EXERCISE CLASS 3 (Part 2/3)

EXERCISE 2

A study was performed by ComputerTek Co to determine the time series of order processing durations. Data in the file "dataset_ese3_es2.csv" refer to the period 1995, July – 1997, October. Each datum represents the time (in days) to ship the order.

Design a 95% **prediction interval** for future observations.

Suggestion

Remind that if:

$$X \sim N(\mu, \sigma^2)$$

then:

$$rac{X-\mu}{s} \sim t_{n-1}$$

Confidence intervals

 $L \le \theta \le U$ such that $P(L \le \theta \le U) = 1 - \alpha$ is called $100(1 - \alpha)\%$ confidence interval for the (unknown) parameter θ

Interpretation: if, in repeated random samplings, a large number of such intervals is constructed, $100(1 - \alpha)\%$ of them will contain the true value of θ .

Prediction intervals

 $L \le Y \le U$ such that $P(L \le Y \le U) = 1 - \alpha$ is called $100(1 - \alpha)\%$ prediction interval for the **future process outcome** Y

Interpretation: if, in repeated random samplings, a large number of such intervals is constructed, $100(1 - \alpha)\%$ of them will contain the future outcome Y

```
In []: # Import the necessary libraries
import numpy as np
import matplotlib.pyplot as plt
import pandas as pd
from scipy import stats

# Import the dataset
data = pd.read_csv('dataset_ese3_es2.csv')
```

```
data.head()
```

```
Out[]: Ex2

0 29

1 21

2 17

3 9

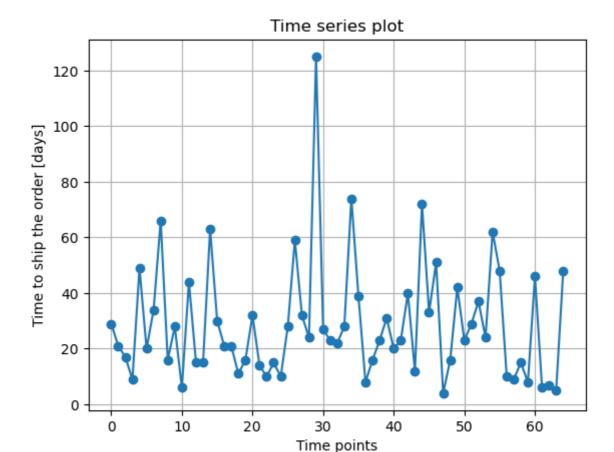
4 49
```

We need a model of process output to make predictions. Which kind of model? **Time series** model or **distributional** model.

We can verify if the process is random by using:

- 1. time series plot (qualitative)
- 2. ACF/PCAF (qualitative)
- 3. runs test (quantitative)
- 4. Bartlett's test (quantitative)
- 5. LBQ test (quantitative)
- 1. Time series plot

```
In [ ]: # Time series plot
  plt.plot(data, 'o-')
    plt.xlabel('Time points')
    plt.ylabel('Time to ship the order [days]')
    plt.title('Time series plot')
    plt.grid()
    plt.show()
```



1. Runs test

```
In []: # Import the necessary libraries for the runs test
    from statsmodels.sandbox.stats.runs import runstest_1samp

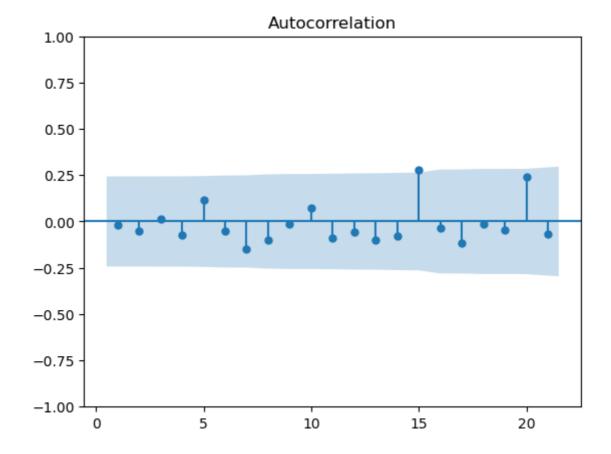
    stat_runs, pval_runs = runstest_1samp(data['Ex2'], correction=False)
    print('Runs test statistic = {:.3f}'.format(stat_runs))
    print('Runs test p-value = {:.3f}'.format(pval_runs))

Runs test statistic = 0.325
Runs test p-value = 0.745
```

