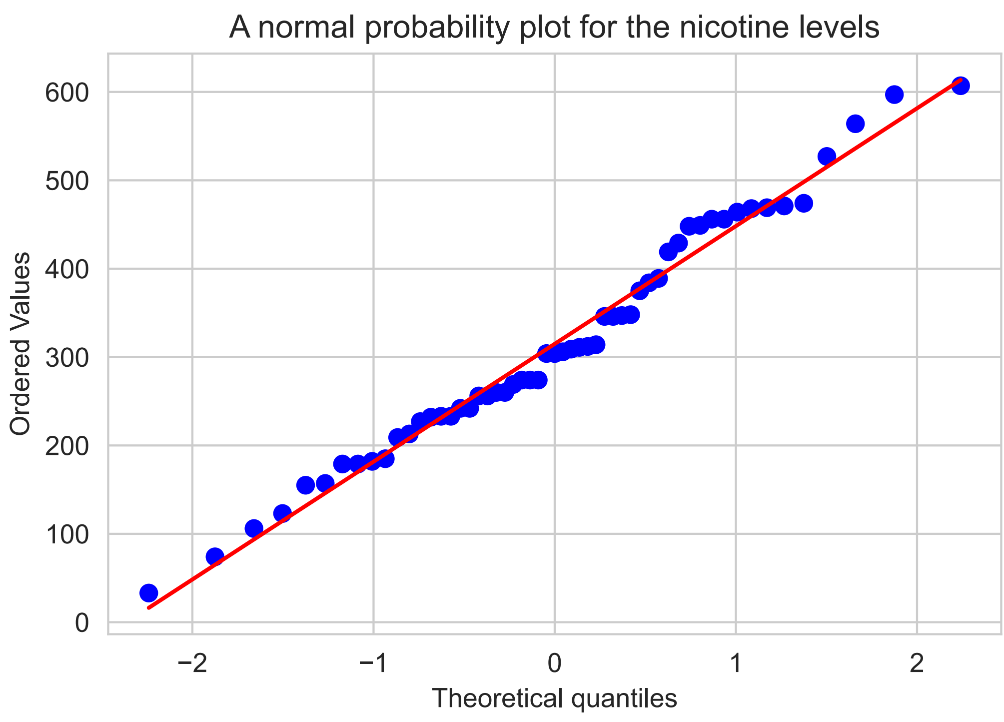
> Data on the blood plasma nicotine levels of 55 smokers are contained in the worksheet plasma.mwx. Obtain a normal probability plot for these data. Is a normal distribution a plausible model for the variation in blood plasma nicotine levels?

```python
# import the dataset
data = pd.read_csv("plasma.csv")
```

We will use `scipy.stats.probplot` to produce the Normal probability plot. (See documentation).

The method returns a tuple of arrays. The data used to produce the plot is the 0th element of the tuple. For example, using `res`, the data is stored in `res[0]`.

```python
fig = plt.figure()
ax = fig.add_subplot()
res = stats.probplot(data["Level"], plot=ax)
ax.set_title("A normal probability plot for the nicotine levels")
plt.show()
```



Plot 1: Draw a plot reflected in $y = x$

The variable `res` holds a reference to a tuple of tuples. From the documentation, this tuple contains:

> (`osm`, `osr`) : tuple of ndarrays
>
> Tuple of theoretical quantiles (`osm`, or order statistic medians) and ordered responses (`osr`). osr is simply sorted input x.
>
> (`slope`, `intercept`, `r`) : tuple of floats, optional
>
> Tuple containing the result of the least-squares fit, if that is performed by `probplot`. `r` is the square root of the coefficient of determination. If `fit=False` and `plot=None`, this tuple is not returned.

For this activity, we are interested in the first tuple. Let us append `res[0]` to two columns in a DataFrame.

```
df = pd.DataFrame()

df["X"] = res[0][1]  # Append x (osr)
df["Quantiles"] = res[0][0]  # Append quantiles (osm)
```

```
df.head()
```