1. ACF/PACF

```
In [ ]: # Plot the acf using the statsmodels library
import statsmodels.graphics.tsaplots as sgt

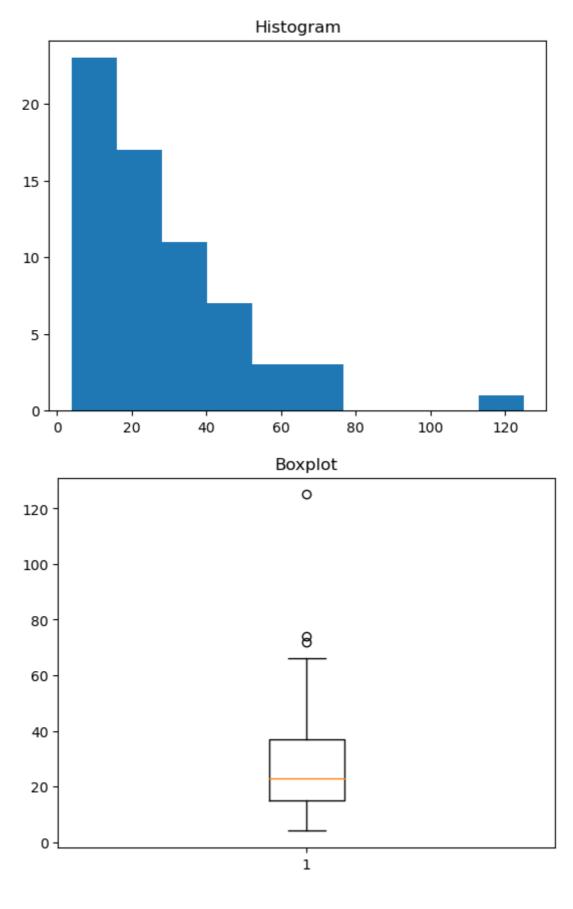
sgt.plot_acf(data['Ex2'], lags = int(len(data)/3), zero=False)
plt.show()
```



1. Histogram and Boxplot

```
In []: plt.hist(data)
    plt.title('Histogram')
    plt.show()

    plt.boxplot(data)
    plt.title('Boxplot')
    plt.show()
```



Let's check normality

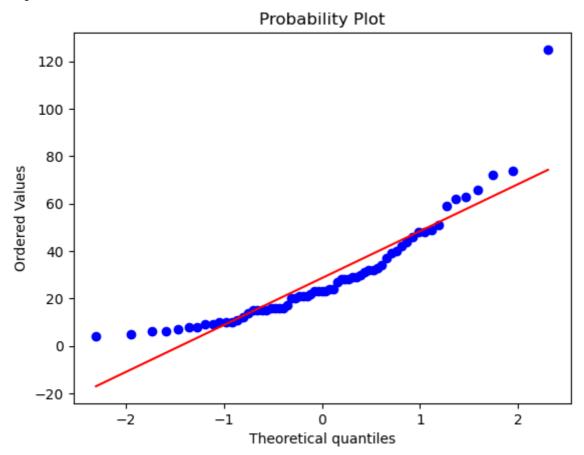
```
In []: #Normality test
    #Shapiro-Wilk test
    import matplotlib.pyplot as plt

stat_shapiro, p_shapiro = stats.shapiro(data)
```

```
print('Statistic = %.3f, p-val = %.3f' % (stat_shapiro, p_shapiro))
# interpret
alpha = 0.05
if p_shapiro > alpha:
    print('Fail to reject H0')
else:
    print('Reject H0')

# Plot the qqplot
stats.probplot(data['Ex2'], dist="norm", plot=plt)
plt.show()
```

Statistic = 0.844, p-val = 0.000 Reject H0



How much is this result influenced by the outlier? We can try to remove the outlier and check for normality again.

```
In []: # Remove outlier (point 30) and check normality
    data_out = data.drop(index=29)

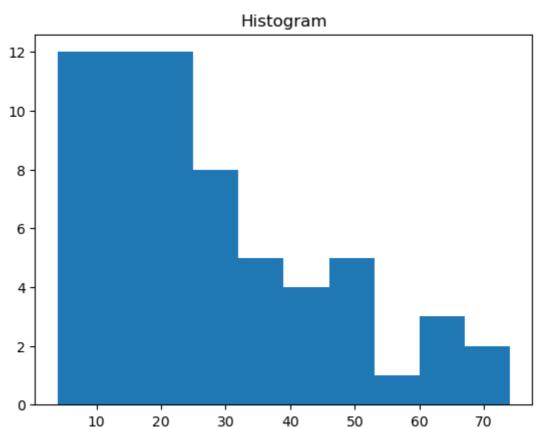
plt.hist(data_out)
plt.title('Histogram')
plt.show()

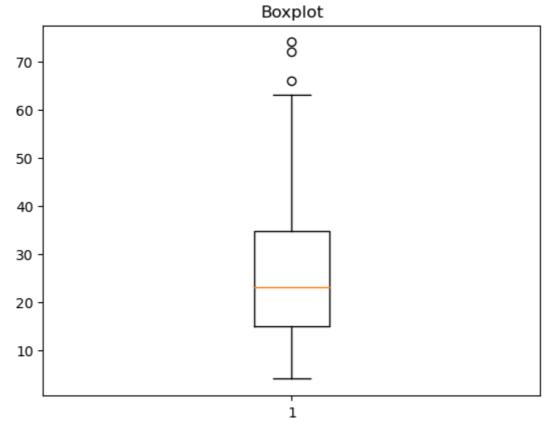
plt.boxplot(data_out)
plt.title('Boxplot')
plt.show()

#Normality test
#Shapiro-Wilk test
from scipy.stats import shapiro
stat_shapiro_out, p_shapiro_out = shapiro(data_out)
```

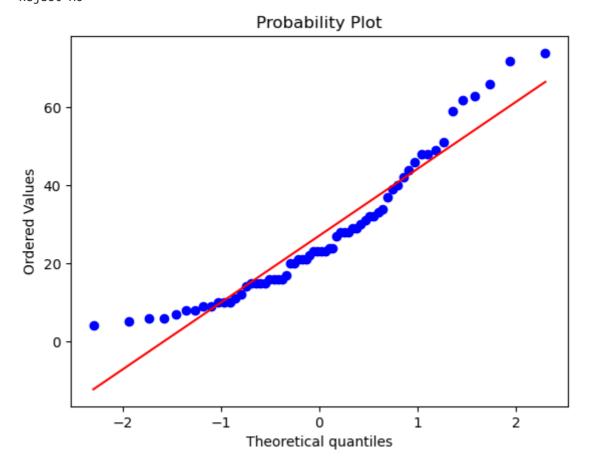
```
print('Statistic = %.3f, p-val = %.3f' % (stat_shapiro_out, p_shapiro_out))
# interpret
alpha = 0.05
if p_shapiro > alpha:
    print('Fail to reject H0')
else:
    print('Reject H0')

# Plot the qqplot
stats.probplot(data_out['Ex2'], dist="norm", plot=plt)
plt.show()
```





Statistic = 0.914, p-val = 0.000 Reject H0



Even after removing the outlier, normality is still violated.

Try with the Box-Cox transformation.