	X	Quantiles
0	33	-2.240674
1	74	-1.875104
2	106	-1.660060
3	123	-1.502274

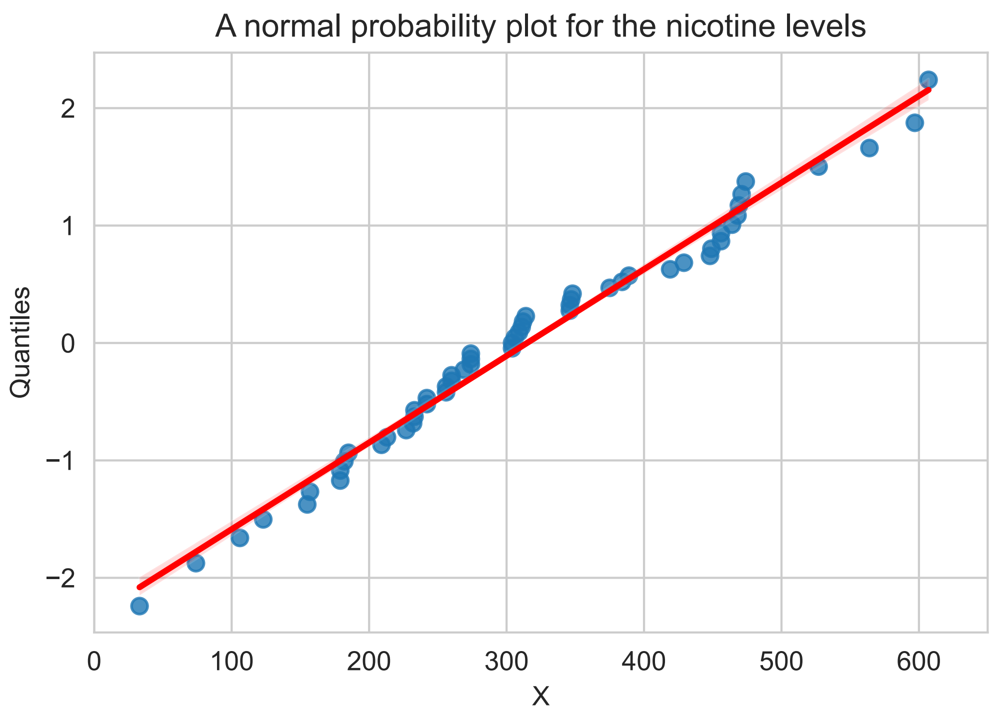
	X	Quantiles
4	155	-1.374940

The default `probplot()` output maps `Quantiles` to the $x-$axis, and `X` to the $y-$axis. However, we can draw a plot with a line of best fit for this data that matches the output of **M248** by changing the column that is mapped to each axis. We will use `seaborn.regplot()` for this activity. (See documentation).

```
# declare the plot
ax = sns.regplot(data=df,
                 x="X",
                 y="Quantiles",
                 line_kws={"color": "r"})

# adjust x-axis, set the title
ax.set(xlim=(0, 650),
       title="A normal probability plot for the nicotine levels")

plt.show()
```



The plot now better fits that drawn by Minitab in **M248**. It is not a *perfect* match because the theoretical quantiles are different: Rather than using $(1/n+1)$ quantiles, `probplot()` uses **Filliben's estimate**, which outputs a different set of quantiles. (See *Notes* in the `sciply.stats.probplot()` documentation for further information).

Plot 2: Draw a residual plot

The returned tupled referenced by the variable `res` holds the parameters of the equation of the original best-fit line in `res[1]`. Its slope is held in `res[1][0]`, and intercept in `res[1][1]`. We can use this information to draw a residual plot of the original normal probability plot.

Recall that `residual = data - fit = y - (a + bx)`, where

- x refers to the column `Quantiles`

- y to column X
- `fit = a + bx`

Let us add a third column to our `DataFrame` that will hold the residual value.

```
df["Residual"] = df["X"] - (res[1][1] + res[1][0]*df["Quantiles"])
```

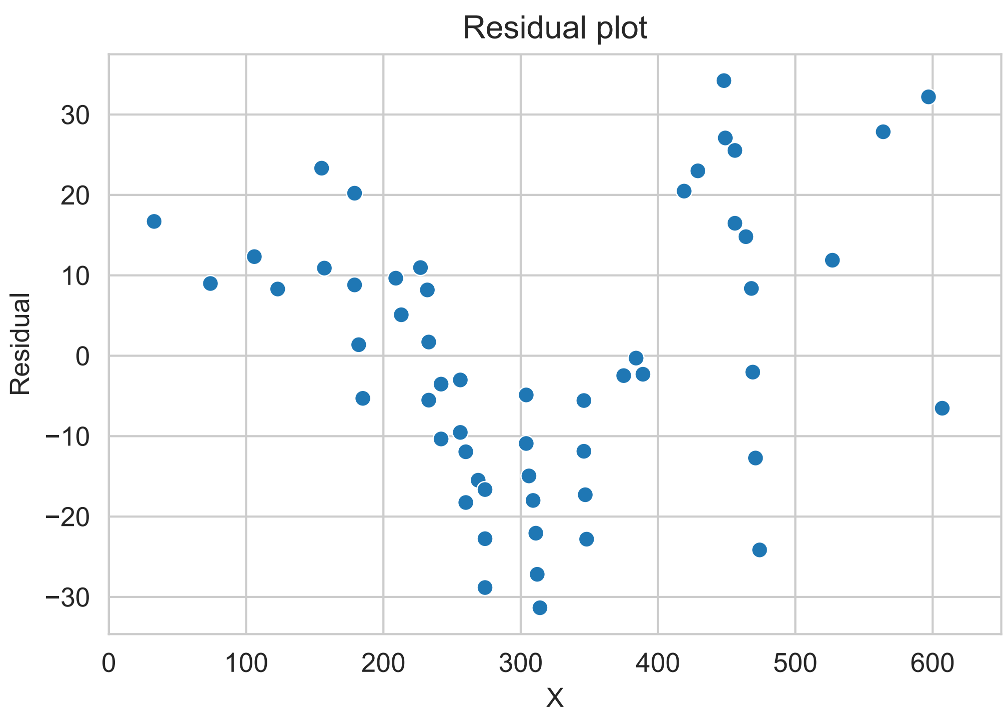
```
df.head()
```

	X	Quantiles	Residual
0	33	-2.240674	16.706013
1	74	-1.875104	8.986353
2	106	-1.660060	12.327451
3	123	-1.502274	8.299315
4	155	-1.374940	23.329385

Let us draw the residual plot.

```
ax1= sns.scatterplot(data=df,
                     x="X",
                     y="Residual")

# adjust the axes, set the title
ax1.set(xlim=(0, 650),
        title="Residual plot")
plt.show()
```



The activity concludes that the points lie roughly on a straight line, so a normal distribution is plausible. However there does seem to a pattern in the distribution of the residuals, with a possible turning point at approximately $x = 300$, indicating the relationship may not be strictly linear.