Remind:

```
y=(x^{\lambda}-1)/\lambda, for \lambda 
eq 0 y=ln(x), for \lambda=0
```

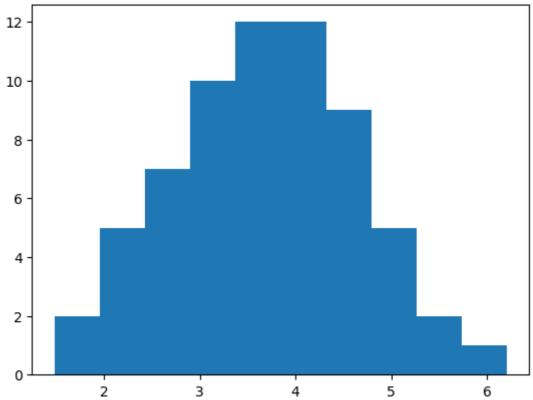
```
In [ ]: #Box-Cox transformation
    [data_norm, lmbda]=stats.boxcox(data['Ex2'])

print('Lambda = %.3f' % lmbda)

plt.hist(data_norm)
plt.title('Histogram of Box-Cox transformed data')
plt.show()
```

Lambda = 0.100

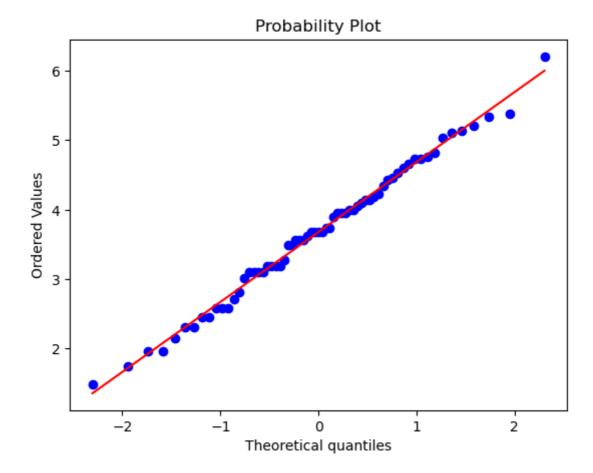
Histogram of Box-Cox transformed data

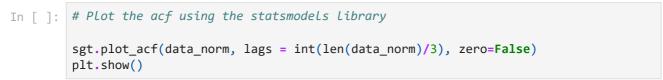


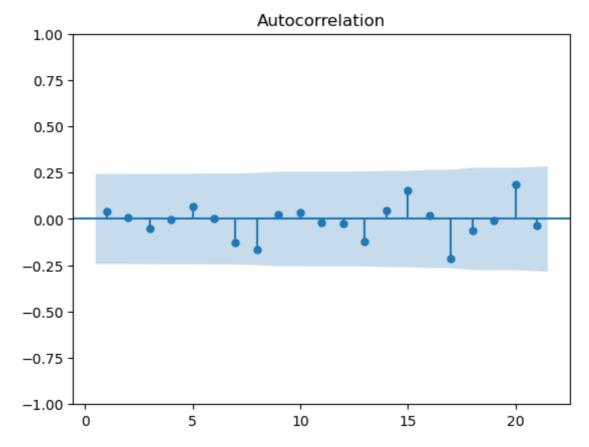
```
In [ ]: stat, p_shapiro = stats.shapiro(data_norm)
    print('Statistics=%.3f, p=%.3f' % (stat, p_shapiro))
    # interpret
    alpha = 0.05
    if p_shapiro > alpha:
        print('Fail to reject H0')
    else:
        print('Reject H0')

# Plot the qqplot
    stats.probplot(data_norm, dist="norm", plot=plt)
    plt.show()
```

Statistics=0.992, p=0.959 Fail to reject H0







No graphical evidence of auto-correlation from the sample acf plot. We can verify it with quantitative tests, e.g.:

- Bartlett's test
- LBQ test

On transformed data

Bartlett's test for a specific lag k

 $H_0: \rho_k = 0$

 $H_1:
ho_k
eq 0$

 ρ_k : true autocorr at lag k

 r_k : sample autocorr at lag k

Rejection region $|r_k|>rac{z_{lpha/2}}{\sqrt{n}}$

Rejection region starts at 0.243108 The null hypothesis is accepted

LBQ test

$$H_0:
ho_k=0, k=1,\ldots,L$$

 $H_1:\exists k\in[1,L]$ such that $ho_k
eq 0$

LBQ test statistic:

$$LBQ = n(n+2)\sum_{k=1}^L rac{r_k^2}{n-k}$$

Under H_0 ($ho_k=0, k=1, \ldots L$), $LBQ\sim \chi_L^2$, and its rejection region is:

$$LBQ > \chi^2_{\alpha,L}$$

```
# Generally speaking: how many lags?
# Rule of thumb: L<sqrt(n)
Q0_LBQ = lbq[lag_test-1]
print('Q0 LBQ = %f' % Q0 LBQ)
#Rejection region for chi square distribution
dof = lag test
chi2_alfa= stats.chi2.ppf(1-alpha,dof)
print('Rejection region starts at %f' % chi2_alfa)
if Q0_LBQ>chi2_alfa:
  print('The null hypothesis is rejected')
  print('The null hypothesis is accepted')
# Compute the p-value for the LBQ test
pval = 1 - stats.chi2.cdf(Q0_LBQ, lag_test)
print('p-value = %f' % pval)
Q0 LBQ = 0.621926
Rejection region starts at 12.591587
The null hypothesis is accepted
p-value = 0.996024
```

Alternatively, you can use the acorr_ljungbox function.

```
In [ ]: #LBQ test for autocorrelation
        from statsmodels.stats.diagnostic import acorr_ljungbox
        lbq_test = acorr_ljungbox(data_norm, lags=[lag_test], return_df=True)
        print('LBQ test statistic at lag %d = %f' % (lag_test, lbq_test.loc[lag_test,'lb_s'
        print('LBQ test p-value at lag %d = %f' % (lag_test, lbq_test.loc[lag_test,'lb_pvalue)
        LBQ test statistic at lag 6 = 0.621926
        LBQ test p-value at lag 6 = 0.996024
```

...to finally answer the question (Design a 95% prediction interval for future observations):

Process data are **normal** and **independent** (NID)

$$X \sim N(\mu, \sigma^2) \rightarrow \frac{X - \mu}{s} \sim t_{n-1}$$
 Attention: this is not $T = \frac{\bar{X} - \mu}{S/\sqrt{n}}$

Prediction interval:

$$\Pr\biggl(-t_{\alpha/2,n-1} \leq \frac{X-\mu}{s} \leq t_{\alpha/2,n-1}\biggr) = 1-\alpha \quad \Longrightarrow \quad \mu - t_{\alpha/2,n-1} s \leq X \leq \mu + t_{\alpha/2,n-1} s$$

Approximated prediction interval (95%): Approximated because we use the sample mean in place of the true mean

$$\overline{X} \pm t_{0.025,64} \cdot s$$

```
In [ ]: alpha = 0.05
        df = len(data norm) - 1
        Xbar = data_norm.mean()
        s = data norm.std()
```

```
t_alpha = stats.t.ppf(1 - alpha/2, df)

[pred_lo, pred_up] = [Xbar-t_alpha*s,Xbar+t_alpha*s]
print('Two-sided confidence interval for transformed data: [%.3f %.3f]' % (pred_lo
```

Two-sided confidence interval for transformed data: [1.719 5.640]

Attention: this is the prediction interval on the transformed data. To estimate the prediction interval on the **original data** we need to back transform.

```
Remind: y=(x^{\lambda}-1)/\lambda , for \lambda \neq 0
```

Thus:
$$x=(y\lambda+1)^{(1/\lambda)}$$

```
In [ ]: [pred_lo_ORIG, pred_up_ORIG] = [(pred_lo*lmbda+1)**(1/lmbda),(pred_up*lmbda+1)**(1/lmbda),(pred_up*lmbda+1)**(1/lmbda),(pred_up*lmbda+1)**(1/lmbda),(pred_up*lmbda+1)**(1/lmbda),(pred_up*lmbda+1)**(1/lmbda),(pred_up*lmbda+1)**(1/lmbda),(pred_up*lmbda+1)**(1/lmbda),(pred_up*lmbda+1)**(1/lmbda),(pred_up*lmbda+1)**(1/lmbda),(pred_up*lmbda+1)**(1/lmbda),(pred_up*lmbda+1)**(1/lmbda),(pred_up*lmbda+1)**(1/lmbda),(pred_up*lmbda+1)**(1/lmbda),(pred_up*lmbda+1)**(1/lmbda),(pred_up*lmbda+1)**(1/lmbda),(pred_up*lmbda+1)**(1/lmbda),(pred_up*lmbda+1)**(1/lmbda),(pred_up*lmbda+1)**(1/lmbda),(pred_up*lmbda+1)**(1/lmbda),(pred_up*lmbda+1)**(1/lmbda),(pred_up*lmbda+1)**(1/lmbda),(pred_up*lmbda+1)**(1/lmbda),(pred_up*lmbda+1)**(1/lmbda),(pred_up*lmbda+1)**(1/lmbda),(pred_up*lmbda+1)**(1/lmbda),(pred_up*lmbda+1)**(1/lmbda),(pred_up*lmbda+1)**(1/lmbda),(pred_up*lmbda+1)**(1/lmbda),(pred_up*lmbda+1)**(1/lmbda),(pred_up*lmbda+1)**(1/lmbda),(pred_up*lmbda+1)**(1/lmbda),(pred_up*lmbda+1)**(1/lmbda),(pred_up*lmbda+1)**(1/lmbda),(pred_up*lmbda+1)**(1/lmbda),(pred_up*lmbda+1)**(1/lmbda),(pred_up*lmbda+1)**(1/lmbda),(pred_up*lmbda+1)**(1/lmbda),(pred_up*lmbda+1)**(1/lmbda),(pred_up*lmbda+1)**(1/lmbda),(pred_up*lmbda+1)**(1/lmbda),(pred_up*lmbda+1)**(1/lmbda),(pred_up*lmbda+1)**(1/lmbda),(pred_up*lmbda+1)**(1/lmbda),(pred_up*lmbda+1)**(1/lmbda),(pred_up*lmbda+1)**(1/lmbda),(pred_up*lmbda+1)**(1/lmbda),(pred_up*lmbda+1)**(1/lmbda),(pred_up*lmbda+1)**(1/lmbda),(pred_up*lmbda+1)**(1/lmbda),(pred_up*lmbda+1)**(1/lmbda),(pred_up*lmbda+1)**(1/lmbda),(pred_up*lmbda+1)**(1/lmbda),(pred_up*lmbda+1)**(1/lmbda),(pred_up*lmbda+1)**(1/lmbda),(pred_up*lmbda+1)**(1/lmbda),(pred_up*lmbda+1)**(1/lmbda),(pred_up*lmbda+1)**(1/lmbda),(pred_up*lmbda+1)**(1/lmbda),(pred_up*lmbda+1)**(1/lmbda),(pred_up*lmbda+1)**(1/lmbda),(pred_up*lmbda+1)**(1/lmbda),(pred_up*lmbda+1)**(1/lmbda),(pred_up*lmbda+1)**(1/lmbda),(pred_up*lmbda+1)**(1/lmbda),(pred_up*lmbda+1)**(1/lmbda),(pred_up*lmbda+1)**(1/lmbda),(pred_up*lmbda+1)**(1/lmbda),(pred_up*lmbda+1)**(1/lmbda),
```

Two-sided confidence interval for original data: [4.887 87.689]